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155454

From: Chernyshev, Olga
Sent: Saturday, June 04, 2005 12:48 PM
To: STIC-Biotech/ChemLib
Subject: 09/869,486; sequence search request

US case 09/869,486

Please search SEQ ID NO: 25, SEQ ID NO: 29 (full length and fragment 73-3714) and SEQ ID NO: 30 in regular and pending databases.

Thank you very much!

Olga N. Chernyshev, Ph.D.

AU 1646

REM 3C89

2-0870

mail 4C70

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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

11

BEST AVAILABLE COPY

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[illegible]

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Db 1390 CCGTGAATCCGCGGCGTATTCATCTGAGGCTGAGGCTCCTTGGGGTAAACAGGACA 1449
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RESULT 2
US-09-030-607-109
; Sequence 109, Application us/09030607
; Patent No. 6262245
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; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-109
;
Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1,86-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;
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RESULT 3
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Reiter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-109

Query Match      52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

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Db 250 ATCTTCAGGTCACAAACAGCTGGGCCCCAAGATGTCATGTCAGGCAAGATGAAG 309
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Db 610 CTCGAGGCAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
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Db 670 AAAGTACAGGGCAACAGGCAATCTCTAAGAGGCGACGCTTACCCGCTCATCCGGGAA 729
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RESULT 4
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; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.42708
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-109

Query Match 52.7%; Score 1149.8; DB 3; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1,

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Db 310 GACGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 369
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QY 1633 CTCAGGCAATTGTGAGGCGACCCGSGAGACCCCGAGCCGCTCTCCCGGCTCGAGCAT 1692
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DB 850 TTCGGGGTTTACCTTTCTTAAGGAGCCGAGCGGAAAGCTGTCTAACCTGGGAAATCGGTGCAT 909
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DB 1210 ATTTTGTCTCTAAGTAAGGCTCATCTGGGCTCTGGGCGCCCGCACCTGTGTGCTGTGCTC 1269
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QY 2066 CTGTGATCCGAGCGCTTATTCATCTGGAGGCTGAGGCTCTTGGGGTAAACAGGACCA 2125
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RESULT 6
US-09-159-812-109
; Sequence 109; Application US/09159812A
; Patent No. 6613872
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
; FILE REFERENCE: 210121.428C5
; CURRENT APPLICATION NUMBER: US/09/159, 812A
; NUMBER OF SEQ ID NOS: 306
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-109

Query Match 52.7%; Score 1149.8; DB 4; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

QY 853 CTGGCGCAGGCGCTGAGCGAGAGCGGAGGAGAGCTTCGCAAGCGGAGGCGCCCGGCGCTGGC 912
DB 10 CTGGCGCAGGCGCTGAGCGAGAGCGGAGGAGAGCTTCGCAAGCGGAGGCGCCCGGCGCTGGC 69
QY 913 CATGCTCACTGAGCCAGCGGCTGCGCTTACTCTGCGCAGACTGGAACCAAGTGCAG 972
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QY 1333 GAGCAAGCAACATGCTGTGGAGCCGCGCTTGGGCGACCCCTCGGGGCGCCAGCG 1392
DB 490 GAGCAAGCAACATGCTGTGGAGCCGCGCTTGGGCGACCCCTCGGGGCGCCAGCG 549
QY 1393 GGCACTGCGCTCTCCAGTATGCAATGCTGTGTGTCTCTCTGATCTTCTG 1452
DB 550 GGCACTGCGCTCTCCAGTATGCAATGCTGTGTGTGTCTCTCTGATCTTCTG 609
QY 1453 CTGCTGCAACATCTGCTGTGTCACTTGTCAATGTCATGTTCAATTAACATTCGCG 1512
DB 610 CTGCTGCAACATCTGCTGTGTCACTTGTCAATGTCATGTTCAATTAACATTCGCG 669
QY 1513 AAAGTAAGGCGCAACAGGATCTCACTGAAAGCGGAGGTTACCGCTCATCCGGAA 1572
DB 670 AAAGTAAGGCGCAACAGGATCTCACTGAAAGCGGAGGTTACCGCTCATCCGGAA 729
QY 1573 TTCACTCTGCGCCCGGCTGCGCCCGCTTATGTCATCTCCACTTGGGCTCTG 1632
DB 730 TTCACTCTGCGCCCGGCTGCGCCCGCTTATGTCATCTCCACTTGGGCTCTG 789
QY 1633 CTCAGGCAATTGTGAGGCGACCCGSGAGACCCCGAGCCGCTCTCCGAGCAT 1692
DB 790 CTCAGGCAATTGTGAGGCGACCCGSGAGACCCCGAGCCGCTCTCCGAGCAT 849
QY 1693 TTCGGGGTTTACCTTTCTTAAGGAGCCGAGCGGAAAGCTGTCTAACCTGGGAAATCGGTGCAT 1752
DB 850 TTCGGGGTTTACCTTTCTTAAGGAGCCGAGCGGAAAGCTGTCTAACCTGGGAAATCGGTGCAT 909
QY 1753 AAGGAGAACTTTCTGTGCGACCGGCTAGGAGCAAGCGGAGAGGAGTCTCCGAGMGTCGTG 1812
DB 910 AAGGAGAACTTTCTGTGCGACCGGCTAGGAGCAAGCGGAGAGGAGTCTCCGAGMGTCGTG 969
QY 1813 AAGCGCAGTCCCAAGAGGTGACTTTGGCACTGAAACAGCTGGAGACATCCGCGAGTAC 1872
DB 970 AAGCGCAGTCCCAAGAGGTGACTTTGGCACTGAAACAGCTGGAGACATCCGCGAGTAC 1029
QY 1873 GAACAGCGCTTGAAAGTGTCTGGAGCGGAGGCTCCAGCATGTGA----- 1915
DB 1030 GAACAGCGCTTGAAAGTGTCTGGAGCGGAGGCTCCAGCATGTGAGCCGCTCTGGGGTGTG 1089

QY 1916 ----- 1915
Db 1090 GTGGCCGAGGCCCTGAGCCGCTGTGCTTGTGCTGCCCCAGGTGGGCCGCCACCCCTGAC 1149
QY 1916 ----- 1915
Db 1150 CTGCCTGGTCCAAGACTGAGCCCTGCTGGCGGACTTCAAGAGAAAGCCCCACAGGG 1209
QY 1916 ----- 1915
Db 1210 ATTTGCTCTAGAGTGAAGGCTCATCTGGGCTCTGGCCCCCGACCTGGTGGCTTGTCC 1269
QY 1946 TTGAGGTGAGCCCATGTCCATCTGGGCACTGTACAGAACCACTTTGGAGTGTATCC 2005
Db 1270 TTGAGGTGAGCCCATGTCCATCTGGGCACTGTACAGAACCACTTTGGAGTGTATCC 1329
QY 2006 TTACAAACCAAGCATGCGGCTCTCCAGAACGATCCAGCCTGGAGGATCAAG 2065
Db 1330 TTACAAACCAAGCATGCGGCTCTCCAGAACGATCCAGCCTGGAGGATCAAG 1389
QY 2066 CCGGATCCCGGCGCTTATCCATCTGGAGCTGGAGGCTTGGGGTAAAGGACCA 2125
Db 1390 CCGGATCCCGGCGCTTATCCATCTGGAGCTGGAGGCTTGGGGTAAAGGACCA 1449
QY 2126 CAGACCCCTCAGCACTCAGATTTCTCAGCACTGGGGAATTAAGCATTTCAGA 2180
Db 1450 CAGACCCCTCAGCACTCAGATTTCTCAGCACTGGGGAATTAAGCATTTCAGA 1504

RESULT 7

US-09-636-215-109
Sequence 109, Application US/09636215
Patent No. 6620922

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqun
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 109
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapien
US-09-636-215-109

Query Match 52.7%; Score 1149.8; DB 4; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

QY 853 CTGCGCCAGGCGCTTGAAGCGAGCGGGGCAAGCTCGCCAGCGGGGCCCCCGGCTGGC 912
Db 10 CTGCGCCAGGCGCTTGAAGCGAGCGGGGCAAGCTCGCCAGCGGGGCCCCCGGCTGGC 69
QY 913 CATGCTCACTAGCAAGCGGCTGGCGCTCTACTCGCCGACAGCTGGAACAGTGGAC 972

Db 70 CATGCTCACTAGCAAGCGGCTGGCGCTCTACTCGCCGACAGCTGGAACAGTGGAC 129
QY 973 CTAGTGGCTCTCACTGCTTCTCTGCGGCTGAGGCTGCCGCTGACCCCGGTTGTAC 1032
Db 130 CTAGTGGCTCTCACTGCTTCTCTGCGGCTGAGGCTGCCGCTGACCCCGGTTGTAC 189
QY 1033 CACTGGGCGGCACTGCTCTGTCATGCACTTATGTTTCAAGGCTGGCTGTAC 1092
Db 190 CACTGGGCGGCACTGCTCTGTCATGCACTTATGTTTCAAGGCTGGCTGTAC 249
QY 1093 ATCTTACGCTCAACAAAGCTGGGCGCCAGATGTCATCTGAGCAAGATGATGAG 1152
Db 250 ATCTTACGCTCAACAAAGCTGGGCGCCAGATGTCATCTGAGCAAGATGATGAG 309
QY 1153 GACGTGTTCTTCT 1212
Db 310 GACGTGTTCTTCT 369
QY 1213 GAGGGGCTCTGAGGCGACGAGGACAGTGACTTCCAAATCTCTGGGCGGCTTCTAC 1272
Db 370 GAGGGGCTCTGAGGCGACGAGGACAGTGACTTCCAAATCTCTGGGCGGCTTCTAC 429
QY 1273 CGTCCCTACCTGAGATCTTTCGGGCAAGTTCACAGAGACATGACGTGGCCCTGATG 1332
Db 430 CGTCCCTACCTGAGATCTTTCGGGCAAGTTCACAGAGACATGACGTGGCCCTGATG 489
QY 1333 GAGCAGACGACATGCTGTGTGGAGCCCGCTTCTGGGCAACCTCTCTGGGGCCAGGCG 1392
Db 490 GAGCAGACGACATGCTGTGTGGAGCCCGCTTCTGGGCAACCTCTCTGGGGCCAGGCG 549
QY 1393 GGCACCTGGGCTCCAGATATGCAATGCGCTGGTGTGTGCTCTCCGTCATCTTCCTG 1452
Db 550 GGCACCTGGGCTCCAGATATGCAATGCGCTGGTGTGTGCTCTCCGTCATCTTCCTG 609
QY 1453 CTGTGGCCAACTCTGCTGTCACTTGTCTTCCATGTTCACTTCACTTCCGCTGAGC 1512
Db 610 CTGTGGCCAACTCTGCTGTCACTTGTCTTCCATGTTCACTTCCGCTTCCGCTGAGC 669
QY 1513 AAGTACAGGCGCAACGCGATCTTACTGAGAGCGGCGATTAACGCTCATCCGGAA 1572
Db 670 AAGTACAGGCGCAACGCGATCTTACTGAGAGCGGCGATTAACGCTCATCCGGAA 729
QY 1573 TTCCACTCTGCGCGCGGCTGGCGGCGGCTTATGTATCTCCACTTGGGCTTCCTG 1632
Db 730 TTCCACTCTGCGCGCGGCTGGCGGCGGCTTATGTATCTCCACTTGGGCTTCCTG 789
QY 1633 CTGAGCAATTGTGACAGCGACCCGAGGCGCCCAAGCTCTCCCGGCTCTGAGCAT 1692
Db 790 CTGAGCAATTGTGACAGCGACCCGAGGCGCCCAAGCTCTCCCGGCTCTGAGCAT 849
QY 1693 TTCCGGGTTTACCTTTCTAAGAGGCGGAGGAGCTGTAACTGGGATGCTGAT 1752
Db 850 TTCCGGGTTTACCTTTCTAAGAGGCGGAGGAGGAGCTGTAACTGGGATGCTGAT 909
QY 1753 AAGGAACTTTTGTGCTGAGCGGCTAAGGAAACCGGGAAGGAGGAGCTCCGAGGCTG 1812
Db 910 AAGGAACTTTTGTGCTGAGCGGCTAAGGAAACCGGGAAGGAGGAGCTCCGAGGCTG 969
QY 1813 AAGCGACGTCAGAGAGGAGGAGCTTGGCACTGAAACAGCTGGGAGACATCCGAGTAC 1872
Db 970 AAGCGACGTCAGAGAGGAGGAGCTTGGCACTGAAACAGCTGGGAGACATCCGAGTAC 1029
QY 1873 GAAACAGCGCTGAAAGTGTGAGCGGAGGAGTCCAGAGTGA----- 1915
Db 1030 GAACAGCGCTGAAAGTGTGAGCGGAGGAGTCCAGAGTGAAGCTGCTGGGCTGAG 1089
QY 1916 ----- 1915
Db 1090 GTGGCCGAGGCCCTGAGCCGCTGTGCTTGTGCTGCCCCAGGTGGGCCGCCACCCCTGAC 1149
QY 1916 ----- 1915

1946 TTGAGGTGAGCCCATATGCTCATCTGAGCCACTGTCAAGACCACCTTTGGAGTGTATCC 2005
1270 TTGAGGTGAGCCCATATGCTCATCTGAGCCACTGTCAAGACCACCTTTGGAGTGTATCC 1329
2006 TTACAAACCAAGACATGCCCCGCTCTCCAGAAACAGTCCAGCTGGAGAGATCAAG 2065
1330 TTACAAACCAAGACATGCCCCGCTCTCCAGAAACAGTCCAGCTGGAGAGATCAAG 1389
2066 CCGGATCCCGGCGCTTATCCATCTGAGAGCTGAGAGGCTCTTGGGTTAAAGAGCA 2125
1390 CCGGATCCCGGCGCTTATCCATCTGAGAGCTGAGAGGCTCTTGGGTTAAAGAGCA 1449
2126 CAGACCCCTCACTCAAGATTTCTCACTGAGAGAAATAAGCATTTTCA 2180
1450 CAGACCCCTCACTCAAGATTTCTCACTGAGAGAAATAAGCATTTTCA 1504

RESULT 9
US-09-115-453-109
; Sequence 109, Application US/09115453B
; Patent No. 6657056
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
; FILE REFERENCE: 210121.427C4
; CURRENT APPLICATION NUMBER: US/09/115.453B
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-115-453-109

Query Match 52.7%; Score 1149.8; DB 4; Length 1524;
Best Local Similarity 88.6%; Pred. No. 1.8e-260;
Matches 1325; Conservative 3; Mismatches 0; Indels 167; Gaps 1;

853 CTGCGCAGAGGCGCTGAGCGAGCGAGCGAGCGCTGCGCAGCGAGGCGCGCGGCTGGC 912
10 CTGCGCAGAGGCGCTGAGCGAGCGAGCGAGCGCTGCGCAGCGAGGCGCGCGGCTGGC 69
913 CATGCTCACTGAGCGAGCGAGCGAGCGCTGCGCAGCGAGCGAGCGAGCGAGCGAGCG 972
70 CATGCTCACTGAGCGAGCGAGCGAGCGAGCGCTGCGCAGCGAGCGAGCGAGCGAGCG 129
973 CTGAGGCTCTACCTGCTCTCTCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1032
130 CTGAGGCTCTACCTGCTCTCTCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 189
1033 CACTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1092
190 CACTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 249
1093 ATCTTCAAGGTCAACAAACAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1152
250 ATCTTCAAGGTCAACAAACAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 309
1153 GAGGTGCTTCTTCT 1212
310 GAGGTGCTTCTTCT 369
1213 GAGGTGCTTCTTCT 1272
370 GAGGTGCTTCTTCT 429
1273 GGTCCCTCACTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1332
430 GGTCCCTCACTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 489

1333 GAGCAGCAAGCACTGCTGCTGAGAGCGCGCTTCTGAGCAGACCTCTCTGAGCGCG 1392
490 GAGCAGCAAGCACTGCTGCTGAGAGCGCGCTTCTGAGCAGACCTCTCTGAGCGCG 549
1393 GGCACCTGCTCTCCAGATGCGAACTGAGCTGAGCTGCTCTCTCTCTCTCTCTCTCT 1452
550 GGCACCTGCTCTCCAGATGCGAACTGAGCTGAGCTGAGCTGCTCTCTCTCTCTCTCT 609
1453 CTGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1512
610 CTGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 669
1513 AAGTACAGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1572
670 AAGTACAGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 729
1573 TTCCACTCTGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1632
730 TTCCACTCTGAGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 789
1633 CTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1692
790 CTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 849
1693 TTCCGAGTTTACCTTCTTAAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1752
850 TTCCGAGTTTACCTTCTTAAAGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 909
1753 AAGAGAACTTTCTGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1812
910 AAGAGAACTTTCTGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 969
1813 AAGCGCAGCTTCCAGAGAGCTGAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1872
970 AAGCGCAGCTTCCAGAGAGCTGAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1029
1873 GAACAGCGCTTGAAGAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1915
1030 GAACAGCGCTTGAAGAGCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 1089
1916 ----- 1915
1090 GTGCGCAGGCGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1149
1916 ----- 1915
1150 CTGCTGAGTCCAAAGAGCTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1209
1916 ----- 1915
1210 ATTTGCTCTTAAGAGTAAAGCTATCTGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 1269
1946 TTGAGGTGAGCCCATATGCTCATCTGAGCCACTGTCAAGACCACCTTTGGAGTGTATCC 2005
1270 TTGAGGTGAGCCCATATGCTCATCTGAGCCACTGTCAAGACCACCTTTGGAGTGTATCC 1329
2006 TTACAAACCAAGACATGCCCCGCTCTCCAGAAACAGTCCAGCTGGAGAGATCAAG 2065
1330 TTACAAACCAAGACATGCCCCGCTCTCCAGAAACAGTCCAGCTGGAGAGATCAAG 1389
2066 CCGGATCCCGGCGCTTATCCATCTGAGAGCTGAGAGGCTCTTGGGTTAAAGAGCA 2125
1390 CCGGATCCCGGCGCTTATCCATCTGAGAGCTGAGAGGCTCTTGGGTTAAAGAGCA 1449
2126 CAGACCCCTCACTCAAGATTTCTCACTGAGAGAAATAAGCATTTTCA 2180
1450 CAGACCCCTCACTCAAGATTTCTCACTGAGAGAAATAAGCATTTTCA 1504

RESULT 10
US-09-688-489-109
; Sequence 109, Application US/09688489
; Patent No. 6664377

Query Match 45.9%; Score 1000.4; DB 2; Length 1297;
Best Local Similarity 97.9%; Pred. No. 2.3e-225;
Matches 1051; Conservative 2; Mismatches 16; Indels 4; Gaps 4;

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QY      854  TCCGCGAGGCGCTGAGCCGGA-GGCGGGGAGACCTTCGCGAGGGGGGCGGGGCTTGGC 912
DB      1  TCCGCGAGGCGCTGAGCCGGAAGGTGTGCGACCTTCGCGAGGGGGGCGGGGCTTGGC 60
QY     913  CA-TGCTCACTGAGCCAGCGCCTGAGCTTCACTCGCCGCAAGCTGGAACAGATGGCA 971
DB      61  CATTGCCCTCACTGAGCCAGCGCCTGAG-CTNCTACTCGCCGCAAGCTGGAACAGATGGCA 119
QY     972  CTTAGTGGCTCTCACTGCTTCTCTCTGAGGCGTGGGCTCGCGCTGACCGCGGTTTGT 1031
DB     120  CTTAGTGGCTCTCACTGCTTCTCTCTGAGGCGTGGGCTCGCGCTGACCGCGGTTTGT 179
QY     1032  CCAGCTGGGCGGCACTGTCTCTGTGATGACTTCAATGTTTTCAGGTCGCGCTCTTCA 1091
DB     180  CCAGCTGGGCGGCACTGTCTCTGTGATGACTTCAATGTTTTCAGGTCGCGCTCTTCA 239
QY     1092  CATCTTCACGGTCAACAACAAGCTGGGGCCCAAGATCGCATCGTAGCAAGATGATA 1151
DB     240  CATCTTCACGGTCAACAACAAGCTGGGGCCCAAGATCGCATCGTAGCAAGATGATA 299
QY     1152  GAGCGTGTCTTCTTCTTCTTCTCTGCGGCTGTGCTGTGAGCTTATGGCGTGGCCAC 1211
DB      300  GAGCGTGTCTTCTTCTTCTTCTTCTCTGCGGCTGTGCTGTGAGCTTATGGCGTGGCCAC 359
QY     1212  GGAGGGGCTCTGAGGCGCAAGGAGATGACTTCCCAAGTACTTCCGAGGAGGAGTCTTCT 1271
DB     360  GGAGGGGCTCTGAGGCGCAAGGAGATGACTTCCCAAGTACTTCCGAGGAGGAGTCTTCT 419
QY     1272  CGGTCCCTACCTGAGATCTTCTGAGGAGATTTCCCGAGAGGAGATGAGTGGGCTCTAT 1331
DB     420  CGGTCCCTACCTGAGATCTTCTGAGGAGATTTCCCGAGAGGAGATGAGTGGGCTCTAT 479
QY     1332  GGAGACAGCAACCTGCTGTGAGGCGCGGCTTCTGAGCAACCTCTCTGGGGCCCAAGC 1391
DB     480  GGAGACAGCAACCTGCTGTGAGGCGCGGCTTCTGAGCAACCTCTCTGGGGCCCAAGC 539
QY     1392  GGGGACCTGCGCTCTCCAGTATGCCAATGTGGTGTGCTGCTCTCTGCTATCTTCT 1451
DB     540  GGGGACCTGCGCTCTCCAGTATGCCAATGTGGTGTGCTGCTCTCTGCTATCTTCT 599
QY     1452  GCTCGTGGCCAAACATCTGTGTGCACTTGTCTATGCGATGTTCACTTACATTCG 1511
DB     600  GCTCGTGGCCAAACATCTGTGTGCACTTGTCTATGCGATGTTCACTTACATTCG 659
QY     1512  CAAAGTACAGGGCAACAGCATCTTCTAGTGAAGGCGAGCGTTACCGCTCATCCGGA 1571
DB     660  CAAAGTACAGGGCAACAGCATCTTCTAGTGAAGGCGAG-GTTACCGCTCATCCGGA 718
QY     1572  ATTCCACTCTGGGCGCGGCTGTGGCCCGCTTTATGTCTATCTCCACTTGGCGCTCT 1631
DB     719  ATTCCACTCTGGGCGCGGCTGTGGCCCGCTTTATGTCTATCTCCACTTGGCGCTCT 778
QY     1632  GCTCAGCAATTGTGACAGGCGACCCGAGGCGCCGAGCGTCTCTCCCGGCGCTGACGA 1691
DB     779  GCTCAGCAATTGTGACAGGCGACCCGAGGCGCCGAGCGTCTCTCCCGGCGCTGACGA 838
QY     1692  TTTCCGGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGTAAAGTGGGAATCGGTGA 1751
DB     839  TTTCCGGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGTAAAGTGGGAATCGGTGA 898
QY     1752  TTAAGGAACCTTTCTGCTGCGACCGGCTAAGGACAGCGGAGAGCGACTCCGAGMGTCT 1811
DB     899  TTAAGGAACCTTTCTGCTGCGACCGGCTAAGGAGGAGGAGCGACTCCGAGCGCTCT 958
QY     1812  GAAAGCGACGTCCCAAGAGTGAATTTGGAAGCTGGAACAGCGTGGGAGCATTCGAGATA 1871
DB     959  GAAAGCGACGTCCCAAGAGTGAATTTGGAAGCTGGAACAGCGTGGGAGCATTCGAGATA 1018
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QY     1872  CGAAGCGGCTGTAAAGTGTGAGCGGGAGCTCCAGAGTGTACTTCGCGCC 1924
DB     1019  CGAAGCGGCTGTAAAGTGTGAGCGGGAGGTCCAGAGTGTAGCGCGCTCC 1071
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RESULT 15
US-09-949-016-1003
; Sequence 1003, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTUR, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1003
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1003
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Query Match 24.7%; Score 538.6; DB 4; Length 3498;
Best Local Similarity 58.6%; Pred. No. 1.1e-116;
Matches 1105; Conservative 1; Mismatches 680; Indels 99; Gaps 6;

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QY      35  AGGCCCCCTGAGGAGACCTGCTTGTGGGACATGTTGTGAAGGAGCAAGATGGCCA 94
DB     1544  AGAACCCTGCGGAGACTGTCTGTGGGCTGTGAGCAAGCAAGCAAGATGGCCA 1603
QY      95  TGTACTTCTGGAGATGGGTTCCATGCACTTCTCTGAGCTTGTGGGCTGTTGTGTC 154
DB     1604  CTTACTTCTGGGCGCATGGGCGAGAGAGTGTGGAGCGGAGCGGCGGCTGCAAAATCC 1663
QY     1655  TCCGGGTGATGACAGCGCTGAGCGCTTACGCTGAGAGGAGCAAGAGAAAGACTGG 214
DB     1664  TCAAGAGATGTCCGACCTGAGAGCGAGGCGGAGGCGCGCCGAGCAGC-----CGCG 1717
QY     215  CGTTCAAGTTTGAAGGAGATGGGCTTGAACCTTTTGGCGAGTGTATTCGACAGTGA 274
DB     1718  AGGCGAAATACGAGCGGCTGCGCTTGAACCTTCTCCGAGTGTACAGCAAGTGAAG 1777
QY     275  TGAAGGCTGCCCGCTCTCTCTGCGTGCCTCCGCTCTGGGGGAGATGCACTTGGCTCC 334
DB     1778  CCGCGGCTTGTGCGCTGCTGTGTGGCGGAGAACCGCTGTGAGCAAGCACTTGGCTGC 1837
QY     335  AGCTGGCCATGCAAGCTGACGCGCGTGTCTTTTGGCCAGAGATGGGATACATCTGTC 394
DB     1838  ACTGGCCACCGAAGCTGACGCGCAAGGCTTTTGGCCAGAGAGGCGTTCAGGCTTTC 1897
QY     395  TGAACAGAAAGTGTGGGAGATATGCGCAGCACTACCAACCATGTGGGCTGCTTCTCG 454
DB     1898  TGACCAAGATCTGTGTGGGGGACATGTGGCGGAGCAGCGCCATCTCGGCTGTAGAG 1957
QY     455  CCTTCTTTTGGCTTCACTACACCGGCTCATCACTTTCAGGAAATCAGAAAGAG 514
DB     1958  CTTTCTTCTGCGCGGCTCTGTCTATACCAACCTATCACTTTCAGTGAAGAGCTCCCC 2017
QY     515  AGCCCAACGAGAGAGCTTGAAGTTTGAATGATGATGATTAATGAGGAGGCGCTG 574
DB     2018  TGAAGACAGGCTGAGGAGACTGTGAGGAGCTTGAAGAGCTTGAAGAGAGAGCGCG 2077
QY     575  TCGGAGAGGCGGAGACCGAGCGAGAGAGCGCTGTGGGGGTTCGCGGCGCAATCGGCGCTC 634
DB     2078  TGTATGGCTGTGACAGGCGGAGTGAAGAGCTGTGTGAGAGCGCGCGAG----- 2123
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QY 635 CGGGTTGCTGCGGGGCGCTGCGGGGCGCGGTCCTAACCGCCGCTGCTTCTCT 694
DB 2124 -GGCTCAGGGGTGACCGAGGCCCAAGTGTCTCTTCCGCTCACAAGCTGGCGGAATTC 2182
QY 695 GGGGCGCGCGGTGACCACTTTCATGAGGCAACGTGTCACTACCTGTCTCTCTGTC 754
DB 2183 GGGGCGCTCCGCTGACTGTCTCTGGGGAACGTGGCATGTACTTCTGCTCTCTTCC 2242
QY 755 TTTTCTCGGGGTGTCTGTGATTTCAAGCCGGGCGCGCCGCTCC-----CTGG 808
DB 2243 TGTTCACCTAACGCTGTGTGTGACTTCAAGCGCGCCCGCCCGGCTTCAGGGCCG 2302
QY 809 AGCTGCTGCTCTATTTTCTGGGCTTTTCAAGCTGTGTGAGGAACCTGCGCGGCTTGA 868
DB 2303 AGGTCAACCTCTTACTTCTGTGGGTCTTTACGCTGTGTGAGGAATCCGGACGGCTTCT 2362
QY 869 GCGGAGCGCGGGGCAAGCTTGCACAGCGGGGCGCCCGGCTGTGACCTCACTGAGCC 928
DB 2363 TCACAGACGAGGACACACAC-----CTGGTGA 2389
QY 929 AGCGCTGCGCTCTTACTTCTGCGGCAAGCTGGAACAGTGCACCTAGTGGCTTCACT 988
DB 2390 AGAAGTTCAACATGTATGTGGGGGACAACTGGAACAGTGTGACATGTGTGCATCTTCC 2449
QY 989 GCTTCCCTCGGGGCTGTGGGCTGCGGCTGACCCCGGGTTGTACCACTGGGGCGGCACTG 1048
DB 2450 TGTTCATGTGGGTGTACCTTGAAGAGTGTGCGCTGCGGCTTTGAGGCTGGCCGACGG 2509
QY 1049 TCCTTGCATGCACTTTCATGATGTTTTCAGGCTGGGCTGCTTCACTTCTCAAGCTCAACA 1108
DB 2510 TCCTTGCATGCACTTTCATGATGTTTTCAGGCTGGGCTGCTTCACTTCTTGCATACACA 2569
QY 1109 AACAGCTGGGGCCCAAGATGTCACTGTAGCAAGATGATGAAGAGCTGTTCTTCC 1168
DB 2570 AGCAGCTGGGGCCCAAGATGTCACTGTAGCAAGATGATGAAGAGCTGTTCTTCC 2629
QY 1169 TCTTCTTCCCGGCTGTGGCTGTGAGCTATGGCGGTGGCCACGAGAGGGCTCTGAGGC 1228
DB 2630 TCTTCTTCTGAGCGTGTGGCTGTGAGCTATGGCGGTGGCCACGAGAGGGCTCTGAGGC 2689
QY 1229 CACGGGACAGTGACTTCCCAAGTATCTGTGCGCGCGCTTCTTCACTGCTTCACTGCGAGA 1288
DB 2690 CCGATGACGGCGCGCTGTGAGTGTATCTTCCGCGGGGTCTTACCGGCTTCACTGCGAGA 2749
QY 1289 TCTTGGGGCAAGTTCCTCCAGAGAGACATGACGTGCGCTCATGAGACACAGCACTGCT 1348
DB 2750 TCTTGGGGCAAGTTCCTCCAGAGAGACATGACGTGCGCTCATGAGACACAGCACTGCT 2809
QY 1349 CGTCGAGCGCGGCTTGTGGGACACCCCTCTGGGGGCCAGGGGGGCACTGTGCTTCC 1408
DB 2810 CACTGTGCTGAGAGACTCAC-----TCTGTGCCCGAGCC 2845
QY 1409 AGTATGCACTAGCTGT 1468
DB 2846 TCTATGCACTAGCTGT 2905
QY 1469 TGTGTGCACTTGTCTATTTCCATGTTTCAAGTTCACATTTGGGCAAGTACAGGGCAACA 1528
DB 2906 TGTCTCATGAACCTGTCTATGCTGATGTTTCAAGTTCACATTTGGGCAAGTACAGGGCAACA 2965
QY 1529 GCGATCTCTACTGGAAGGCGGAGGTTTCCGCTCATCGGGAATTCCACTTGTGGCCG 1588
DB 2966 CAGACATGTTCTGGAAGTTCAGGCTTCAACCTGATTTGTGAGTACACAGAGCGCCG 3025
QY 1589 CGCTGGCGCGCGCTTATGTGTCTTCCACTTGGCTCTCTGCTCAGGCAATTTGTGA 1648
DB 3026 CCTTGGCGCGCGCTTATGTGTCTTCCACTTGGCTCTCTGCTCAGGCAATTTGTGA 3085
QY 1649 GCGGACCGGAGAGCGCGGCTCTCCCGGCTTGAAGCAATTTCCGGGTTTACCTTT 1708
DB 3086 AGAAGAGGCTGAGCACACGCG-----GAGCACCTGGAAGAGACCTGCG 3130

QY 1709 CTAAAGAGCCGAGCGGAAGCTGTCTAACCTGGAATCGTGTCAATTAAGAGAACTTCTGC 1768
DB 3131 CAGACCCCTTGACACAGAAAGTGTCTACCTGGGAGACAGTCCAGAAAGAACTTCTGGA 3190
QY 1769 TGGCAGCGCTTAAAGGACAGCGGAGAGGATCTCGAGGTCTGAAAGCGGACCTCCAGA 1828
DB 3191 GCAAGATGAGGAAGCGAGAGGAGACAGCGAGGGGAGGTGTGCGGAAAAACGCCACACA 3250
QY 1829 AGGTGACCTTGGCACTGAAACAGCTGGGACACATCCGCGAGTACGAACAGCGCTGAAG 1888
DB 3251 GAGTGAACCTTCAATTCGCAAGTACCTGAGGGGCTGAGAGGCAAGAAAGCGATCAAGT 3310
QY 1889 TGTGAGCGGGAGGTCCAGCAGTG 1913
DB 3311 GTCTGAGTACAGATCACTACTG 3335

Search completed: June 13, 2005, 08:38:50
Job time : 256.801 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 16:55:33 ; Search time 4466.1 Seconds
(without alignments)
18579.996 Million cell updates/sec

Title: US-09-869-486B-25
Perfect score: 2180
Sequence: 1 tcggcgcccaagcattcgca.....ggaataaagccattcaga 2180

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1088.2	49.9	4293	3 AK044094	AK044094 Mus muscu
2	770	15.3	912	6 CA488162	CA488162 AGENCOURT
3	719	33.0	879	5 B0858032	B0858032 AGENCOURT
4	651.6	29.9	883	5 BQ723742	BQ723742 AGENCOURT
5	647	29.7	864	6 CA488844	CA488844 AGENCOURT
6	634.4	29.1	672	4 B1759746	B1759746 603045620
7	609.8	28.0	613	5 BX474984	BX474984 DKP2686M
8	579.8	26.6	599	4 B1910079	B1910079 603067915
9	577	26.5	580	5 BP265210	BP265210
10	527	24.2	725	7 CK955668	CK955668 4095493 B
11	525.6	24.1	551	6 CB266373	CB266373 1005278 B
12	514.4	23.6	1090	6 BF111909	BF111909 601897749
13	499.2	22.9	540	7 CN335029	CN335029 170004277
14	487.4	22.8	895	5 BQ918283	BQ918283 AGENCOURT
15	483	22.3	625	4 B1199159	B1199159 602758878
16	465.6	21.4	3449	5 BQ084154	BQ084154 K-BST0148
17	465.6	21.4	3998	3 AK035197	AK035197 Mus muscu
18	463.2	21.2	997	2 AK044908	AK044908 Mus muscu
19	451	20.7	933	5 BQ942718	BQ942718 AGENCOURT
20	449.2	20.6	3523	3 AK044423	AK044423 Mus muscu
21	447.4	20.3	624	7 CK832049	CK832049 4056009 B
22	443	20.3	444	4 BM821224	BM821224 K-BST0090
23	411.6	18.9	601	7 CO261067	CO261067 4133160 B

25	395	18.1	519	4 B1198633	B1198633 602761709
26	391.2	17.9	392	4 BM797899	BM797899 K-BST0081
27	389	17.8	569	7 CN677997	CN677997 E014H02
28	387.6	17.8	611	2 B313619	B313619 60153249
29	387.2	17.8	580	7 CK942304	CK942304 4065798 B
30	382.8	17.6	869	4 B1488582	B1488582 603021110
31	379.6	17.4	444	2 AW816479	AW816479 QVO-ST023
32	374.6	17.2	883	2 BF582966	BF582966 602097824
33	371.2	17.0	869	6 CB193845	CB193845 AGENCOURT
34	370.2	17.0	774	4 BQ759687	BQ759687 602713380
35	368.8	16.9	734	6 CA312705	CA312705 UI-CF-FNO
36	367.8	16.9	733	5 BQ687299	BQ687299 UI-CF-B01
37	362.2	16.6	3498	9 AY401205	AY401205 Homo sapi
38	361.6	16.6	484	2 BF652205	BF652205 275703 MA
39	356	16.3	545	7 CO895866	CO895866 Bowden 24
40	352.6	16.2	676	7 CN790827	CN790827 4125460 B
41	343.8	15.8	486	4 BQ243789	BQ243789 602357809
42	343	15.7	495	5 BQ371603	BQ371603 PML-FN021
43	341.4	15.7	410	7 H18835	H18835 YM45d10.r1
44	341.2	15.7	432	2 BF041933	BF041933 BP250006A
45	341.2	15.7	671	4 B1198267	B1198267 602760054

ALIGNMENTS

RESULT 1
AK044094
LOCUS
DEFINITION
AK044094 4293 bp mRNA linear HTC 03-APR-2004
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length
enriched library, clone:A830089H13 product:similar to TRP-RELATED
CATION INFLUX CHANNEL (Homo sapiens), full insert sequence.

ACCESSION
AK044094.1 GI:26336171
VERSION
HTC; CAP trapper.
KEYWORDS
Mus musculus (house mouse)
SOURCE
ORGANISM
Mus musculus

REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
2 Carninci, P., Shibata, Y., Hayatsu, N., Suganara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
3 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kikunari, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matshiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research

REFERENCE
JOURNAL
MEDLINE
PUBMED
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

QY 1106 ACAACAGCTGGGGCCCAAGATCGTCATCGTAGACAAGATGATGAAGACCGGTTCTTCT 1165
 DB 2403 ACAAGCACTGGGGCCCAAGATTCATAGTAGCAAAATATGAAGATGATATTTCTTCT 2462
 QY 1166 TCTCTTCTTCTCGGCGTGTGTGAGTACCTATGCGTGGCCACGAGAGGGCTCTCTGA 1225
 DB 2463 TCTCTTCTTCTCGGCGTGTGTGAGTACCTATGCGTGGCCACGAGAGGGATCTCTGA 2522
 QY 1226 GGGCCAGGAGACAGTACTTCCCAAGTATCTTCCGCGCGCTCTTCTACCGCTTCACTTGC 1285
 DB 2523 GGGCCAGGAGACAGTACTTCCCAAGTATCTTCCGCGCGCTCTTCTACCGAGCTATCTGC 2582
 QY 1286 AGATCTTGGGAGATTCGCCAGAGAGACATGAGACGTCGCTCATGAGACAGCAACT 1345
 DB 2583 AGATCTTGGGAGATTCGCCAGAGAGAAATGAGAGTGGCCCTCATGATTCAGGTAATCT 2642
 QY 1346 GCTCGTGGAGCCCGGCTTCTGGGACACCCCTCTGGGGCCAGCGGGCACTTCCGCTCT 1405
 DB 2643 GCTCAATGGAGCGGGGCTCTCGGGCTCATCCGAGGGGCCCGTGGCAAGCTCTGTGTGT 2702
 QY 1406 CCCAGTATGCCAATCTGGTGTGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1465
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 QY 1526 ACACGAGTCTTCTAGTGAAGGCGAGCTTACCGCTCATCCGGGAATTCACCTCTCGGC 1585
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 QY 1586 CCGGCTGGGCCCCGCTTATTCGTATCTCCCACTTGGCGCTCTCTCTCTCTCTCTCT 1645
 DB 2883 CTTGCTGGGCCCCGCTTATTCGTATCTCCCACTTGGCGCTCTCTCTCTCTCTCTCT 2916
 QY 1646 GCAAGGCAACCCGAGAGCCCGAGCGCTCTCCCGGCTCTGAGATTTCCGGGTTTACC 1705
 DB 2917 -----TGTGCTGTCT 2926
 QY 1706 TTTCTAAGAAAGCCGAGCGGAAGCTGCTAAGTGGGAATCGTGATGAAGAACTTTC 1765
 DB 2927 TCTGTAAAGAAAGCGAGCGGAAGCTGCTAAGTGGGAATCGTGATGAAGAACTTTC 2986
 QY 1766 TGTCTGCAACGCGCTAAGGAGCAAGCGGAGAGCACTCCGAGTGTGAAGCGCACTGCC 1825
 DB 2987 TGTCTGCAACGCGCTAAGGAGCAAGCGGAGAGCACTCCGAGTGTGAAGCGCACTGCC 3046
 QY 1826 AGAAGCTGGAATTTGGCACTGTAAGACAGCTGGGACATCCGAGATGACGAAGCGCTTGA 1885
 DB 3047 AGAAGCTGGAATTTGGCACTGTAAGACAGCTGGGACATCCGAGATGACGAAGCGCTTGA 3106
 QY 1886 AAGTCTGAGAGCGGAGGATCCAGAGTGTACCTCGGCC 1924
 DB 3107 GGGGGCTGGAGAGAGAGGTCCAACTGTCTCCAGTCC 3145

RESULT 2
 CA488162
 LOCUS
 DEFINITION AGNCOURT_10808068 MAPcl Homo sapiens cDNA clone IMAGE:6719903 5',
 mRNA sequence.
 ACCESSION CA488162
 VERSION CA488162.1 GI:24949318
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 912)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
 COMMENT
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 CDNA Library Preparation: Invitrogen Corp
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
 http://image.lnl.gov
 Plate: LLM4278 row: 1 column: 23
 High quality sequence start: 28
 High quality sequence stop: 728.
 Location/Qualifiers
 1. 912
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6719903"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 HRTBT-HMB1, LNCaP"
 /lab_host="EMDH10B"
 /clone_id="MAPCL"
 /note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bungkok Lee & Ira Pastan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

ORIGIN
 Query Match 35.3%; Score 770; DB 6; Length 912;
 Best local similarity 98.8%; Pred. No. 1e-163;
 Matches 773; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1146 GATGAAGAGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1205
 DB 46 GATGAAGAGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 105
 QY 1206 GGCACGAGAGGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1265
 DB 106 GGCACGAGAGGGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 165
 QY 1266 CTTTCAACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1325
 DB 166 CTTTCAACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 225
 QY 1326 CTTTCAACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1385
 DB 226 CTTTCAACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 285
 QY 1386 CCAGCGGGGACCTGCGCTCTCCAGTATGCAACTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 1445
 DB 286 CCAGCGGGGACCTGCGCTCTCCAGTATGCAACTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 345
 QY 1446 CTTTCTGCTGTCGCAACATCTCTGCTGCTCACTTCTCTCACTTCTCTCACTTCTCTCACT 1505
 DB 346 CTTTCTGCTGTCGCAACATCTCTGCTGCTCACTTCTCTCACTTCTCTCACTTCTCTCACT 405
 QY 1506 ATTGCGCAAGTACAGGCGCAACAGCATCTTACTGGAAGCGCAAGCGGTATACCGCTCAT 1565
 DB 406 ATTGCGCAAGTACAGGCGCAACAGCATCTTACTGGAAGCGCAAGCGGTATACCGCTCAT 465
 QY 1566 CCGGGAATTCACATCTGGGCGCGGCTGGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 1625
 DB 466 CCGGGAATTCACATCTGGGCGCGGCTGGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 525
 QY 1626 CTTCTCTCTCAGGCAATTTGTGACAGCGACCCGAGAGCCCGAGCGCTCTTCCCGGCGCT 1685
 DB 526 CTTCTCTCTCAGGCAATTTGTGACAGCGACCCCGAGAGCCCGAGCGCTCTTCCCGGCGCT 585

QY 1686 CGAGCATTTCCGGGTTTACCTTTCTAAGAGCCGAGCGGAAGCTGCTAACGTGGAAATC 1745
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QY 1746 GGTGATATAGAGAACTTCTGCTGACAGCGCTAGGGACAAGCGGAGAGAGACTCCGA 1805
DB 646 GGTGATATAGAGAACTTCTGCTGACAGCGCTAGGGACAAGCGGAGAGAGACTCCGA 705
QY 1806 GGTGATATAGAGAACTTCTGCTGACAGCGCTAGGGACAAGCGGAGAGAGACTCCGA 1865
DB 706 GGTGATATAGAGAACTTCTGCTGACAGCGCTAGGGACAAGCGGAGAGAGACTCCGA 765
QY 1866 CGAGTACGAAACAGCGCTGAAAGTGTGAGCGGAGGTCACAGTGTACCTCGGCCCC 1925
DB 766 CGAGTACGAAACAGCGCTGAAAGTGTGAGCGGAGGTCACAGTGTACCTCGGCCCC 825
QY 1926 CG 1927
DB 826 CG 827

RESULT 3
BU858032 879 bp mRNA linear EST 16-OCT-2002
LOCUS AGENCOURT_1047874 NIH_MGC_107 Homo sapiens cDNA clone
DEFINITION IMAGE:6647959 5', mRNA sequence.
ACCESSION BU858032
VERSION BU858032.1 GI:24043024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 879)
NIH-MGC http://mgi.nci.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2889 row: d column: 07
High quality sequence start: 11
High quality sequence stop: 612.
Location/Qualifiers
1..879
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6647959"
/tissue="type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pOTB; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

ORIGIN
Query Match 33.0%; Score 719; DB 5; Length 879;
Best Local Similarity 96.6%; Pred. No. 3.8e-152;
Matches 799; Conservative 0; Mismatches 20; Indels 8; Gaps 6;
QY 708 GACCATCTTCATGGGCAAGGTGCTACCTGCTCTGCTGCTTTCTTCGCGGGT 767

DB 1 GACCATCTTCATGGGCTACCTGCTACCTACCTGCTGCTTTCTTCGCGGGT 60
QY 768 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 827
DB 61 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 120
QY 828 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 887
DB 121 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 180
QY 888 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 947
DB 181 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 240
QY 948 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 1007
DB 241 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 300
QY 1008 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 1067
DB 301 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 360
QY 1068 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 1127
DB 361 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 420
QY 1128 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 1187
DB 421 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 480
QY 1188 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 1247
DB 481 GCTGCTCGATATTTCCAGCGGAGCGCGCGGCTCCCTGAGAGCTGCTATATTTCTG 540
QY 1248 AAGTATCTGCGCGCGCGCTGCTTCTACCTGCTTCTGCTGCTGCTGCTGCTGCTG 1307
DB 541 AAGTATCTGCGCGCGCGCTGCTTCTACCTGCTTCTGCTGCTGCTGCTGCTGCTG 600
QY 1308 GAGAGCATATGACGCGCGCTCATGAGACAGCAAGCTGCTGCTGCTGCTGCTGCTG 1366
DB 601 GAGAGCATATGACGCGCGCTCATGAGACAGCAAGCTGCTGCTGCTGCTGCTGCTG 660
QY 1367 GAGAGCATATGACGCGCGCTCATGAGACAGCAAGCTGCTGCTGCTGCTGCTGCTG 1423
DB 661 GAGAGCATATGACGCGCGCTCATGAGACAGCAAGCTGCTGCTGCTGCTGCTGCTG 720
QY 1424 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1482
DB 721 TGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 1483 CTCATTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1526
DB 781 CTCATTGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 827

RESULT 4
BO723742 883 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8241174 Lupski_sympathetic_trunk Homo sapiens cDNA clone
DEFINITION IMAGE:6186968 5', mRNA sequence.
ACCESSION BO723742
VERSION BO723742.1 GI:21862639
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 883)
NIH-MGC http://mgi.nci.nih.gov/
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

Email: cgabbs-remail.nih.gov
 Tissue Procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM13580 row: d column: 09
 High quality sequence stop: 557.
 Location/Qualifiers

FEATURES

source

1. .883
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 /db_xref="taxon:9606"
 /clone="IMAGE:6186968"
 /sex="male"
 /tissue_type="sympathetic trunk"
 /dev_stage="adult, 16 yr"
 /lab_host="DH10B"
 /clone_lib="lupski, sympathetic trunk"
 /note="Vector: PCMV-SPORT6 (Life Technologies); Site 1:
 NotI; Site 2: SalI; cDNA made by oligo-dt priming.
 Directionally cloned using the following adaptors:
 5'-TCGACCCAGCGCCG-3' and
 5'-GACTAGTTCTAGATCGGAGCGCGCCCT(15)-3'. Size selected >
 1 kb for average insert length 1.9 kb. This is a primary
 library, non-amplified. Library constructed by Life
 Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
 College of Medicine); available through Life
 Technologies."

ORIGIN

Query Match 29.9%; Score 651.6; DB 5; Length 883;
 Best Local Similarity 94.3%; Pred. No. 7.3e-137;
 Matches 709; Conservative 0; Mismatches 39; Indels 4; Gaps 3;

QY 321 TGGCACTTGCTCGAGTGGCCATGCAAGCGCCGCTTTGGCCAGAGATGG 380
 Db 1 TGGCACTTGCTCGAGTGGCCATGCAAGCGCCGCTTTGGCCAGAGATGG 60

QY 381 GGTACAGTCTCTGTGACACAGAGTGGTGGAGATATGAGCACTACACCATCTG 440
 Db 61 GGTACAGTCTCTGTGACACAGAGTGGTGGAGATATGAGCACTACACCATCTG 120

QY 441 GGCCCTGCTTCCGCTTTCTTTGCTCCCTCACTATCAACCCGCTCATACCTTCAG 500
 Db 121 GGCCCTGCTTCCGCTTTCTTTGCTCCCTCACTATCAACCCGCTCATACCTTCAG 180

QY 501 GAAATCAGAGAGAGCCCAACAGGAGAGACTGATTTGACATGATATGATTTAA 560
 Db 181 GAAATCAGAGAGAGCCCAACAGGAGAGACTGATTTGACATGATATGATTTAA 240

QY 561 TGGGGAAGAGGCTCTGCGGAGCGGAGCCAGCGAGAGAGCGCTGGGGGTCCGCG 620
 Db 241 TGGGGAAGAGGCTCTGCGGAGCGGAGCCAGCGAGAGAGCGCTGGGGGTCCGCG 300

QY 621 CCACTGCGGCGCTGCGGAGTCTGCGGAGCGCGCTGCGGAGCGCGCTGACCGCG 680
 Db 301 CCACTGCGGCGCTGCGGAGTCTGCGGAGCGCGCTGCGGAGCGCGCTGACCGCG 360

QY 681 CTGCTTCACTTCTGCGGAGCGCGGAGCACTTCAATGAGGCAACGTGTCACTACT 740
 Db 361 CTGCTTCACTTCTGCGGAGCGCGGAGCACTTCAATGAGGCAACGTGTCACTACT 420

QY 741 GCTGTTCTGCTGCTTTTCTGCGGAGTCTGCTGATTTTCAAGCGGCGCGCGCG 800
 Db 421 GCTGTTCTGCTGCTTTTCTGCGGAGTCTGCTGATTTTCAAGCGGCGCGCGCG 480

QY 801 CTCCTTGAAGTGTGCTTATTTCTGAGCTTTTCAAGTGTGTGAGAGAACTGCGCA 860
 Db 481 CTCCTTGAAGTGTGCTTATTTCTGAGCTTTTCAAGTGTGTGAGAGAACTGCGCA 540

QY 861 GGGCTGAGCGAGCGGAGCGGAGCACTCGCCAGCGGAGCCCGGAGCTGACCTC 920
 Db 541 GGGCTGAGCGAGCGGAGCGGAGCACTCGCCAGCGGAGCCCGGAGCTGACCTC 600

QY 921 A-CTGAGCAGCGGCTCGGCTTCTTACTTCTGCGGAGCTGAGCACTGACTAGTG 979
 Db 601 ACTGAGCAGCGGCTCGGCTTCTTACTTCTGCGGAGCTGAGCACTGAGCACT 659

QY 980 CTCACCTGCTTCTCTCTGAGC--GTGGGCTGCGGAGTCCCGGCTTTGACCACT 1037
 Db 660 CTCACCTGCTTCTCTCTGAGC--GTGGGCTGCGGAGTCCCGGCTTTGACCACT 719

QY 1038 GGGCGGACCTGCTCTGATGCACTTCATG 1069
 Db 720 GGGCGGACCTGCTCTGATGCACTTCATG 751

RESULT 5
 CA488844
 LOCUS
 DEFINITION AGNCOURT_10808212 MAREL Homo sapiens cDNA clone IMAGE:6721042 5',
 mRNA sequence.
 ACCESSION CA488844
 VERSION CA488844.1 GI:24951635
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)

REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLM14281 row: 1 column: 10
 High quality sequence stop: 571.
 Location/Qualifiers

FEATURES

source

1. .864
 /organism="Homo sapiens"
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 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 hTERT-HME1, LNCaP"
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 /clone_lib="MAPCL"
 /note="Vector: PCMV-SPORT6, Site 1: EcoRV; Site 2: Not I;
 Subtracted with brain, liver, lung, kidney and muscle.
 Directionally cloned. Priming method: oligo-dt. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bunkook Lee & Ira Pastan. Discovery of new breast
 cancer genes encoding membrane and secreted proteins.
 Manuscript submitted."

ORIGIN

Query Match 29.7%; Score 647; DB 6; Length 864;
 Best Local Similarity 85.6%; Pred. No. 8.1e-136;
 Matches 703; Conservative 3; Mismatches 114; Indels 1; Gaps 1;

QY 1262 GCGTCTTACCGTCTCTTACTGCAATCTTGGGAGATTTCCAGAGAGCATGACG 1321
 Db 1 GCGTCTTACCGTCTCTTACTGCAATCTTGGGAGATTTCCAGAGAGCATGACG 60

QY 1322 TGGCCCTCATGAGCAGACATGCTGTCGAGCCCGGCTTGGGCAACCTCTCG 1381

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Db      61 TGGCCCTCATGAGACAGACAACTGCTCGTGGAGCCGGCTTCTGGGACACCTCTCG 120
Qy      1382 GGGGCCAGGGGGGACCTGCGTCTCCAGTATGCGCAATGCGTGGTGGTCTCTCG 1441
Db      121 GGGGCCAGGGGGGACCTGCGTCTCCAGTATGCGCAATGCGTGGTGGTCTCTCG 180
Qy      1442 TCATCTCTGCTGCTGAGCAACATCTGCTGCTCACTTGTCTCATTTGCTCATTTGCTCATTT 1501
Db      181 TCATCTCTGCTGCTGAGCAACATCTGCTGCTCACTTGTCTCATTTGCTCATTTGCTCATTT 240
Qy      1502 ACACATTTGGGCAAGTACAGGGGCAACAGGATCTCTAATGAAAGGCGCAGCGTTACCGCC 1561
Db      241 ACACATTTGGGCAAGTACAGGGGCAACAGGATCTCTAATGAAAGGCGCAGCGTTACCGCC 300
Qy      1562 TCATCGGGGAATTCACCTCGGCGCGGCTGGCCCGCCCTTATTCGTCATCTCCACT 1621
Db      301 TCATCGGGGAATTCACCTCGGCGCGGCTGGCCCGCCCTTATTCGTCATCTCCACT 360
Qy      1622 TCGGCTCTGCTGCTGAGCAATTTGTCAGAGCGACCCGAGCCCGCTCTCCCGG 1681
Db      361 TCGGCTCTGCTGCTGAGCAATTTGTCAGAGCGACCCGAGCCCGCTCTCCCGG 420
Qy      1682 CCCTGAGCATTTCCGGGTTTACCTTTCTAAGAAAGCGAGGAACTGCTAACGTGG 1741
Db      421 CCCTGAGCATTTCCGGGTTTACCTTTCTAAGAAAGCGAGGAACTGCTAACGTGG 480
Qy      1742 AATCGGTGATTAAGAGAACTTTCTGCTGCGACGCGCTGAGGACAAAGCGGAGAGCACT 1801
Db      481 AATCGGTGATTAAGAGAACTTTCTGCTGCGACGCGCTGAGGACAAAGCGGAGAGCACT 540
Qy      1802 CCGAGGTGTAAGGCGACGCTCCAGAAAGTGAATTTGCACTGAAACAGCTGGAGACA 1861
Db      541 CCGAGGTGTAAGGCGACGCTCCAGAAAGTGAATTTGCACTGAAACAGCTGGAGACA 600
Qy      1862 TCCGGAGTACGAACAGCGCTGAAAGTCT-GAGCGGAGAGTCCAGCAGTGAATCTCG 1920
Db      601 TCCGGAGTACGAACAGCGCTGAAAGTCTGCGAGCGGAGAGTCCAGCAGTGAATCTCG 660
Qy      1921 GCGCCCGACGCTGCTGCTTCTCTGAGTGAAGCCCATGTCATCTGGGCGCACTGTC 1980
Db      661 TCCCTCTGGGGGTTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 720
Qy      1981 AGGACCACTTTGGAGTGTCTTCAATCAAAACCAAGCATGCGGCTCTCTCCAGAAC 2040
Db      721 GCGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Qy      2041 CAGTCCCAAGCTTGGAGAGATCAAGGCTGATCCCGGCG 2081
Db      781 CCCCCNNCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 821

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RESULT 6
B1759746 672 bp mRNA linear EST 25-SEP-2001
LOCUS 603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5',
DEFINITION mRNA sequence.
ACCESSION B1759746
VERSION B1759746.1 GI:15751324
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 672)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgephs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

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FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5185949"
/lab_host="DH10B"
/clone_1ib="NIH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon, 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH MGC Library."

ORIGIN
Query Match 29 1%; Score 634.4; DB 4; Length 672;
Best Local Similarity 99.4%; Pred. No. 5,6e-133;
Matches 668; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

Qy      706 GTGACCATCTTCATGAGGACAGTGTCA-GTACCTGCTGTTCTGCTGCTTTCTCGCG 764
Db      1 GTGACCATCTTCATGAGGACAGTGTCA-GTACCTGCTGTTCTGCTGCTTTCTCGCG 60
Qy      765 GGTGCTGCTCGTGATTTTCAGCCGCGCGCGCGCTCCCTGAGCTGCTGCTTATT 824
Db      61 GGTGCTGCTCGTGATTTTCAGCCGCGCGCGCGCTCCCTGAGCTGCTGCTTATT 120
Qy      825 CTGGGCTTTCAACGCTGCTGTCGAGAGAACTGCGGAGGCGCTGAGCGGAGCGGCGAG 884
Db      121 CTGGGCTTTCAACGCTGCTGTCGAGAGAACTGCGCA-GGCTGAGCGGAGCGGCGAG 179
Qy      885 CTTGCGCAAGGGGGGCGCC-GGGCTGCGCAATGCTCACTAGCAGCGGCTGCGCTCT 943
Db      180 CTTGCGCAAGGGGGGCGCCCTTGGGCTGCGCAATGCTCACTAGCAGCGGCTGCGCTCT 239
Qy      944 ACTTGGCGAAGCTGGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1003
Db      240 ACTTGGCGAAGCTGGAACCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 299
Qy      1004 TGGGCTGCGCGTGAACCGCGGGTTTGTACCACTGAGGCGGACGTCCTGCACTGACT 1063
Db      300 TGGGCTGCGCGTGAACCGCGGGTTTGTACCACTGAGGCGGACGTCCTGCACTGACT 359
Qy      1064 TCATGATTTTCAAGTGGGCGCTGCTTCACTTTCAGCGTCAACAAAGCTGGGGCCCA 1123
Db      360 TCATGATTTTCAAGTGGGCGCTGCTTCACTTTCAGCGTCAACAAAGCTGGGGCCCA 419
Qy      1124 AGATGTCATGTCGTGAAGAAATGATGAAGAGAGTGTCTTCTCTTCTTCTCTGAGCG 1183
Db      420 AGATGTCATGTCGTGAAGAAATGATGAAGAGAGTGTCTTCTCTTCTTCTCTGAGCG 479
Qy      1184 TGTGCTGTGATGCTTATGCGTGGCGACAGGAGGGCTCTTGAAGCGACAGGACAGTACT 1243
Db      480 TGTGCTGTGATGCTTATGCGTGGCGACAGGAGGGCTCTTGAAGCGACAGGACAGTACT 539
Qy      1244 TCCCAAGTATCTGAGCGCGCGCTTCTTCAAGCGCTTCACTGCAAGTCTTCCGAGCATTC 1303
Db      540 TCCCAAGTATCTGAGCGCGCGCTTCTTCAAGCGCTTCACTGCAAGTCTTCCGAGCATTC 599
Qy      1304 CCCAGAGACATGACGTGGCCCTCATGAGACACAGCACTGCTGTCGAGACCGCGCT 1363

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Db 600 CCCAGAGACATGAGCGTGGCCCTCATGAGACAGCAACTGCTGCTGGAGCCCGCT 659
Qy 1364 TCTGGCAGCACC 1375
Db 660 TCTGGCAGCACC 671

RESULT 7
LOCUS BX474984 613 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp686m22173.1 686 (synonym: h1cc3) Homo sapiens cDNA clone
BX474984 DKFZp686m22173.5', mRNA sequence.
VERSION BX474984.1 GI:31669181
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 613)
AUTHORS Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fodor,G., Han,M. and Wiemann,S.
EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS

MIPS
Ingolstaedter Landstr.1, D-85764 Neubertberg, Germany
This is the 5' sequence of the clone insert
clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No 5' sequence available.
This clone (DKFZp686m22173) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
1..613
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686m22173"
/dev_string="adult"
/lab_host="DH10B"
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/note="Vector: pTribEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 28.0%; Score 609.8; DB 5; Length 613;
Best Local Similarity 99.7%; Pred. No. 2.1e-127;
Matches 611; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 896 GGGGCCCCGGGCTGGCCATGCTCAGTACGAGCCGCGCTTACTTACCGCCGACA 955
Db 1 GGGGGCCCGGGCTGGCCATGCTCAGTACGAGCCGCGCTTACTTACCGCCGACA 60
Qy 956 GCTTGAACCACTGAGCTAGTGGCTCTCAGCTGCTTCTTCTGGGCGTGGAGTCCGGC 1015
Db 61 GCTGGAACCACTGAGCTAGTGGCTCTCAGCTGCTTCTTCTGGGCGTGGAGTCCGGC 120
Qy 1016 TGACCCCGGGTTTGTACCACTGGGCGGCACTGTCTTGCATGACATTCATGGTTTCA 1075
Db 121 TGACCCCGGGTTTGTACCACTGGGCGGCACTGTCTTGCATGACATTCATGGTTTCA 180
Qy 1076 CGGTGGCGGCTCTTCACTTCTTCAAGGTCAAAAGAGTGGGCGCAAGATCGCATCG 1135
Db 181 CGGTGGCGGCTCTTCACTTCTTCAAGGTCAAAAGAGTGGGCGCAAGATCGCATCG 240
Qy 1136 TGACCAAGATGATGAAGAGCGTGTCTTCTTCTTCTTCTTCTGCGCGTGTGGCTGTAG 1195
Db 241 TGACCAAGATGATGAAGAGCGTGTCTTCTTCTTCTTCTTCTGCGCGTGTGGCTGTAG 300

Qy 1196 CCTATGCGTGGCCAGGAGGCGCTCTTGAAGCCACCGGACAGTGAATCCCAAGTATCC 1255
Db 301 CCTATGCGTGGCCAGGAGGCGCTCTTGAAGCCACCGGACAGTGAATCCCAAGTATCC 360
Qy 1256 TGGCGCGCGTCTTCTTACCGTTCCTTACCTGAGATCTTTCGGGAGATTTCCCGAGAGACA 1315
Db 361 TGGCGCGCGTCTTCTTACCGTTCCTTACCTGAGATCTTTCGGGAGATTTCCCGAGAGACA 420
Qy 1316 TGACCGTGGCCCTTATGAGACAGACAACTGCTGTGGAGCCCGGCTTCTGGGACACACC 1375
Db 421 TGACCGTGGCCCTTATGAGACAGACAACTGCTGTGGAGCCCGGCTTCTGGGACACACC 480
Qy 1376 CTCTGGGGCCAGGCGGAGCACTGCGTCTCCAGTATGCAACTGAGTGGTGTCTGC 1435
Db 481 CTCTGGGGCCAGGCGGAGCACTGCGTCTCCAGTATGCAACTGAGTGGTGTCTGC 540
Qy 1436 TCTCTGATCTTCTCTGCTGCGGCAACATCTGCTGATCACTTCTCATTTCCATGT 1495
Db 541 TCTCTGATCTTCTCTGCTGCGGCAACATCTGCTGATCACTTCTCATTTCCATGT 600
Qy 1496 TCACTTACATTT 1508
Db 601 TCACTTACATTT 613

RESULT 8

BI910079

LOCUS BI910079 599 bp mRNA linear EST 16-OCT-2001
DEFINITION 60306791.F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5217194.5',
mRNA sequence.
ACCESSION BI910079
VERSION BI910079.1 GI:16173416
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 599)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs@emall.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM1545 Row: m Column: 03
High quality sequence stop: 589.

FEATURES

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/note="Vector: pCMV-SPORT6, Site_1: NotI; Site_2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 26.6%; Score 579.8; DB 4; Length 599;

Best Local Similarity 99.2%; Pred. No. 1,3e-120;
Matches 592; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

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QY 1187 GGCTGTACCTATGGCGGCGGACGAGAGGGCTCTGTAGAGGACAGGACATGATTTCC 1246
DB 1 GGCTGTACCTATGGCGGCGGACGAGAGGGCTCTGTAGAGGACAGGACATGATTTCC 59
QY 1247 CAAGTATCTTGGCGGCGGCTCTTCTACCGTCCCTACCTGAGAGATCTTGGGAGATTTCCC 1306
DB 60 CAAGTATCTTGGCGGCGGCTCTTCTACCGTCCCTACCTGAGAGATCTTGGGAGATTTCCC 119
QY 1307 AGGAGACATGACGTCGCTCTGATGAGACACAGCACTGCTGTGAGAGCCCGGCTTCT 1366
DB 120 AGGAGACATGACGTCGCTCTGATGAGACACAGCACTGCTGTGAGAGCCCGGCTTCT 179
QY 1367 GGGACACCTCTGTGGGGCGGAGGGGGGACGTCGCTCCAGATATGCACTGCTGAG 1426
DB 180 GGGACACCTCTGTGGGGCGGAGGGGGGACGTCGCTCCAGATATGCACTGCTGAG 239
QY 1427 TGGTGTGCTCTGCTGATCTTCTGCTGTCGTCGAGCAACATCTGCTGATCACTTGTCA 1486
DB 240 TGGTGTGCTCTGCTGATCTTCTGCTGTCGTCGAGCAACATCTGCTGATCACTTGTCA 299
QY 1487 TTGCGATGTTCACTTACATTCGATTCGCAATGACAGGCAACAGCGATCTTCACTGAGG 1546
DB 300 TTGCGATGTTCACTTACATTCGCAATGACAGGCAACAGCGATCTTCACTGAGG 359
QY 1547 GCGAGGTTACGCGGCTCATCGGAGAAATTCACATCTGCGGCGGCGGCGGCGGCTTTA 1606
DB 360 GCGAGGTTACGCGGCTCATCGGAGAAATTCACATCTGCGGCGGCGGCGGCGGCTTTA 419
QY 1607 TCGTATCTTCCCACTTTCGCTCTGCTGAGCAATTTGTCAGAGGACCCGAGAGCCCG 1666
DB 420 TCGTATCTTCCCACTTTCGCTCTGCTGAGCAATTTGTCAGAGGACCCGAGAGCCCG 479
QY 1667 AGCGTCTTCCCGGCGGCTGAGCATTTCCGGGTTTACCTTTCTAAGAGCCGAGCGGA 1726
DB 480 AGCGTCTTCCCGGCGGCTGAGCATTTCCGGGTTTACCTTTCTAAGAGCCGAGCGGA 539
QY 1727 AGCTGTACGTCGGGAATGTCATAGAGGAACCTTCTGTCGAGCGGCTAAGG 1783
DB 540 AGCTGTACGTCGGGAATGTCATAGAGGAACCTTCTGTCGAGCGGCTAAGG 596
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RESULT 9
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LOCUS BP265210 mRNA 580 bp linear EST 16-SEP-2004
DEFINITION BP265210, mRNA sequence.
ACCESSION BP265210
VERSION BP265210.1 GI:52180441
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 580)
Suzuki, Y., Yamashita, R., Shiota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
JOURNAL CONTACT: Yutaka Suzuki
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp.
TITLE Location/Qualifiers
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/db_xref="taxon:9606"
/clone="JTH00250"

/tissue_type="thyroid"
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/note="thyroid tumor"

Query Match
Best Local Similarity 100.0%; Pred. No. 5,8e-120;
Matches 577; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 GTTCCACTTTGGGGCGGCGGAGTACCAATCTTCAATGGGCAACGTCGATGCTTACTGCT 63
QY 744 GTTCCGTCGCTTTCTGGCGGAGTCGTCGTCGATTTTCAAGCGGCGGCGGCGGCTC 803
DB 64 GTTCCGTCGCTTTCTGGCGGAGTCGTCGTCGATTTTCAAGCGGCGGCGGCGGCTC 123
QY 804 CTTGAGCTGCTCTTATTTCTGGGCTTTCACGCTGCTGTCGAGAACTGCGCAGAG 863
DB 124 CTTGAGCTGCTCTTATTTCTGGGCTTTCACGCTGCTGTCGAGAACTGCGCAGAG 183
QY 864 CTTGAGCGGAGCGGCGGAGCTTGGCAGCGGGGGCCCGGAGCTGTCATGCTTACT 923
DB 184 CTTGAGCGGAGCGGCGGAGCTTGGCAGCGGGGGCCCGGAGCTGTCATGCTTACT 243
QY 924 GAGCGAGGCGTGGCGCTCTACCTGCGGACAGCTGGAACAGATGAGCTTATGAGCTCT 983
DB 244 GAGCGAGGCGTGGCGCTCTACCTGCGGACAGCTGGAACAGATGAGCTTATGAGCTCT 303
QY 984 CACTGCTTCTTCTGCGGCGTGGGCTGCGGCTGACCCCGGCTTGTACCACTTGGGCG 1043
DB 304 CACTGCTTCTTCTGCGGCGTGGGCTGCGGCTGACCCCGGCTTGTACCACTTGGGCG 363
QY 1044 CACTGCTTCTGTCATGCACTTATGTTTTCACGCTGCGCTGCTTCACTTTACGCT 1103
DB 364 CACTGCTTCTGTCATGCACTTATGTTTTCACGCTGCGCTGCTTCACTTTACGCT 423
QY 1104 CAACAAAGAGCTGGGGCCCAAGATGTCATGTCGTCGAGAAATGATGAAGAGCTTCTT 1163
DB 424 CAACAAAGAGCTGGGGCCCAAGATGTCATGTCGTCGAGAAATGATGAAGAGCTTCTT 483
QY 1164 CTTCTCTTCTTCTGCGGCGTGTGCTGTAAGCTTATGCGCTGACGAGAGGCTCTCT 1223
DB 484 CTTCTCTTCTTCTGCGGCGTGTGCTGTAAGCTTATGCGCTGACGAGAGGCTCTCT 543
QY 1224 GAGGCCACGGGACAGTACTTCCCAAGTATCTGCGC 1260
DB 544 GAGGCCACGGGACAGTACTTCCCAAGTATCTGCGC 580
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RESULT 10
CK955668 725 bp mRNA linear EST 15-MAR-2004
LOCUS CK955668
DEFINITION 4095493 BARC 10BOV Bos taurus cDNA clone 10BOV34_D12 5', mRNA
sequence.
ACCESSION CK955668
VERSION CK955668.1 GI:45470048
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 725)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubinfeld, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically
activated bovine gut
Unpublished (2004)
JOURNAL CONTACT: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute

Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 540 Std Error: 0.00.

FEATURES

Source

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/organism="Homo sapiens"
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derived from H1, H7 and H9 cells"
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from embryoid body outgrowths derived from hES cell lines
H1 (p32), H7 (p25), and H9 (p26) maintained in feeder-free
conditions."

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ORIGIN

Query Match	22.9%	Score 499.2;	DB 7;	Length 540;
Best Local Similarity	98.9%	Pred. No. 2.5e-102;		
Matches 524;	Conservative 0;	Mismatches 3;	Indels 3;	Gaps 2

QY	511	CCGACCGGGAGAGCTAAGTTTGAACATGATACTGTCATTAAATGGGAAAGGGCCGTG	576
Db	11	CGCACCGGAGAGGAGCTAAGATTGACATGATAGTATGTCATTAAATGGGAAAGGGCCGTG	70
QY	577	GGGACGGCGGACCCAGCCGAGAAAGACGGCCGTGGGGGGTCCC--GGCCAGTCGGGCGGTG	634
Db	71	GGGACGGCCGAGCCGACGCCAAGAAAGACGCCGTGGGGGGTCCCTGCAGGCCAGTCGGGCCGTG	130
QY	635	CGGGTTGCTGCGGGGGGCGGCTGCGGGGGGGCGCCGGTGCCTACGCGCTGTTCCACTTCT	694
Db	131	CGGGTTGCTGCGGGGGGCGGCTGCGGGGGGGCGCCGGTGCCTACGCGCTGTTCCACTTCT	190
QY	695	GGGGCGCGCGCGGAGACATCTTCAATGGGCAAGTGGTCACTACTGTGTTCTGCTGC	754
Db	191	GGGGCGCGCGCGGAGACATCTTCAATGGGCAAGTGGTCACTACTGTGTTCTGCTGC	250
QY	755	TTTTCTCGGGGGTGCCTCGTGGATTTCCAGCCGGGCGCGCCCGGGCTCCCTGGAGCTGC	814
Db	251	TTTTCTCGGGGGTGCCTCGTGGATTTCCAGCCGGGCGCGCCCGGGCTCCCTGGAGCTGC	310
QY	815	TGCTATTATTCTGGGCTTTCAAGCTGCTGTGGAGAACTGCGCAAGGACTGAGCGAG	874
Db	311	TGCTATTATTCTGGGCTTTCAAGCTGCTGTGGAGAACTGCGCAAGGACTGAGCGAG	370
QY	875	GCGGGGGGACGCTCGCCAGCGGGGGCGCCGGGCTGGCCATGCTCACTGACAGCCAGGCC	934
Db	371	GCGGGGGGACGCTCGCCAGCGGGGGCGCCGGGCTGGCCATGCTCACTGACAGCCAGGCC	430
QY	935	TGCGCTCTAAGCTCGGCCGACAGCTGGAAACAGTCGACCTAAGTGGCTTCACTGCTTCC	994
Db	431	TGCGCTCTAAGCTCGGCCGACAGCTGGAAACAGTCGACCTAAGTGGCTTCACTGCTTCC	490
QY	995	TGCTGGGCGTGGGCTGGCGGCTGACCC--GGTTTGTACCACTGGGCGG	1043
Db	491	TGCTGGGCGTGGGCTGGCGGCTGACCCCGGGGTTTGTACCACTGGGCGG	540

RESULT 14

LOCUS	BO918283	895 bp	mRNA	linear	EST 20-AUG-2002
DEFINITION	AGAGCNCURT 8880984	NCI_CGAP_Co24	Mus	musculus	CDNA clone
IMAGE	6396337 5',	mRNA	sequence.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 895)	NIH-MGC	http://mgc.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.			

FEATURES

Source

```

/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6396337"
/lab_host="DH10B (r1 phage-resistant)"
/clone_1lib="NCI CGAP_C024"
/site_1="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NCI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

```

ORIGIN

Query Match	22.8%	Score 497.4	DB 5	Length 895
Best Local Similarity	73.6%	Pred. No. 7.1e-107		
Matches 666	Conservative 0	Mismatches 226	Indels 13	Gaps 2
Qy	478	TACACCCGCGCTCAVACACCTTCAGGAATTCAGAAAGAGAGGCCACACGCGAGAGCTAGAG	537	
Db	1	TACACCAACCTTATTCGTCTTCAGGAAGTCAGAGAGAGGCCACACAGAAAGATCTTGAC	60	
Qy	538	TTTGACATGGATAGTGTTCATTATATGGGAGAGGCTGTCCGGACCGGCGAACCCACGCGAG	597	
Db	61	TTTGATATATGACACAGACGATCAATAGAGACAGAGTCTCTCTGGAGCTGTGAACCCCTTCGA	120	
Qy	598	AAGACGCGCGCTGGGGGTCCCGCGCAGTCGCGGCGCTCCGGGTGCTGCGGGGCGCGTGC	657	
Db	121	AAGGTGCGCTTG-----AAGAGCGGAGCGGCGCAGCGCCAGAGAGTGCCTTC	168	
Qy	658	GAGGAGGCGCGGTCCTACGCGCGTGTTCACCTTGTGGGCGCGCGCGGTAGCAATCTTC	717	
Db	169	TGCTGTGGCAAGTTCCTCAAGCGCTGTGCAGACTTCTGGGGGTGCCCCAGTGACTCTTC	228	
Qy	718	ATGGGCAAGTGTCTACGTACTGTCTGTCTCTGCTCTTCTCGCGGGTGTCTGTCTGTG	777	
Db	229	CTGGGTATGTGTGTCAGTAACTGTCTGTCTCTGTCTGTGTGTCCTCAAGTGTGTGTGTG	288	
Qy	778	GATTTCAGCGCGGCGCGCGCGCTCCCTCTGAGGCTGCTCTAATTTCTGGGCTTTCACG	837	
Db	289	GATTTCAGGCCCAAAAGCCAAAGTGTCTCCGAGCTGTCTGTACTTCTGGGGCTTTCACG	348	
Qy	838	CTGCTGTGCGAGGAATCTGCGCAGAGGCTCTGAGCGAGAGCGGAGGCAAGCTTCGCCAGCGG	897	
Db	349	TTGCTGTGCGAGGAGCTGTGCGCAGAGGCGCTGGGTGTGTGAGTGGGGTAGCGCTGCAGTGGG	408	
Qy	898	GGCGCCGCGGCTGGGCCATGTCTCTAAGCCAGGCGCTGCGGCTCTACTCTGGCGGACAGC	957	
Db	409	GGAGGTGTCCGACAGAGCTCCCTCGCGCATGTGGCTGACACTTTCATCTTCAGAAATCC	468	
Qy	958	TGGAACAGATGCGACTAGTGGCTCTACACTGTCTTCCTCTGAGGCGTGGGCTGCCGCTG	1017	
Db	469	TGGAACCAATGTGACTGTGTGCACTGTCACTGTCTTCGTGCTGGGGTATGAGCTGCCGCGTG	528	
Qy	1018	ACCCCGGGTTTGTACCAACTGGGCGGACGTGTCTCTGTGACATGACTTATAGGTTTTCAG	1077	
Db	529	ACCCCTGGGCTTTTGTGACTTGGAGCGGACGCTCTCTGCTGTGACTTATATATCTTTCACA	588	

QY	1078	GTGGCGGCTGCTTCATCTTCACCGGTCAACAAACAGCTGGGGGCCCAATGCGTATCGTG	1137
Db	589	CTGCCCTCGCTGCACATCTTCACGGTGAACAGACGCTGGGGGCCCAATGTCTAATGTC	648
QY	1138	AGCAAGATGATGAAGACGTCGTTCTTCTTCTCTTCTCTCTGCGCGTGTGCTGGTAGCC	1197
Db	649	AGCAAAATGATGAAGAGATGTAATCTTCTTCTCTCTTCTCTCTCTGCGTGTGCTGTAGCT	708
QY	1198	TATGGCGTGCGCACGAGAGGGGCTCTCTGAGCGCACGGGACAGTGAATCTTCCCAAGTATCCTG	1257
Db	709	TATGGGGTGCGCACAGAGGGGATCTGAAGCCCAAGACCGCAGTCTACCGAGTATCCTG	768
QY	1258	CGCCGCGCTTCTTACCCGTCCTTACTCTGCAATC-TTCCGGGAGATTTCCCAAGAGACAT	1316
Db	769	CGCAAGGCTCTTCAACCCGACGAATTTGGAGATCTTTCCGAAATTTCCCAAGAGGAAT	828
QY	1317	GGAGCTGGCCCTCAATGAGACACAGCAATGTCGTGCGAGGCCGCGCTTCTGGGACACACC	1376
Db	829	GGAAGGGGCCCTCAATGATTTCCAGGTAAATGTGCTCAATGGAAGCGGGGCTCCTCGGGCTCAT	888
QY	1377	TCCTG 1381	
Db	889	TCGCG 893	

RESULT 15	625 bp	mRNA	linear	EST 10-JUL-2001
LOCUS	B1199159			
DEFINITION	B1199159	607258878P1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:4894242 5',		
	mRNA sequence.			
ACCESSION	B1199159			
VERSION	B1199159.1	GI:14654180		

SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 625)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES
source

Location/Qualifiers
1. .625

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/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4894242"
/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH MGC 19"
/notes="Organ: brain; Vector: pOT8; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC library."

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ORIGIN

Query Match	22.3%;	Score 485.4;	DB 4;	Length 625;
Best Local Similarity	98.6%;	Pred. NO. 3.5e-99;		

Matches	500	Conservative	0	Mismatches	6	Indels	1	Gaps	1
OY	16	CGGCAAGAGGGCCTTGGGCAAGGCCCCCTTGAGACCACTGCTCTTTGGGCACTGTTGCTG	75						
Db	119	CTGATGTGTGGCCCTTCGGGCAAGGCCCCCTTGAGAGCGACTGCTCTTTGGGCACTGTTGCTG	178						
OY	76	AACA-GGGCAGAGATGGCCATGTACTTCTGGGAGATGGGTTCCAAATGACAGTTTCCCTCAGC	134						
Db	179	AACATGTGTCAAGATGGCCATGTACTTCTGGGAGATGGGTTCCAAATGACAGTTTCCCTCAGC	238						
OY	135	TCTTGGGGCCTGTTTGTCTGCTCCGGGTATGCAAGCCTGAGCCCTGACGCTGAGAGAGC	194						
Db	239	TCTTGGGGCCTGTTTGTCTGCTCCGGGTATGCAAGCCTGAGCCCTGACGCTGAGAGAGC	298						
OY	195	AGCAGGAGGAGAAACCTGSGCGTTCAAGTTTGAAGGGGATGGGCGTTGACCTTTTGGCGA	254						
Db	299	AGCAGGAGGAGAAAGCTGGGCGTTCAAGTTTGAAGGGGATGGGCGTTGACCTTTTGGCGA	358						
OY	255	GTGCTATGCGACAGTAGTAGTGAAGGCGCCGCGCTCTCTCGTCGCTGCGCCGCTGTG	314						
Db	359	GTGCTATGCGACAGTAGTAGTGAAGGCGCCGCGCTCTCTCTCGTCGCTGCGCCGCTGTG	418						
OY	315	GGGGGATGCCACTTGCTCCAGCTGGCCATGCAAGCTGACGCGCGTGCTTTTGGCCCA	374						
Db	419	GGGGGATGCCACTTGCTCCAGCTGGCCATGCAAGCTGACGCGCGTGCTTTTGGCCCA	478						
OY	375	GGATGGGGTAAAGTCTCTGCTGACACAGAAATGTGGTGGGAAATATGGCAGACATACAC	434						
Db	479	GGATGGGGTAAAGTCTCTGCTGACACAGAAATGTGGTGGGAAATATGGCAGACATACAC	538						
OY	435	CATCTGGGCGCTTGATTCGCGCTTCTTTTGGCCCTCACTCATCTACACCCGCTCATCAC	494						
Db	539	CATCTGGGCGCTTGATTCGCGCTTCTTTTGGCCCTCACTCATCTACACCCGCTCATCAC	598						
OY	495	CTTCAAGGAATCAGAGAGAGAGCCAC	521						
Db	599	CTTCAAGGAATCAGAGAGAGAGCCAC	625						

Search completed: June 13, 2005, 08:20:41
 Job time : 4477.1 secs

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Search completed: June 13, 2005, 08:20:41
Job time : 4477.1 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 04:57:16 ; Search time 728.137 Seconds
(without alignments)
17723.358 Million cell updates/sec

Title: US-09-869-486b-25

Perfect score: 2180

Sequence: 1 tcgagccacgaacatcgscgca.....ggaaataaagccattccaga 2180

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: N Geneseqn1980s: *
2: geneseqn1980s: *
3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
6: geneseqn2002as: *
7: geneseqn2002bs: *
8: geneseqn2003as: *
9: geneseqn2003bs: *
10: geneseqn2003cs: *
11: geneseqn2003ds: *
12: geneseqn2004as: *
13: geneseqn2004bs: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2178.8	99.9	2180	3	AAA49921 Human cal
2	1978.8	90.8	3583	11	ADL33391 Human tra
3	1978.8	90.8	3676	12	ADQ83682 Human tum
4	1978.8	90.8	3676	13	ADQ85834 Human tum
5	1978.8	90.8	3676	13	ADQ86998 Human tum
6	1978.8	90.8	3900	5	AAH76383 Human TLC
7	1978.8	90.8	3900	8	ABSS8041 Human tra
8	1978.8	90.8	3900	12	ADH51622 Human 186
9	1978.8	90.8	4061	3	AAA49923 Human cal
10	1978.8	90.8	4061	10	ADH62711 Ca activa
11	1978.8	90.8	4061	13	ADR73511 Human TRP
12	1978.8	90.8	4061	13	ADSL2774 Transient
13	1978.8	90.8	4641	11	ADN39239 Cancer/an
14	1977.2	90.7	2695	6	AAAD32373 Human Trp
15	1977.2	90.7	4042	6	AAAD32372 Human Trp
16	1975.6	90.6	3810	6	ABK32167 Prostate
17	1975.6	90.6	3810	13	ADRE6772 Human pro
18	1975.6	90.6	3810	13	ADRE6869 Human pro
19	1975.6	90.6	3810	13	ADSL2778 Human TRP
20	1975.6	90.6	3898	12	ADL06463 Human tum

ALIGNMENTS

21	1974	90.6	3701	13	ADSL2776	Adsl2776 Transient
22	1968.2	90.3	3599	6	ABK28677	Abk28677 Human CDN
23	1943.8	89.2	2459	12	ADL06424	Adl06424 Human tum
24	1892.2	86.8	3387	5	AAH76384	Aah76384 Human TLC
25	1892.2	86.8	3390	12	ADH51624	Adh51624 Human 186
26	1892.2	86.8	3501	6	ABK92224	Abk92224 Prostate
27	1892.2	86.8	3501	11	ADN39597	Adn39597 Cancer/an
28	1891	86.7	2393	2	AAV26656	Aav26656 Human P51
29	1891	86.7	2393	3	AAAG4090	Aaag4090 Consensus
30	1202	55.1	2176	12	ADQ96621	Adq96621 Human P51
31	1149.8	52.7	1524	2	AAV58585	Aav58585 Prostate
32	1149.8	52.7	1524	2	AAV61200	Aav61200 Full leng
33	1149.8	52.7	1524	3	AAAO6348	Aaao6348 Human imm
34	1149.8	52.7	1524	3	ABSL71253	Absl71253 Human pro
35	1149.8	52.7	1524	4	AAH93464	Aah93464 Human pro
36	1149.8	52.7	1524	4	AAAS3556	Aaas3556 Human pro
37	1149.8	52.7	1524	4	AAH02529	Aah02529 Prostate
38	1149.8	52.7	1524	4	AAH84778	Aah84778 Human pro
39	1149.8	52.7	1524	5	ACAS9365	Acas9365 Prostate
40	1149.8	52.7	1524	5	AAAI0107	Aaai0107 Human pro
41	1149.8	52.7	1524	6	ABL94928	AbL94928 Human pro
42	1149.8	52.7	1524	6	ABSS8637	Abss8637 Prostate
43	1149.8	52.7	1524	8	ACC95092	Acc95092 Prostate
44	1149.8	52.7	1524	10	ADBL3559	Adbl3559 Human pro
45	1149.8	52.7	1524	10	ADG55975	Adg55975 Human pro

RESULT 1
AAA49921 standard; CDN; 2180 BP.

AC	AAA49921;
DT	10-OCT-2000 (first entry)
DE	Human calcium channel SOC-3/CRAC-2 partial cDNA.
DE	
XX	
XX	SOC-3/CRAC-2; calcium channel; human; store operated channel;
KW	calcium release activated channel; therapy; diagnosis;
KM	lymphocyte proliferative disorder; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..2180
FT	/*tag= a
FT	/partial
PN	WC000040614-A2.
XX	
PD	13-JUL-2000.
XX	
PF	20-DEC-1999; 99MO-US029996.
XX	
PR	30-DEC-1998; 98US-0114220P.
PR	29-JAN-1999; 99US-0120018P.
PR	22-JUN-1999; 99US-0140415P.
XX	
PA	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
PI	Scharenberg AM;
XX	
DR	WPI; 2000-465957/40.
DR	P-PDB; AAY95434.
XX	
PT	New SOC/CRAC calcium channel polynucleotides and polypeptides used to
PT	diagnose and treat proliferative disorders associated with the channel,
XX	and to screen for novel modulators of the channel.
XX	
PS	Claim 1(a); Page 90-91; 108pp; English.

XX The present sequence is a partial nucleotide sequence of human SOC-3/CRAC
CC -2 cDNA. A partial open reading frame encodes the C-terminal portion (see
CC AA9544) of SOC-3/CRAC-2, a member of a novel family of store operated
CC channel (SOC) or calcium release activated channel (CRAC) polypeptides
CC that modulate Ca²⁺ flux into and out of a cell, and which may be
CC activated upon depletion of Ca²⁺ from intracellular calcium stores,
CC allowing Ca²⁺ influx into a cell. SOC-3/CRAC-2 (full-length cDNA given in
CC AA9544) is expressed predominantly in the kidney and colon.
CC Compositions for expressing SOC/CRAC calcium channel polypeptides in
CC cells may be useful for treating patients that have reduced extracellular
CC calcium influx into their SOC/CRAC-expressing cells. They will also be
CC useful for delivering therapeutic and/or imaging agents to such cells to
CC modulate proliferation and growth. SOC/CRAC polypeptides also represent
CC targets for designing and/or identifying inhibitors that block lymphocyte
CC proliferation and binding agents that selectively bind to SOC/CRAC
CC polypeptides to which drugs or toxins can be conjugated for delivery to
CC SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used as probes
CC and primers to identify other members of the SOC/CRAC family of calcium
CC channels, as diagnostic reagents for identifying the presence of SOC/CRAC
CC polypeptides in biological samples, as agents for generating SOC/CRAC
CC binding polypeptides, and in gene therapy. Methods for determining the
CC presence, or absence, or stage of a proliferative disorder, e.g. a
CC lymphocyte proliferative disorder
XX
XX Sequence 2180 BP, 365 A; 694 C; 667 G; 451 T; 0 U; 3 Other;

Query Match 99.9%; Score 2178.8; DB 3; Length 2180;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGAGGCCAAGATTGCGACAGAGGCTCGGGCAGGCCCCCTGAGGACCTGTTCTT 60
Db 1 TCGAGGCCAAGATTGCGACAGAGGCTCGGGCAGGCCCCCTGAGGACCTGTTCTT 60
Qy 61 TGGGCACTGTTGCTGAAACAGGSCACAGATGGCATGTACTTCTGGGAATGGGTTCCAT 120
Db 61 TGGGCACTGTTGCTGAAACAGGSCACAGATGGCATGTACTTCTGGGAATGGGTTCCAT 120
Qy 121 GCAGTTTCTCAGCTCTTGGGGGCTGTTGCTGCTCGGGTGATGGSCACGCTGGAGGCT 180
Db 121 GCAGTTTCTCAGCTCTTGGGGGCTGTTGCTGCTCGGGTGATGGSCACGCTGGAGGCT 180
Qy 181 GACGCTGAGGAGGCGACGAGAAAGACCTGCGGTTCAAGTTTGAAGGAGTGGGCTT 240
Db 181 GACGCTGAGGAGGCGACGAGAAAGACCTGCGGTTCAAGTTTGAAGGAGTGGGCTT 240
Qy 241 GACCTCTTGGGAGTGTATGCGACAGTAGAGTGAGGGCTGCCGCTCTCTCCCT 300
Db 241 GACCTCTTGGGAGTGTATGCGACAGTAGAGTGAGGGCTGCCGCTCTCTCCCT 300
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Db 301 CGCTGCCGCTCTGGGGGGATGSCACTTGGCTCCAGCTGGGCGATGCAAGCTGAGCCCGT 360
Qy 361 GCTTCTTGGCCAGAGTGGGTTACGTCCTGCTGACACAGAGTGGTGGGAGATATG 420
Db 361 GCTTCTTGGCCAGAGTGGGTTACGTCCTGCTGACACAGAGTGGTGGGAGATATG 420
Qy 421 GCGACACTACACCATCTGGGCTCTGCTTCTGCTTCTTCTTCTGCTCACTATCTAC 480
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Qy 481 ACCGCGCTCATCCTTCAGGAAATCAGAAAGAGGCCACAGGAGAGACTGAGTTT 540
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Qy 541 GACATGATAGTATTAATGAGGAGAGGCTGTGCGGACGCGGACCCAGCCGAGAG 600
Db 541 GACATGATAGTATTAATGAGGAGAGGCTGTGCGGACGCGGACCCAGCCGAGAG 600
Qy 601 AGCGCGCTGGGAGTCCGCGCAAGTGGGCGCTCGGGTTGCTCGGGGGCGCTGCGGG 660

Db 601 AGCGCGCTGGGAGTCCGCGCAAGTGGGCGCTCGGGTTGCTCGGGGGCGCTGCGGG 660
Qy 661 GGGGCGCGGTCCTAACGCGCTGGTTCATCTTGGGGGCGGCGGTAGACCATCTTCAATG 720
Db 661 GGGGCGCGGTCCTAACGCGCTGGTTCATCTTGGGGGCGGCGGTAGACCATCTTCAATG 720
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Qy 841 CTGTGCGAGAACTGCGCAGAGGCTGAGCGGAGGCGGAGGCTGCGCAGCGGGGCG 900
Db 841 CTGTGCGAGAACTGCGCAGAGGCTGAGCGGAGGCGGAGGCTGCGCAGCGGGGCG 900
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Db 1021 CCGGGTTTGTACACTGCGGCGGAGCTGCTCTGCACTGCACTGATTTTACAGGCTG 1080
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Db 1081 CGGCTGCTTCACTTCACTGCGGCGGAGCTGCTCTGCACTGCACTGATTTTACAGGCTG 1140
Qy 1141 AAGATGATGAAAGAGCTGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200
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Qy 1261 GCGCTCTTCACT 1320
Db 1261 GCGCTCTTCACT 1320
Qy 1321 GTGGCCCTCATGAGGACAGCACTGCTGCTGCGAGGCGGCTTCTGGGACACCTCTCT 1380
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Qy 1381 GGGGCGCAGGCGGAGCAGCTGCTCTCCAGATATCACTGAGTGTGAGTGTGCTCTCT 1440
Db 1381 GGGGCGCAGGCGGAGCAGCTGCTCTCCAGATATCACTGAGTGTGAGTGTGCTCTCT 1440
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Db 1441 GTCACT 1500
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Db 1621 TTGCGCT 1680
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Db 1681 GCCCTCGAGCATTTCCGGGTTTACCTTTCTTAAGAGAGCCGGAAGCTGCTAACGGG 1740
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Db 1741 GAATCGGTGCAATAGAGAACTTTCTGTGCGAGCGCTAGAGCAAGCGGAGAGGAC 1800
Qy 1801 TCCGAGGTCTGAAGCCGACCTCCAGAGAGGTGACTTGGCACTGAAACAGCTGGGACAC 1860
Db 1801 TCCGAGGTCTGAAGCCGACCTCCAGAGAGGTGACTTGGCACTGAAACAGCTGGGACAC 1860
Qy 1861 ATCCGCGAGTACGAACAGCGCTTGAAGTGTGAGCGGGAGTCCAGCACTGTACCTCG 1920
Db 1861 ATCCGCGAGTACGAACAGCGCTTGAAGTGTGAGCGGGAGTCCAGCACTGTACCTCG 1920
Qy 1921 GCCCGCCACCTGGTGGCTTGTCTTGAAGTGAAGCCCAAGTCCATCTGGGCCACTGTC 1980
Db 1921 GCCCGCCACCTGGTGGCTTGTCTTGAAGTGAAGCCCAAGTCCATCTGGGCCACTGTC 1980
Qy 1981 AGGACACCTTTGGAGTGTCTATCTTACAAACAGACATGCGCGCTCTCCAGAAC 2040
Db 1981 AGGACACCTTTGGAGTGTCTATCTTACAAACAGACATGCGCGCTCTCCAGAAC 2040
Qy 2041 CAGTCCAGCTTGAGAGATCAAGGCTGATCCCGCGCTTATCCATCTGAGGCTGC 2100
Db 2041 CAGTCCAGCTTGAGAGATCAAGGCTGATCCCGCGCTTATCCATCTGAGGCTGC 2100
Qy 2101 AGGCTCTTGGGGTAAACAGGACCAAGACCCCTCACCACATCAAGATTCTTCACTGG 2160
Db 2101 AGGCTCTTGGGGTAAACAGGACCAAGACCCCTCACCACATCAAGATTCTTCACTGG 2160
Qy 2161 GGAATATAAGCATTTTCA 2180
Db 2161 GGAATATAAGCATTTTCA 2180

RESULT 2
ADL33391
ID ADL33391 standard; DNA; 3583 BP.
XX
AC ADL33391;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human transporter and ion channel (TRICH) gene #36.
XX
KW anti-HIV; antiallergic; antiinflammatory; antianemic; antiparkinsonian;
KW neurotrophic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
KW immunosuppressive; antichryoid; cytostatic; hepatotropic; dermatological;
KW antidiabetic; aephroretropic; antitumor; thyromimetic; neuroprotective;
KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antiporiatic;
KW utrophalic; ophthalmological; antirheumatic; hemostatic; antibacterial;
KW virucide; protozoacide; fungicide; gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT allele /*tag= a
FT allele /*tag= a
FT allele /*tag= b
FT allele /*tag= b
FT allele /*tag= c
XX
PN MO2003083085-A2.
XX
PD 09-OCT-2003.
XX
PF 27-MAR-2003; 2003MO-US009797.
XX
PR 28-MAR-2002; 2002US-0368840P.
XX
PR 26-APR-2002; 2002US-0375637P.
XX
PA (INCY-) INCYTE CORP.
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XX
PI Marquis JP, Lee SY, Emerling BM, Hafalia AJA, Khare R, Kable AE;
PI Richardson TW, Swarnkar A, Chawla NK, Becha SD, Mason PM;
PI Elliott VS, Rankumar J, Griffin JB, Tran UK, Ison CH, Lindquist EA;
PI Jiang X, Jackson AA, Wilson AD, Jin P, Chang H;
XX
DR WPI: 2003-833535/77.
DR P-PSDB: ADL33332.
XX
PT New human transporters and ion channels (TRICH) and polynucleotides,
PT useful for diagnosing, treating or preventing autoimmune or inflammatory
PT disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, cancer or
PT hepatitis.
XX
XX Claim 12; SEQ ID NO 95; 405bp; English.
XX
CC The invention relates to an isolated polypeptide (I), which is a human
CC intracellular signaling molecule, which is a human intracellular
CC signaling molecule, a naturally occurring amino acid sequence at least 90%
CC -96% identical to it or a biologically active fragment or an immunogenic
CC fragment of the polypeptide. The human TRICH, polynucleotides, agonists
CC and antagonists are useful for diagnosing, treating or preventing
CC disorders associated with aberrant expression of TRICH, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding TRICH are useful for creating transgenic animals
CC to model human disease. This sequence corresponds to the gene encoding
CC one of the proteins of the invention.
XX
SQ Sequence 3583 BP; 633 A; 1119 C; 1124 G; 707 T; 0 U; 0 Other;
XX
Query Match 90.8%; Score 1978.8; DB 11; Length 3583;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;
Qy 16 CGGACGAGGCGCTCGGCGAGGCGCCCTGAGCGACTGCTTTGGGCACTGTGCTG 75
Db 1205 CTGGATCTGGGCTCGGCGAGGCGCCCTGAGCGACTGCTTTGGGCACTGTGCTG 1264
Qy 76 AACAGGCGACAGATGCGCATGTACTTTGGGAGATGGGTTCCATGAGATTCTTCAAGCT 135
Db 1265 AACAGGCGACAGATGCGCATGTACTTTGGGAGATGGGTTCCATGAGATTCTTCAAGCT 1324
Qy 136 CTTGGGCGCTGTTTGTCTCGGGATGATGAGCGACTGAGCGCTGAGCGCTGAGAGGCA 195
Db 1325 CTTGGGCGCTGTTTGTCTCGGGATGATGAGCGACTGAGCGCTGAGAGGCA 194
Qy 196 GCACGAGAGAAAGACTTGGGCTTCAAGTTGAGGGATGGGCGCTTGA 255
Db 1385 GCACGAGAGAAAGACTTGGGCTTCAAGTTGAGGGATGGGCGCTTGA 255
Qy 256 TGCATTCGACAGCTAGGAGGAGGCGCGGCTCTCTCTCGGCGCTCGGCTG 315
Db 1445 TGCATTCGACAGCTAGGAGGAGGCGCGGCTCTCTCTCGGCGCTCGGCTG 315
Qy 316 GGGGATGCACTTGGCTCCAGCTGAGCGCATGAGCGCGGCTCTTGTGAGCCAG 375
Db 1505 GGGGATGCACTTGGCTCCAGCTGAGCGCATGAGCGCGGCTCTTGTGAGCCAG 375
Qy 376 GATGGGATGAGTCTGCTGACACAGAGTGTGGGAGATATGCGACACTACACC 435
Db 1565 GATGGGATGAGTCTGCTGACACAGAGTGTGGGAGATATGCGACACTACACC 435
```

QY	436	ATTGAGGCGCCCTGAGTCTCTGCGCTCTCTTTTGACCTTCCATCTCATTTTAAACACCGGCTCATCAAC	493
Db	1625	ATCTGGGCGCTGAGTCTCGCCCTCTCTTTTGCCCTTCCATCTATTAAACCGGCTCATCAAC	1684
QY	496	TTTCAGGAATTCAGAGAGAGAGCCCAACACCGAGAGAGACTAGATTGACATGATGATGTGTC	555
Db	1685	TTTCAGGAATTCAGAGAGAGAGCCCAACACCGAGAGAGACTAGATTGACATGATGATGTGTC	1744
QY	556	ATTAAATGAGGAGAGGCGCTGTGAGGACGAGCGAACCCAGCCGAGAAACGCGCTGAGGAGTC	615
Db	1745	ATTAAATGAGGAGAGGCGCTGTGAGGAGCGGAGCCAGCCGAGAAACGCGCTGAGGAGTC	1804
QY	616	CGCGGCGAGTGGGCGCGCTTCGAGTGTCTGCGGGGGGCGCTGCGGGGGGCGCGGTGCTTA	675
Db	1805	CGCGGCGAGTGGGCGCGCTTCGAGTGTCTGCGGGGGGCGCTGCGGGGGGCGCGGTGCTTA	1864
QY	676	CGCGGCGTGGTTCACATTCCTGGGGGCGCGCGGAGCATTCCTATAGGGGCAACGTGGTCAACG	735
Db	1865	CGCGGCGTGGTTCACATTCCTGGGGGCGCGCGGAGCATTCCTATAGGGGCAACGTGGTCAACG	1924
QY	736	TACCTGCTGTTCTCTGCTGCTTTTCTCGCGGAGTCTGCTGAGATTTTCAGCGCGGCGCG	795
Db	1925	TACCTGCTGTTCTCTGCTGCTTTTCTCGCGGAGTCTGCTGAGATTTTCAGCGCGGCGCG	1984
QY	796	CCCGGCTCCCTGGAGCTGCTCTATTCTTGGGCTTTCACGCTGCTGTGAGAGAACTG	855
Db	1985	CCCGGCTCCCTGGAGCTGCTCTATTCTTGGGCTTTCACGCTGCTGTGAGAGAACTG	2044
QY	856	CGCCAGGGGCTGAGGCGAGGCGGGGGGAGCCCTCGCACCGGGGGGCGCGGGCGTGGCCAT	915
Db	2045	CGCCAGGGGCTGAGGCGAGGCGGGGGGAGCCCTCGCACCGGGGGGCGCGGGCGTGGCCAT	2104
QY	916	GCCCTCACTGAGGCGACGCGCTGCGCTCTTACCTCGCGGACAGCTGAGAACAGTGCAGACTTA	975
Db	2105	GCCCTCACTGAGGCGACGCGCTGCGCTCTTACCTCGCGGACAGCTGAGAACAGTGCAGACTTA	2164
QY	976	GTCGCTCTCACTGCTCTTCTCTCTGGGGCGTGGGCTGCGGCTGACCCCGGGTTTGTATCAAC	1035
Db	2165	GTCGCTCTCACTGCTCTTCTCTCTGGGGCGTGGGCTGCGGCTGACCCCGGGTTTGTATCAAC	2224
QY	1036	CTGGGCGCGCACGTGCTCTGCGCATCGACTCATAGTTTCAAGGTCGGGCTGCTTCAACATC	1095
Db	2225	CTGGGCGCGCACGTGCTCTGCGCATCGACTCATAGTTTCAAGGTCGGGCTGCTTCAACATC	2284
QY	1096	TTCAACGCTCAACAAACAGCTGGGGGCCAAGATCGTCATCTGTAGAGCAAGATGATGAAGAC	1155
Db	2285	TTCAACGCTCAACAAACAGCTGGGGGCCAAGATCGTCATCTGTAGAGCAAGATGATGAAGAC	2344
QY	1156	GTCGTTCTTCTTCTCTTCTTCTCTCGGCGTGTGAGCTGTAGCCATAGCGTGGCCACGAG	1215
Db	2345	GTCGTTCTTCTTCTCTTCTTCTCTCGGCGTGTGAGCTGTAGCCATAGCGTGGCCACGAG	2404
QY	1216	GGGCGCTCCGAGAGCCACGGGAGCAGTGAATTCCCAAGTATCCCTGGCGGCGGTCTTCAACGT	1275
Db	2405	GGGCGCTCCGAGAGCCACGGGAGCAGTGAATTCCCAAGTATCCCTGGCGGCGGTCTTCAACGT	2464
QY	1276	CCCTAATCTGACAGATCTTTCGGGCGAGTTTCCCAAGAGGACATGAGAGTGGACCTCATGAG	1335
Db	2465	CCCTAATCTGACAGATCTTTCGGGCGAGTTTCCCAAGAGGACATGAGAGTGGACCTCATGAG	2524
QY	1336	CACAGCAACTGCTCGTGGAGCGCGGCTTGTGGGACACCTCTCTGGGGCCCAAGCGGGC	1395
Db	2525	CACAGCAACTGCTCGTGGAGCGCGGCTTGTGGGACACCTCTCTGGGGCCCAAGCGGGC	2584
QY	1396	ACCTGCGCTCCCAAGTATGCCAACTGGGCTGGTGGTGTGCTCTCTGTATCTTCTGTCTC	1455
Db	2585	ACCTGCGCTCCCAAGTATGCCAACTGGGCTGGTGGTGTGCTCTCTGTATCTTCTGTCTC	2644
QY	1456	GTCGCGCAACATCTGCTGCTGATCACTTGTCTATGTCATGTCAGTTACATTCAGGCAAA	1515
Db	2645	GTCGCGCAACATCTGCTGCTGATCACTTGTCTATGTCAGTTACATTCAGGCAAA	2704
QY	1516	GTCAGGGGCAACAGGACTCTTACTGTGAAGGCGACGCTTACCGGCTCATCGGGAATTC	1575

Db	2705	GTACAGGGCCAA CAGCGATCTTACTGGAAGCGCAGCGTTACCGCTTCATCCGGGAATTCC	2766
Oy	1576	CAC TCTCGGCCCGCGCTGACC CCGGCCTTTATACGATCTCCCACTTGACGCTCTGCTC	1635
Db	2765	CAC TCTCGGCCCGCGCTGACC CCGGCCTTTATACGATCTCCCACTTGACGCTCTGCTC	2822
Oy	1636	AGGCAATTTGTG CAGCGCAGCCSGAGACCCCGACCGCTCTCCCGGCCTTGACGATTTC	1695
Db	2825	AGGCAATTTGTG CAGCGCAGCCCGAGGCCCGACCGCTCTCCCGGCCTTGACGATTTC	2884
Oy	1636	CGGGTTTACCTTTCTTAAGGAAGCGAGCGGAAGCTGTCAATGTGGGAATCGGTGATAAG	1755
Db	2885	CGGGTTTACCTTTCTTAAGGAAGCGAGCGGAAGCTGTCAATGTGGGAATCGGTGATAAG	2944
Oy	1756	GAGA ACTTTCTGCTGGCACGCGCTTAGGGACAAGCGGAGAGCGACTCCGAGMGCTGAAG	1815
Db	2945	GAGA ACTTTCTGCTGGCACGCGCTTAGGGACAAGCGGAGAGCGACTCCGAGMGCTGAAG	3004
Oy	1816	CGCAGTCC CAGAAAGTGGACTTTGGCATCTGAACAGCTGGGACACATCCGAGTAGCA	1875
Db	3005	CGCAGTCC CAGAAAGTGGACTTTGGCATCTGAACAGCTGGGACACATCCGAGTAGCA	3066
Oy	1876	CAGCGCTTGA AAGTCTGAGCGGAGGTCCA GCACTTA-----	1915
Db	3065	CAGCGCTTGA AAGTCTGAGCGGAGGTCCA GCACTTA-----	3124
Oy	1916	-----	1915
Db	3125	GCCCCAGGCC CTGAGCCGCTCTGCTTGCTGCCCCCAGSTGGGCGGCCA CCCCCTGACTG	3184
Oy	1916	-----	1915
Db	3185	CTGGGTCCAA AAGACTGAGCCCTGTGGCGGACTTAAGAGAAAGCC CCACAGGGAGTT	3244
Oy	1916	-----CTTGGCCCCCGCACCTTGGTGGCTTTGTCTTG	1948
Db	3245	TTGCTCTTAG AGTAGGCTCATCTGGGCTCTGGGCCCGGCACCTGGTGGCTTTGTCTTG	3304
Oy	1949	AGGTAGGCCCAT GTGCATCTGGGCGCACTGCAGGACCA CACTTTGGGAGTGCATCCTTA	2008
Db	3305	AGGTAGGCCCAT GTGCATCTGGGCGCACTGCAGGACCA CACTTTGGGAGTGCATCCTTA	3364
Oy	2009	CAAAC CAGCATG CCGGCTCTTCCAGAAC CAGTCC CAGCCTTGGAGATCAAGGCT	2068
Db	3365	CAAAC CAGCATG CCGGCTCTTCCAGAAC CAGTCC CAGCCTTGGAGATCAAGGCT	3422
Oy	2069	GGATCCCGG CCGTTATCATCTGGAGCTGCAGGGTCTTTGGGGTAA CAGGACACACAG	2128
Db	3425	GGATCCCGG CCGTTATCATCTGGAGCTGCAGGGTCTTTGGGGTAA CAGGAGCACACAG	3484
Oy	2129	A C C C C T C A C C T C A C A G A T T C C T C A C A C T G G G G A A T T A A G C C A T T T C A G A	2180
Db	3485	A C C C C T C A C C A C T C A C A G A T T C C T C A C A C T G G G A A A T T A A G C C A T T T C A G A	3536

RESULT_3
AD083682
ID AD083682 standard; cDNA, 3676 BP.

AC AD083682;
XX
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #196.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX

PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003NO-US029126.
XX
PR 18-OCT-2002; 2002JUS-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) MU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT Preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 496; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 3676 BP; 627 A; 1148 C; 1171 G; 730 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 12; Length 3676;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

QY 16 CGGCACGAGGCGCTTGGGACGAGCCCTGAGCAGCTGCTTTCTTGGGCACTGTTGCTG 75
DB 1343 CTGGATCTCTGGCTCGGCGAGGCGCCCTGAGCGACCTGCTTCTTGGGCACTGTTGCTG 1402
QY 76 AACAGGCGACAGATGCGCATGACTTCTGGAGATGGGTTTCAATGACATTTCTCACT 135
DB 1403 AACAGGCGACAGATGCGCATGACTTCTGGAGATGGGTTTCAATGACATTTCTCACT 1462
QY 136 CTGGGCGCTGTTGCTGCTCCGGGTGATGCGACGCTGAGCCTGACGCTGAGAGGCA 195

DB 1463 CTGGGCGCTGTTGCTGCTCCGGGTGATGCGACGCTGAGCTGACGCTGAGAGGCA 1522
QY 196 GCACGAGAGAAAGACTGCGGCTTCAAGTTTGAAGGAGATGGGCGTTGACCTCTTTGGGAG 255
DB 1523 GCACGAGAGAAAGACTGCGGCTTCAAGTTTGAAGGAGATGGGCGTTGACCTCTTTGGGAG 1582
QY 256 TGCTATGCGACGATGAGAGTGAAGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 315
DB 1583 TGCTATGCGACGATGAGAGTGAAGGCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1642
QY 316 GGGGATGCGACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 375
DB 1643 GGGGATGCGACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1702
QY 376 GATGGGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 435
DB 1703 GATGGGTACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1762
QY 436 ATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
DB 1763 ATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1822
QY 496 TTGAGAAATCAGAAAGAGAGCCACACGAGAGAGCTAGAGTTGACATGATAGTGTG 555
DB 1823 TTGAGAAATCAGAAAGAGAGCCACACGAGAGAGCTAGAGTTGACATGATAGTGTG 1882
QY 556 ATTATGAGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 615
DB 1883 ATTATGAGAGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1942
QY 616 CCGCGCGAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 675
DB 1943 CCGCGCGAGTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2002
QY 676 CGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735
DB 2003 CGCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2062
QY 736 TACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
DB 2063 TACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2122
QY 796 CCGCGCTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 855
DB 2123 CCGCGCTCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2182
QY 856 CGCAGGAGCTGAGCGAGGCGGAGGCGAGCTGCGCAGCGGAGGCGCGGAGCTGCGCAT 915
DB 2183 CGCAGGAGCTGAGCGAGGCGGAGGCGAGCTGCGCAGCGGAGGCGCGGAGCTGCGCAT 2242
QY 916 GCTCTACTGAGCGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 975
DB 2243 GCTCTACTGAGCGAGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2302
QY 976 GTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1035
DB 2303 GTGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2362
QY 1036 CTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1095
DB 2363 CTGGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2422
QY 1096 TTGACGCTCAACAAAGAGCTGCGGCGCCAGATGCTCATGCTGAGCAAGATGATGAGGAC 1155
DB 2423 TTGACGCTCAACAAAGAGCTGCGGCGCCAGATGCTCATGCTGAGCAAGATGATGAGGAC 2482
QY 1156 GTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1215
DB 2483 GTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2542
QY 1216 GGGCTCTGAGGCGACGAGGAGAGTGAATTTCCAGTATCTGCGCGCGCTCTTCTACCTG 1275

Db 2543 GGGCTCTGAGGCCAGGAGCAGTGACTTCCCAAGATTCGCGCGGCTTTTACCGT 2602
Qy 1276 CCTACCTGAGATTTCTGGGAGATTCCTCCAGAGAGCAGTGAAGTGGCCCTCATGGAG 1335
Db 2603 CCTACCTGAGATTTCTGGGAGATTCCTCCAGAGAGCAGTGAAGTGGCCCTCATGGAG 2662
Qy 1336 CACAGCAATGCTGCTCGAGAGCCCGGCTTCTGGGACACCTCTCTGGGGCCCAAGCGGAC 1395
Db 2663 CACAGCAATGCTGCTCGAGAGCCCGGCTTCTGGGACACCTCTCTGGGGCCCAAGCGGAC 2722
Qy 1396 ACCCTGCTCCCAATATGAGCCAGTGGCTGGGAGGCTGCTGCTGATCTCTCTGCTC 1455
Db 2723 ACCCTGCTCCCAATATGAGCCAGTGGCTGGGAGGCTGCTGCTGATCTCTCTGCTC 2782
Qy 1456 GTGGCCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515
Db 2783 GTGGCCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2842
Qy 1516 GTACAGGGGCAACAGGATCTCTAATGAGAGGCGCAGCGCTTACCGCTCATCCGGGAATTC 1575
Db 2843 GTACAGGGGCAACAGGATCTCTAATGAGAGGCGCAGCGCTTACCGCTCATCCGGGAATTC 2902
Qy 1576 CACTCTGGGCGCGGCTGGCGCGCGCTTATACGCTCATCTCCAGTGGCTGCTGCTGCTC 1635
Db 2903 CACTCTGGGCGCGGCTGGCGCGCGCTTATACGCTCATCTCCAGTGGCTGCTGCTGCTC 2962
Qy 1636 AGGCAATTTGTGAGGCGAGCCGCGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1695
Db 2963 AGGCAATTTGTGAGGCGAGCCCGGAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3022
Qy 1696 CGGGTTTACCTTTCTAAGAAAGCCAGGCGGAAAGCTGCTAAGTGGGAAATCGGTGATTAAG 1755
Db 3023 CGGGTTTACCTTTCTAAGAAAGCCAGGCGGAAAGCTGCTAAGTGGGAAATCGGTGATTAAG 3082
Qy 1756 GAGAACTTTCTGCTGGACGCGCTAGGAGCAAGCGGAGAGGAGTCCGAGAGTGTGAAG 1815
Db 3083 GAGAACTTTCTGCTGGACGCGCTAGGAGCAAGCGGAGAGGAGTCCGAGAGTGTGAAG 3142
Qy 1816 CGCAGTCCCAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1875
Db 3143 CGCAGTCCCAAGAGTGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3202
Qy 1876 CAGCGCTGAAAGTGTGAGAGCGGAGGCTCCAGCAGTGA----- 1915
Db 3203 CAGCGCTGAAAGTGTGAGAGCGGAGGCTCCAGCAGTGAAGCGGCTGCTGAGGAGGCTG 3262
Qy 1916 ----- 1915
Db 3263 GCCAGGCCCTGAGCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3322
Qy 1916 ----- 1915
Db 3323 CCTGGGTCCAAAGACTGAGCCCTGCTGGGAGCTTCAAGAGAAAGCCCCCAAGGGGATT 3382
Qy 1916 -----CCTGGGCCCCCGCAGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1948
Db 3383 TTGCTCTAGAGTAAAGCTCATCTGGGCTCGGCCCCCGCAGCTGTGTGCTGCTGCTGCTG 3442
Qy 1949 AGGTAGGCCCATGCTCATCTGGGCGCAGTCAAGCAACACTTTGGGAGTGCATCCCTTA 2008
Db 3443 AGGTAGGCCCATGCTCATCTGGGCGCAGTCAAGCAACACTTTGGGAGTGCATCCCTTA 3502
Qy 2009 CAAACCAAGATGCGCGGCTCTCTCCAGAAACAGTCCAGCTGGAGAGTCAAGGCT 2068
Db 3503 CAAACCAAGATGCGCGGCTCTCTCCAGAAACAGTCCAGCTGGAGAGTCAAGGCT 3562
Qy 2069 GGATCCGCGGCTTATCTCATCTGAGGCTGAGGCTCTTGGGGTAAACAGGACACAG 2128
Db 3563 GGATCCGCGGCTTATCTCATCTGAGGCTGAGGCTCTTGGGGTAAACAGGACACAG 3622
Qy 2129 ACCCTTACCACTCAAGATTTCTCACTGGGGAATAAAGCCATTTCAGA 2180
Db 3623 ACCCTTACCACTCAAGATTTCTCACTGGGGAATAAAGCCATTTCAGA 3674

RESULT 4
AD085834
ID AD085834 standard; cDNA; 3676 BP.
XX
AC AD085834;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #2703.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
PR 18-OCT-2002; 2002US-0418988P.
PA (GENTH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
PI Wu TD, Zhou Y;
XX
DR WPI; 2004-534300/51.
XX
PT New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.
PS Claim 1; SEQ ID NO 2703; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentially affecting effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing

CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX

Sequence 3676 BP; 627 A; 1148 C; 1171 G; 730 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 13; Length 3676;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

```
QY 16 CGGACGAGGGGCTCGGGGAGGCCCCCTGAGCGACTGCTTCTTGGGCACTGTGCTG 75
DB 1343 CTGAGTCTGGCCCTCGGGGAGGCCCCCTGAGCGACTGCTTCTTGGGCACTGTGCTG 1402
QY 76 AACAGGGGCAAGATGGGCATGTACTTCTGGAGATGGGTTCCAATGAGTTTCTCAAGT 135
DB 1403 AACAGGGGCAAGATGGGCATGTACTTCTGGAGATGGGTTCCAATGAGTTTCTCAAGT 1462
QY 136 CTTGGGGGCTGTGTTGCTCTCCGGGTGATGGACAGCCTGAGCCTGACGCTGAGAGGCA 195
DB 1463 CTTGGGGGCTGTGTTGCTCTCCGGGTGATGGACAGCCTGAGCCTGACGCTGAGAGGCA 1522
QY 196 GCAAGGAGGAAAGACCTGCGGTTCAAGTTTGAAGGAGATGGGCGTTGACCTTTTGGGAG 255
DB 1523 GCAAGGAGGAAAGACCTGCGGTTCAAGTTTGAAGGAGATGGGCGTTGACCTTTTGGGAG 1582
QY 256 TGGTATCGACGAGTGAAGTGAAGGCTGCCGCTCTCTCTCCGTGCTGCTGCTGCTGCTG 315
DB 1583 TGGTATCGACGAGTGAAGTGAAGGCTGCCGCTCTCTCTCCGTGCTGCTGCTGCTGCTG 1642
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DB 1643 GGGGATGSCACTTGGCTCCAGCTGGCCATGCAAGCTGACGCGGTGCTTCTTTGGCCAG 1702
QY 376 GATGGGATGAGTCTCTGTGACACAGAGTGGTGGGAGATATGGCCAGCACTTACACC 435
DB 1703 GATGGGATGAGTCTCTGTGACACAGAGTGGTGGGAGATATGGCCAGCACTTACACC 1762
QY 436 ATCTGGGCTCTGTTCTCGGCTTCTTTGGCTCCACTCATCAACCCGCTCATACACC 495
DB 1763 ATCTGGGCTCTGTTCTCGGCTTCTTTGGCTCCACTCATCAACCCGCTCATACACC 1822
QY 496 TTGAGAAATCATGAAGAGAGACCACACGAGGAGAGTAGATTGATGATGATGTC 555
DB 1823 TTGAGAAATCATGAAGAGAGACCACACGAGGAGAGTAGATTGATGATGATGATGTC 1882
QY 556 ATTAAATGAGAGAGGCTGTGCGGACCGGACCGACCGAGAAAGACGCGCTGGGGTTC 615
DB 1883 ATTAAATGAGAGAGGCTGTGCGGACCGGACCGACCGAGAAAGACGCGCTGGGGTTC 1942
QY 616 CCGCGGCTGTCGGGCGCTCGGGTGTGCTGCGGGGCGCTGCGGGGGGCGCGGTGCTTA 675
DB 1943 CCGCGGCTGTCGGGCGCTCGGGTGTGCTGCGGGGCGCTGCGGGGGGCGCGGTGCTTA 2002
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QY 916 GCCTCACTGAGCGGCTGCGCTTACTCTGCGCAGACAGCTGGAACAGTGGCACTTA 975
DB 2243 GCCTCACTGAGCGGCTGCGCTTACTCTGCGCAGACAGCTGGAACAGTGGCACTTA 2302
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DB 2363 CTGGGCGGACCTGCTCTGATGACCTTCAATGATTTTCAAGTGGCTGCTTCAATC 2422
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QY 1636 AGGCAATTGTCAGGCGGACCCGAGGCGCTCTCTCCGCGCTGAGCATTTTC 1695
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QY 1876 CAGCGCTGAAAAGTGTGAGCGGAGGCTCCAGCACTGTA----- 1915
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QY 1916 ----- 1915
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QY 676 CGCGCTGATTCCACTTCTGGGGCGCGCCGGTAGCACTTTCATGGGCAAGTGTGAGC 735
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 QY 736 TACCTGCTGTTCTGCTGCTTTTCTCGCGGGTGTGCTGTGATTTTCAAGCCGGCCG 795
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 Db 2123 CCGGCTCCCTGGAGGCTGCTCTATTTCTGGGCTTTCAAGCTGCTGTGAGAACTG 2182
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Db 3083 GAGAACTTTTGTGCGAGCGGCTAGGGAGCAAGCGGAGAGCAAGCTCCGAGCGTCTGAAG 3142
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 Db 3503 CAAACCAAGCATGCGCGGCTCTCTCCAGAACAGTCCAGCTGGAGATCAAGGCTT 3562
 QY 2069 GATCCCGGCGGCTTATCCATCTGAGGCTGAGGCTGAGGCTTGGGGTGAACAGGAGCA 2128
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RESULT 6
 AAH76383
 ID AAH76383 standard; cDNA; 3900 BP.
 AC AAH76383;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Human TLCC polypeptide encoding cDNA.
 XX
 KW TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
 KW hepatotropic; cardiant; antiarteriosclerotic; antiinflammatory; vasculide;
 KW cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;
 KW gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 138..3527
 FT /*tag= a
 FT /product= "TLCC polypeptide"
 FT /note= "coding sequence (AAH76384) specifically claimed"
 PN WO200162794-A2.
 PD 30-AUG-2001.
 XX
 PF 20-FEB-2001; 2001MO-US005529.
 XX
 PR 22-FEB-2000; 2000US-00510706.
 PR 31-MAY-2000; 2000US-00583373.
 PR 08-AUG-2000; 2000US-00634669.
 XX

PA (MILL-) MILLENNIUM PHARM INC.
XX Glucksmann MA, Curtis RAJ, Lora JM;
XX MPI: 2001-557700/62.
DR P-PSDB; AAB85974.
XX New isolated nucleic acid encoding a transient receptor potential-like
PT calcium channel for identifying modulators that can be used to treat
PT hepatic or cardiovascular disorders.
XX
PS Claim 1; Fig 1A-D; 160bp; English.
XX
CC The invention provides isolated nucleic acids encoding a human transient
CC receptor potential (TRP) family member, called TRP-like calcium channel
CC (TRPC) polypeptide. The TRPC polypeptide can be expressed by standard
CC recombinant methodology. The TRPC polynucleotides and polypeptide are
CC used to identify modulators that can be used to treat a hepatic or a
CC cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC the liver, hemochromatosis, liver parasite induced disorders, central
CC nervous system disorders, pain disorders, or disorders of cellular
CC growth, differentiation or migration. The TRPC polynucleotides,
CC polypeptide, protein homologs and antibodies to the proteins can be used
CC in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenetics). Anti-TRPC antibodies
CC can isolate TRPC proteins, regulate the bioavailability of TRPC
CC proteins, and modulate TRPC activity. The present sequence represents a
CC cDNA encoding the human TRCC polypeptide
XX
SQ Sequence 3900 BP, 655 A, 1232 C, 1216 G, 795 T, 0 U, 2 Other;
Query Match 90.8%; Score 1978.8; DB 5; Length 3900;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;
QY 16 CGGACAGAGGCGCTGGGAGAGCCCTGAGAGCACTGCTTTTGGGCACTGTGCTG 75
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Db 2070 ATTAATGGGAAAGGCGCTGTGCGGACGCGCGGACCCAGAGAAAGACGCCGCTGGGGGTC 2129
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Db 3030 GTACAGGGCAAGAGCAGTCTCTATGGAAGGCGAGGTTACCGGCTCATCCGGGAATTC 3089
QY 1576 CACTCTGGGCGCGGCTGGCCCGCTTATGCTATCTTCACTTGGCTGCTGCTGCTG 1635
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QY 1636 AGGCAATTTGACAGCGACCCGAGAGCCCGAGCCGCTCTCCCGGCTTCAAGATTTTC 1695

Db 3150 AGGCAATTGTGACAGCGAGCCCGAGCCCGACCGCTCTCCCGGCGCTCGAGCATTTTC 3209
Qy 1696 CGGGTTTACCTTTCTTAAGGAAGCCGAGCGGAGCTGTAACGTGGGAATCGTGCAATTAAG 1755
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Db 3330 CGCAAGCTCCAGAAAGTGAATTGGCACTGAAACAGCTGGGAGACATCCGCGAGTAGAA 3389
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Qy 1916 ----- 1915
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Db 3810 ACCCTGACACTGACAGATTCTCCACACTGGGGAAATTAAGCATTTTCAAG 3861

RESULT 7

ABSS8041 standard; cDNA; 3900 BP.

ABSS8041;

14-FEB-2003 (first entry)

Human transient receptor potential (TRP)-like calcium channel (TLCC).

Human; gene; ss; transient receptor potential-like calcium channel; TRP; TLCC; 18607; calcium signaling; growth; differentiation; SOC; capacitative calcium channel; store-operated calcium channel; SOC; plasma membrane; calcium ion; cytosol; modulator; membrane excitability; action potential; excitation; neurite outgrowth; synaptogenesis; signal transduction; angiogenesis; cell proliferation; vascular tone; gene therapy; diagnosis; cardiovascular disorder; atherosclerosis; rheumatoid arthritis; diabetes; tumor metastasis; psoriasis; rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis; central nervous system disorder; Alzheimer's disease; Parkinson's disease; multiple sclerosis; epilepsy; cancer; cellular proliferation disorder; migration disorder; therapeutic.

Homo sapiens.

Location/Qualifiers

FT 5'UTR 1. .137
FT /*tag= a
FT CDS 138. .3390
FT /*tag= b
FT /product= "TLCC"
FT /note= "This CDS is specifically claimed in claim 1"
FT 3'UTR 3391. .3900
FT /*tag= c
PN US2002142377-A1.
PD 03-OCT-2002.
XX 20-FEB-2001; 2001US-00789481.
XX 22-FEB-2000; 2000US-00510706.
PR 31-MAY-2000; 2000US-00583373.
PR 08-AUG-2000; 2000US-00634669.
XX (GLUC/) GLUCKSMANN M. A.
PA (CURT/) CURTIS R. A. J.
PA (LORA/) LORA J. M.
XX Glucksmann MA, Curtis RAJ, Lora JM;
PI WPI: 2003-102516/09.
DR P-PSDB; ABG72088.
XX
XX Isolated transient receptor potential-like calcium channel polypeptide, useful for treating cardiovascular, hepatic, central nervous system disorders, pain, cellular proliferation, or migration disorder.
PS Claim 1; Fig 1; 80pp; English.
XX
XX The invention discloses an isolated transient receptor potential (TRP)-like calcium channel (TLCC) polypeptide (18607). Calcium signaling has been implicated in the regulation of a variety of cellular responses, such as growth and differentiation. TLCC is a member of the capacitative calcium channel group or store-operated calcium channel (SOC) which is activated in the plasma membrane to import calcium ions from the extracellular environment to the cytosol. The nucleic acids, polypeptides and antibodies of TLCC are useful for detecting its presence in a sample, for identifying a compound which binds to it and identifying a compound which modulates its activity. Modulators of TLCC can be used to modulate membrane excitability, wave forms and frequencies of action potentials, transduction, angiogenesis, neurite outgrowth and synaptogenesis, signal transduction, angiogenesis, endothelial cell proliferation and vascular tone. The nucleic acid and polypeptide are also useful (using gene therapy) for diagnosing and treating cardiovascular disorders, such as atherosclerosis and restenosis, endothelial cell disorders, such as tumor metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic disorders such as hepatitis and cirrhosis, central nervous system disorders, such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and epilepsy, cellular proliferation disorders, such as cancer, and growth, differentiation or migration disorders. TLCC can also be used in predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment (e.g. therapeutic and prophylactic). The sequence presented is the human TLCC, 18607, cDNA
XX
XX Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;
XX
XX Query Match 90.8%; Score 1978.8; DB 8; Length 3900;
XX Best Local Similarity 92.5%; Pred. No. 0;
XX Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;
Qy 16 CGCAGAGGCGCTCGGAGAGCGCCCTGAGAGCACTGCTTTGGGACATGCTG 75
Db 1530 CTGAGTCTGCGCTCGGAGAGCGCCCTGAGAGCACTGCTTTGGGACATGCTG 1589
Qy 76 AACAGGCAAGATGAGCATGCTTCTGAGAGTGGTTCATGAGATTTCTCTAGCT 135
Db 1590 AACAGGCAAGATGAGCATGCTTCTGAGAGTGGTTCATGAGATTTCTCTAGCT 1649

Qy 136 CTTGGGCGCTGTTGCTGCTCCGGGTGATGGCACGCTGAGCCTGACGCTGAGAGGCA 195
Db 1650 CTTGGGCGCTGTTGCTGCTCCGGGTGATGGCACGCTGAGCCTGACGCTGAGAGGCA 1709
Qy 196 GCAAGAGAGAAAGACTGCGCTTCAAGTTTGAAGGGAGATGGGCTTGAACCTCTTTGGCAG 255
Db 1710 GCACGAGAGAAAGACTGCGCTTCAAGTTTGAAGGGAGATGGGCTTGAACCTCTTTGGCAG 1769
Qy 256 TGCTATCGCAGAGATGAGGTGAGGGCTGCGCGCTCTCTCTCGGTGCTGCGCGCTGCG 315
Db 1770 TGCTATCGCAGAGATGAGGTGAGGGCTGCGCGCTCTCTCTCGGTGCTGCGCGCTGCG 1829
Qy 316 GGGGATGCGCACTGCTGCTGCAAGTGCATGCAAGCTGACGCGCGTGCCTTTTGGCCAG 375
Db 1830 GGGGATGCGCACTGCTGCTGCAAGTGCATGCAAGCTGACGCGCGTGCCTTTTGGCCAG 1889
Qy 376 GATGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATATGGCCAGCATACACC 435
Db 1890 GATGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATATGGCCAGCATACACC 1949
Qy 436 ATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Db 1950 ATCTGGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2009
Qy 496 TTCAAGAAATGAGAGAGAGAGCCACACGGAGAGATGAGATTGACATGATAGTGTG 555
Db 2010 TTCAAGAAATGAGAGAGAGAGCCACACGGAGAGATGAGATTGACATGATAGTGTG 2069
Qy 556 ATTATATGGGAAAGGGCTGTGTGGGACCGCGGACCCAGCCGAGAAAGACCCCGTGGGGTTC 615
Db 2070 ATTATATGGGAAAGGGCTGTGTGGGACCGCGGACCCAGCCGAGAAAGACCCCGTGGGGTTC 2129
Qy 616 CCGGCGCAGTGGGGCGTCCGGGATTGCTGCGGGGGCGCGTGGGGGGGGCGCGGCTTA 675
Db 2130 CCGGCGCAGTGGGGCGTCCGGGATTGCTGCGGGGGCGCGTGGGGGGGGCGCGGCTTA 2189
Qy 676 CGCGCGTGGTTCATTGCGGGCGCGCGGTGACCATTTTCATGGGCAAGTGTGACG 735
Db 2190 CGCGCGTGGTTCATTGCGGGCGCGCGGTGACCATTTTCATGGGCAAGTGTGACG 2249
Qy 736 TACCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 795
Db 2250 TACCTGCTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2309
Qy 796 CCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 855
Db 2310 CCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2369
Qy 856 CGCGAGGCGTGAAGCGAGGCGGGGCGAGCCTGCGCAGCGGGGCGCCCGGCGCTGGCCAT 915
Db 2370 CGCGAGGCGTGAAGCGAGGCGGGGCGAGCCTGCGCAGCGGGGCGCCCGGCGCTGGCCAT 2429
Qy 916 GCGTCACTGAGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 975
Db 2430 GCGTCACTGAGCGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2489
Qy 976 GTGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1035
Db 2490 GTGGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2549
Qy 1036 CTGGGCGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1095
Db 2550 CTGGGCGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2609
Qy 1096 TTCAAGGTCAACAAACAGCTGGGGCCCAAGATCGTCACTGAGAGATATGATGAGAGC 1155
Db 2610 TTCAAGGTCAACAAACAGCTGGGGCCCAAGATCGTCACTGAGAGATATGATGAGAGC 2669
Qy 1156 GTGATCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1215
Db 2670 GTGATCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2729

Qy 1216 GGGCTCTGAGGCCACGAGACAGTACTTCCAAAGTACTGCGCGCGCTTCTTACCGT 1275
Db 2730 GGGCTCTGAGGCCACGAGACAGTACTTCCAAAGTACTGCGCGCGCTTCTTACCGT 2789
Qy 1276 CCTTACCTGAGATCTTCTGGGCAATTTCCCAAGAGACATAGACGTGGCCCTTATGAG 1335
Db 2790 CCTTACCTGAGATCTTCTGGGCAATTTCCCAAGAGACATAGACGTGGCCCTTATGAG 2849
Qy 1336 CACAGCAATGCTGCTGAGAGCCGGCTTCTGGGCAACCTCTGGGGGCCAGGCGGC 1395
Db 2850 CACAGCAATGCTGCTGAGAGCCGGCTTCTGGGCAACCTCTGGGGGCCAGGCGGC 2909
Qy 1396 ACTGCGTCTCCAGATAGCCAACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1455
Db 2910 ACTGCGTCTCCAGATAGCCAACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2969
Qy 1456 GTGGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1515
Db 2970 GTGGCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3029
Qy 1516 GTACAGGCAACAGCGATCTCTACTGGAAGCGCAGGCTTACCGCTCATCCGGGAATTC 1575
Db 3030 GTACAGGCAACAGCGATCTCTACTGGAAGCGCAGGCTTACCGCTCATCCGGGAATTC 3089
Qy 1576 CACTCTGCGCCCGGCTGCGCCCGCTTATGCTGATCTTCCACTTGGCGCTTCTGCTC 1635
Db 3090 CACTCTGCGCCCGGCTGCGCCCGCTTATGCTGATCTTCCACTTGGCGCTTCTGCTC 3149
Qy 1636 AGGCAATTGTGACAGGCGACCCGAGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1695
Db 3150 AGGCAATTGTGACAGGCGACCCGAGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3209
Qy 1696 CGGCTTACCTTCTTAAGAAAGCGAGCGGAGCTGCTAAAGTGGGAATCGTGCATTAAG 1755
Db 3210 CGGCTTACCTTCTTAAGAAAGCGAGCGGAGCTGCTAAAGTGGGAATCGTGCATTAAG 3269
Qy 1756 GAGAACTTCTGCTGCGACCGGCTAGAGGACAGCGGAGAGCGACTCGAGMGTCTGAAG 1815
Db 3270 GAGAACTTCTGCTGCGACCGGCTAGAGGACAGCGGAGAGCGACTCGAGMGTCTGAAG 3329
Qy 1816 CGCACGTGCCAGAAAGTGGACTTGGGCACTGAAACAGCTGGGACATTCGGGAAATTAAG 1875
Db 3330 CGCACGTGCCAGAAAGTGGACTTGGGCACTGAAACAGCTGGGACATTCGGGAAATTAAG 3389
Qy 1876 CAGCGCTGAAAGTGTGAGAGCGGAGATCCAGAGTGA----- 1915
Db 3390 CAGCGCTGAAAGTGTGAGAGCGGAGATCCAGAGTGA----- 3449
Qy 1916 ----- 1915
Db 3450 GCCGAGCGCTGAGCGCTGCTGCTGCTGCGCCAGGTGGCGCCACCCCTGACCTG 3509
Qy 1916 ----- 1915
Db 3510 CTTGGGTCAAAAGCTGAGCCCTGCTGCGGACTTCAAGAGAAAGCCCAAGGGGATT 3569
Qy 1916 -----CTGCGGCCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1948
Db 3570 TTGCTCTAAGTAAGCTCATCTGGGCTTGGGCCCTCCGCACTGCTGCTGCTGCTGCTGCTG 3629
Qy 1949 AGGTAGCCCCCATGCTCATCTGGGCGCACTGTCAAGAACCCCTTTGGAGTGTCACTTGA 2008
Db 3630 AGGTAGCCCCCATGCTCATCTGGGCGCACTGTCAAGAACCCCTTTGGAGTGTCACTTGA 3689
Qy 2009 CAAACCAAGATATCCCGGCTCTCTCCAGAAACAGTCTCCAGGCTGGGAGATCAAGGCT 2068
Db 3690 CAAACCAAGATATCCCGGCTCTCTCCAGAAACAGTCTCCAGGCTGGGAGATCAAGGCT 3749
Qy 2069 GGAATCCCGGCGCTTATCTGCTGAGAGGCTGCTTGGGGTAAAGAGGACCAAG 2128
Db 3750 GGAATCCCGGCGCTTATCTGCTGAGAGGCTGCAAGGCTCTTGGGGTAAAGAGGACCAAG 3809
Qy 2129 ACCCTGACCACTCAAGATTCTCTCAACTGGGGAAATAAGCAATTTCAGA 2180

Db 3610 ACCCTCACCACGATTCCTCACACTGGGAAATAAGCCATTTCAGA 3661

RESULT 8
ADH51622
ID ADH51622 standard; cDNA; 3900 BP.

AC ADH51622;

DT 25-MAR-2004 (first entry)

DE Human 18607 protein cDNA sequence.

XX cytosolic; vasotropic; hemostatic; nephrotropic; gastrointestinal-Gen;
XX respiratory-Gen; muscular-Gen; osteopathic; antiinflammatory;
XX immunosuppressive; cardiovascular-Gen; hepatotropic; vitruclide; analgesic;
XX antianaemic; endocrine-Gen; neuroprotective; nootropic; cardiant;
XX gene therapy; cellular proliferative; differentiative disorder; brain;
XX blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;
XX pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;
XX immune disorder; inflammatory disorder; cardiovascular disorder;
XX endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;
XX neoplastic; endocrine disorder; neurological; heart; tissue typing;
XX chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;
XX ss; 18607.

OS Homo sapiens.

PN US2003219806-A1.

PD 27-NOV-2003.

PF 18-MAR-2003; 2003US-00391399.

XX 22-FEB-2000; 2000US-00510706.
XX 07-APR-2000; 2000US-0195734P.
XX 31-MAY-2000; 2000US-00583373.
XX 26-JUN-2000; 2000US-0214176P.
XX 08-AUG-2000; 2000US-00634669.
XX 31-AUG-2000; 2000US-0229036P.
XX 19-SEP-2000; 2000US-023537P.
XX 01-FEB-2001; 2001US-0267076P.
XX 20-FEB-2001; 2001US-00789481.
XX 12-MAR-2001; 2001US-0275078P.
XX 12-MAR-2001; 2001US-0275172P.
XX 06-APR-2001; 2001US-00828035.
XX 26-JUN-2001; 2001US-00891762.
XX 29-AUG-2001; 2001US-00942447.
XX 17-SEP-2001; 2001US-0322983P.
XX 19-SEP-2001; 2001US-00957683.
XX 27-SEP-2001; 2001US-0325854P.
XX 04-DEC-2001; 2001US-0336936P.
XX 31-JAN-2002; 2002US-00262937.
XX 08-MAR-2002; 2002US-00094214.
XX 11-MAR-2002; 2002US-00095139.
XX 17-SEP-2002; 2002US-00245121.
XX 26-SEP-2002; 2002US-00255532.
XX 04-DEC-2002; 2002US-00309804.

XX (MILL-) MILLENNIUM PHARM INC.

PA Glucksmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;

DR P-PSDB; ADH51623.

XX New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,

PT 55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,
PT useful for diagnosing, preventing or treating e.g. proliferative or brain
XX disorders.

PS Claim 1; SEQ ID NO 1; 276pp; English.

XX This invention relates to novel human DNA sequences (designated 18607,
CC 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,
CC 52991, 59914, 59921 or 33751) and the proteins encoded by them. The
CC invention may be useful for the development of compounds with a
CC cytosolic, vasotropic, hemostatic, nephrotropic, gastrointestinal-Gen,
CC respiratory-Gen, muscular-Gen, osteopathic, antiinflammatory,
CC immunosuppressive, cardiovascular-Gen, hepatotropic, vitruclide, analgesic,
CC antianaemic, endocrine-Gen, neuroprotective, nootropic or cardiant
CC activity. In addition, the sequences may be useful for gene therapy. The
CC invention may be useful in diagnosing, preventing or treating disorders
CC characterised by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433,
CC 38554, 57301, 58324, 55063, 52991, 59914, 59921 or 33751 activity, for
CC example cellular proliferative and/or differentiative disorder, brain
CC disorder, blood vessel disorder, platelet disorder, breast disorder,
CC colon disorder, kidney disorder, lung disorder, ovarian disorder,
CC prostate disorder, pancreatic disorder, skeletal muscle disorder,
CC testicular disorder, hormonal disorder, disorder associated with bone
CC metabolism, immune disorder, inflammatory disorder, cardiovascular
CC disorder, endothelial cell disorder, liver disorder, viral disease, pain,
CC metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder,
CC endocrine disorder, neurological disorder or heart disorder. They may
CC also be used in screening assays, tissue typing, chromosomal mapping,
CC predictive medicine or pharmacogenomics. The present sequence is that of
XX the cDNA which encodes the human 18607 protein of the invention.

SQ Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

Query Match 90.8%; Score 1978.8; DB 12; Length 3900;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

QY 16 CGGCACGAGGCGCTCGGCGAGGCGCCCTGGAGGACCTGCTTTGGGCACTTGTCTG 75
DB 1530 CTGATGCTGCGCTCGGCGAGGCGCCCTGGAGGACCTGCTTTGGGCACTTGTCTG 1589
QY 76 AACAGGCGACAGATGAGCATGTACTTCTGAGAGTGGGTTCCATGAGTTTCTCAAGT 135
DB 1590 AACAGGCGACAGATGAGCATGTACTTCTGAGAGTGGGTTCCATGAGTTTCTCAAGT 1649
QY 136 CTTGGGCGCTGTTGCTGCTCCGGGATGAGGACGCTGAGGCTGACGCTGAGAGGCA 195
DB 1650 CTTGGGCGCTGTTGCTGCTCCGGGATGAGGACGCTGAGGCTGACGCTGAGAGGCA 1709
QY 196 GCACGAGGAGAAAGACTGCGCTTCAAGTTGAGAGGAGTGGCGTTGACCTTTGGCGAG 255
DB 1710 GCACGAGGAGAAAGACTGCGCTTCAAGTTGAGAGGAGTGGCGTTGACCTTTGGCGAG 1769
QY 256 TGCATGCGACAGTGAAGTGAAGGCGCCGCTCTCTCCGTCGTCGCCGCTGTG 315
DB 1770 TGCATGCGACAGTGAAGTGAAGGCGCCGCTCTCTCCGTCGTCGCCGCTGTG 1829
QY 316 GGGGATGCCACTTGCCCTCCAGCTGAGCATGACGACCGGTCCTTTTGGCCAG 375
DB 1830 GGGGATGCCACTTGCCCTCCAGCTGAGCATGACGACCGGTCCTTTTGGCCAG 1889
QY 376 GATGGGATACAGTCTGCTGACACAGAGTGTGGGAGATATGCGACACTACACC 435
DB 1890 GATGGGATACAGTCTGCTGACACAGAGTGTGGGAGATATGCGACACTACACC 1949
QY 436 ATCTGGGCGCTGTTCTCGGCTTTTGGCTTCCACTCATACACCGCCATACACC 495
DB 1950 ATCTGGGCGCTGTTCTCGGCTTTTGGCTTCCACTCATACACCGCCATACACC 2009
QY 496 TTCAGGAATCAGAAAGAGAGCCACACGAGGAGAGCTAGATTGTCATGATAGTGC 555
DB 2010 TTCAGGAATCAGAAAGAGAGCCACACGAGGAGAGCTAGATTGTCATGATAGTGC 2069
QY 556 ATTAATGGGAGAGGCGCTGTGCGAGCGGCGACCTACGCGGAGAAAGCGCGTGGGGGTC 615
DB 2070 ATTAATGGGAGAGGCGCTGTGCGAGCGGCGACCTACGCGGAGAAAGCGCGTGGGGGTC 2129
QY 616 CCGCGCAGTCGGGCGCTCGGGGTTGCTGCGGGGGCGCTGCGGGGGCGCGCGTGTGCTA 675

Db	2130	CGCGCCAGTGGGGCCGTCGGGGTTCGCGGGGGCCGTCGGGGGGCGCGGGCTTA	21888
OY	676	CGCGCTGGTTCATTCTGAGGCGCGCGGTGACCATCTTCATGGGCAACGTGTACG	735
Db	2190	CGCGCTGGTTCATTCTGAGGCGCGCGGTGACCATCTTCATGGGCAACGTGTACG	2249
OY	736	TACCTGCTGTTCCTGCTGCTTTTCTCGGGGTGCTGCTGAGATTTCCAGCCGGCCG	795
Db	2250	TACCTGCTGTTCCTGCTGCTTTTCTCGGGGTGCTGCTGAGATTTCCAGCCGGCCG	2309
OY	796	CCCGGCTCCCTGAGCTGTGCTCTAATTCTGAGCTTTCACGCTGCTGGAGGAATG	855
Db	2310	CCCGGCTCCCTGAGCTGTGCTCTAATTCTGAGCTTTCACGCTGCTGGAGGAATG	2368
OY	856	CGCCAGGGCTGAGCGGAGCGGGGCAAGCTCGCAGCGGGGGCCCGGGCTGGCCAT	915
Db	2370	CGCCAGGGCTGAGCGGAGCGGGGCAAGCTCGCAGCGGGGGCCCGGGCTGGCCAT	2429
OY	916	GCCTCACTGAGCAGCGCTTGCGCTTACCTCGCGACAGCTGGAACCACTGCGACTTA	975
Db	2430	GCCTCACTGAGCAGCGCTTGCGCTTACCTCGCGACAGCTGGAACCACTGCGACTTA	2489
OY	976	GTGGCTCACTGCTTCCTCGGGGCTGGGCTGCGGGCTGACCCCGGGTTTGACAC	1035
Db	2490	GTGGCTCACTGCTTCCTCGGGGCTGGGCTGCGGGCTGACCCCGGGTTTGACAC	2549
OY	1036	CTGGGCGCACGTGCTCTGTCATGCACTTACGTATGATTTTCAAGGTCGGCTCTTCACTC	1095
Db	2550	CTGGGCGCACGTGCTCTGTCATGCACTTACGTATGATTTTCAAGGTCGGCTCTTCACTC	2609
OY	1096	TTCAACGTCAACAAACAGCTGGGGCCCAAGATCGTCATGTGAGCAAGATGAGAGAC	1155
Db	2610	TTCAACGTCAACAAACAGCTGGGGCCCAAGATCGTCATGTGAGCAAGATGAGAGAC	2659
OY	1156	GTGTTCTTCTTCCTCTCTCTCGGCGGTGGTGGCTGATGAGCTATGGGTGGCCACGGAG	1215
Db	2670	GTGTTCTTCTTCTTCTTCTCTCGGCGGTGGTGGCTGATGAGCTATGGGTGGCCACGGAG	2729
OY	1216	GGGCTCTGAGAGGCAACGGGACAGTGACTTCCCAAGTATCTGAGCGCGGTCTTTCACGT	1275
Db	2730	GGGCTCTCTGAGAGGCAACGGGACAGTGACTTCCCAAGTATCTGAGCGCGGTCTTTCACGT	2789
OY	1276	CCCTACCTGACGATCTTGGGCAAGTTCCACAGAGACATGACGTGGCCCTCATGAG	1335
Db	2790	CCCTACCTGACGATCTTGGGCAAGTTCCACAGAGACATGACGTGGCCCTCATGAG	2849
OY	1336	CACAGCACTGCTGTCGGAGCCCGGCTTCTGGGACACCTCTCTGGGGCCCAAGCGGGC	1395
Db	2850	CACAGCACTGCTGTCGGAGCCCGGCTTCTGGGACACCTCTCTGGGGCCCAAGCGGGC	2909
OY	1396	ACCTGCGCTCCAGTATGCCAACGTGGGTGGTGGTGCCTCGTGCATCTTCGTGTC	1455
Db	2910	ACCTGCGCTCCAGTATGCCAACGTGGGTGGTGGTGCCTCGTGCATCTTCGTGTC	2969
OY	1456	GTGGCCAACATCTGCTGGTCAACTTGTCTCATTTGCCATGTTCACTTACACTTGGCAAA	1515
Db	2970	GTGGCCAACATCTGCTGGTCAACTTGTCTCATTTGCCATGTTCACTTACACTTGGCAAA	3029
OY	1516	GTACAGGGCAACAGGATCTTACTGGAAGCGCAGGTTACCGCTCATCCGGAATTTC	1575
Db	3030	GTACAGGGCAACAGGATCTTACTGGAAGCGCAGGTTACCGCTCATCCGGAATTTC	3089
OY	1576	CACCTCGGGCCGGGCTGGGCCCGCCCTTATATGTCATCTCCACTTGGGCTCTGTCTC	1635
Db	3090	CACCTCGGGCCGGGCTGGGCCCGCCCTTATATGTCATCTCCACTTGGGCTCTGTCTC	3149
OY	1636	AGGCAATTTGTCAGAGCGAACCCCGAGCGGTCTCCCGGCGCTTGAGCATTTTC	1695
Db	3150	AGGCAATTTGTCAGAGCGAACCCCGAGCGGTCTCCCGGCGCTTGAGCATTTTC	3209
OY	1696	CGGGTTTACCTTTTGAAGAGCCGAGCGAAGCTGTTAAGTGGGATCGGTGCATTAAG	1755

Db	3210	CGGGTTTACCTTTCTTAAGGAACCGAGCGGAAGCTGCTAAGTGGAAATGCGTGCATTAAG	3265
Qy	1756	GAGAACTTTCTGCTGGCA CGCGCTTAAGGACAAGCGGGAGACGCACTCCGAGMGTCTGAAG	1815
Db	3270	GAGAACTTTCTGCTGGCA CGCGCTTAAGGACAAGCGGGAGACGCACTCCGAGMGTCTGAAG	3328
Qy	1816	CGCAGCTCCGAAAGGTGGAATTTGGCACTTGAAACAGCTGGGACATCCGGAGATACGAA	1875
Db	3330	CGCAGCTCCGAAAGGTGGAATTTGGCACTTGAAACAGCTGGGACATCCGGAGATACGAA	3389
Qy	1876	CAGCGCTGAAAGTCTGGAACGGGAGGTCCAGCAGTGA-----	1915
Db	3330	CAGCGCTGAAAGTCTGGAACGGGAGGTCCAGCAGTGA-----	3449
Qy	1916	-----	1915
Db	3450	GCCGAGGCGCTGAGCGGCTCTGCTTGCCGCCAGAGGTGGGCCGCCACCCCTGACCTTG	3509
Qy	1916	-----	1915
Db	3510	CCTGGGTCCAAAGACTGAGCCCTGTGGGACTTCAAGGAAGCCCCACAGGGGAT	3565
Qy	1916	-----	1948
Db	3570	TTGCTCTTGAAGTAAAGGCTCATCTGGGCTTGCGCCCGCACCTGGTGGCTTGTCTTG	3629
Qy	1949	AGGTGAGCCCGCATGTCACTTGAGGCACTGTCAAGAACCACTTTGGAGTGTCACTCTTA	2008
Db	3630	AGGTGAGCCCGCATGTCACTTGAGGCACTGTCAAGAACCACTTTGGAGTGTCACTCTTA	3689
Qy	2009	CAAAACACAGCATGCCCGGCTCTCCAGAACCAAGTCCAGGCTGGAGATCAAGGCT	2068
Db	3690	CAAAACACAGCATGCCCGGCTCTCCAGAACCAAGTCCAGGCTGGAGATCAAGGCT	3749
Qy	2069	GGATCCCGGCGGTTATCATCTGGAAGCTGCAAGGTCCTTGGGGTAAACAGGGACCAAG	2128
Db	3750	GGATCCCGGCGGTTATCATCTGGAAGCTGCAAGGTCCTTGGGGTAAACAGGGACCAAG	3809
Qy	2129	ACCCCTCACCACTCACAGATTCCTCACACTGGGGGAAATAAGCATTTCAGA	2180
Db	3810	ACCCCTCACCACTCACAGATTCCTCACACTGGGGGAAATAAGCATTTCAGA	3861
RESULT 9			
AAAA9923			
ID	AAAA9923	standard; cDNA; 4061 BP.	
XX	AAAA9923;		
AC			
XX			
DT	10-OCT-2000	(first entry)	
XX			
DE	Human calcium channel SOC-3/CRAC-2 cDNA.		
XX			
KW	SOC-2/CRAC-1, calcium channel; human; store operated channel;		
KM	calcium release activated channel; therapy; diagnosis;		
KW	lymphocyte proliferative disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	382..5979	
FT		/*tag= a	
XX	WO2000040614-A2.		
XX			
PD	13-JUL-2000.		
XX			
PF	20-DEC-1999;	99WO-US029996.	
XX			
PR	30-DEC-1998;	98US-0114220P.	
PR	29-JAN-1999;	99US-0120018P.	
PR	22-JUN-1999;	99US-0140415P.	
XX			

PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

XX Scharenberg AM;

XX WPI, 2000-465957/40.

DR P-SDB; AAY95436.

XX New SOC/CRCAC calcium channel polynucleotides and polypeptides used to
PT diagnose and treat proliferative disorders associated with the channel,
and to screen for novel modulators of the channel.

PS Claim 1(a); Page 99-100; 108pp; English.

XX The present sequence is a full-length nucleotide sequence of human SOC-
3/CRCAC-2 cDNA. It includes an open reading frame encoding SOC-3/CRCAC-2
(see AAY95436), a member of a novel family of store operated channel
(SOC) or calcium release activated channel (CRAC) polypeptides that
modulate Ca²⁺ flux into and out of a cell, and which may be activated
upon depletion of Ca²⁺ from intracellular calcium stores, allowing Ca²⁺
influx into a cell. SOC-3/CRCAC-2 is expressed predominantly in kidney and
colon. Compositions for expressing SOC/CRCAC calcium channel polypeptides
in cells may be useful for treating patients that have reduced
extracellular calcium influx into their SOC/CRCAC-expressing cells. They
will also be useful for delivering therapeutic and/or imaging agents to
such cells to modulate proliferation and growth. SOC/CRCAC polypeptides
also represent targets for designing and/or identifying inhibitors that
block lymphocyte proliferation and binding agents that selectively bind
to SOC/CRCAC polypeptides to which drugs or toxins can be conjugated for
delivery to SOC/CRCAC expressing cells. SOC/CRCAC polynucleotides are used
as probes and primers to identify other members of the SOC/CRCAC family of
calcium channels, as diagnostic reagents for identifying the presence of
SOC/CRCAC polypeptides in biological samples, as agents for generating
SOC/CRCAC binding polypeptides, and in gene therapy. Methods for
determining the level of SOC/CRCAC expression in a subject can be used to
assess the presence, or absence, or stage of a proliferative disorder,
e.g. a lymphocyte proliferative disorder

XX Sequence 4061 BF; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 3; Length 4061;

Best Local Similarity 92.5%; Pred. No. 0;

Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

QY 16 CGGACACAGGGCCCTGGGAGAGCCCTTGAGAGCACTGCTTTTGGGACCTTTCTG 75
DB 1720 CTGAGTGTGCTGCTGGGAGAGCCCTTGAGAGCACTGCTTTTGGGACCTTTCTG 1779
QY 76 AACAGGACAGATGGCATGTAATCTTGAGAGATGGGATTCAGATGCACTTCTCAAGT 135
DB 1780 AACAGGACAGATGGCATGTAATCTTGAGAGATGGGATTCAGATGCACTTCTCAAGT 1839
QY 136 CTGGGGGCTGTTTGTCTCTCGGGATGAGCAGCTTGAGAGCTGAGAGAGCA 195
DB 1840 CTGGGGGCTGTTTGTCTCTCGGGATGAGCAGCTTGAGAGCTGAGAGAGCA 1899
QY 196 GCACGAGAGAAAGCTGGGGCTTCAGATTGAGAGGAGATGGGCTGTGACCTCTTGGGAG 255
DB 1900 GCACGAGAGAAAGCTGGGGCTTCAGATTGAGAGGAGATGGGCTGTGACCTCTTGGGAG 1959
QY 256 TGCTATGACAGAGATGAGAGTGGGCTGCGCTCTCTCGCTGCTGCGCTGCGCTGCG 315
DB 1960 TGCTATGACAGAGATGAGAGTGGGCTGCGCTCTCTCGCTGCTGCGCTGCGCTGCG 2019
QY 316 GGGGATGCCACTTGTCTCTCAAGCTGGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 375
DB 2020 GGGGATGCCACTTGTCTCTCAAGCTGGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 2079
QY 376 GATGGGATCAAGTCTGCTGACACAGAGTGGGAGATGATGAGGACAGATCAACCC 435
DB 2080 GATGGGATCAAGTCTGCTGACACAGAGTGGGAGATGATGAGGACAGATCAACCC 2139
QY 436 ATCTGGGCGCTGCTTCTGCTCTTCTTGTGCTCTCACTCATCTCAACCGGCTATAC 495

DB 2140 ATCTGGGCGCTGCTTCTGCTCTTCTTGTGCTCTCACTCATCTCAACCGGCTATAC 2199
QY 496 TTGAGAAATACAGAGAGAGCCACAGGAGAGAGTGAAGTTTGCATGATAGTGC 555
DB 2200 TTGAGAAATACAGAGAGAGCCACAGGAGAGAGTGAAGTTTGCATGATAGTGC 2259
QY 556 ATTAATGGGAGAGGCTGTGAGGACGAGCCAGCCAGAGAGAGAGAGAGAGAGAGAG 615
DB 2260 ATTAATGGGAGAGGCTGTGAGGACGAGCCAGCCAGAGAGAGAGAGAGAGAGAGAG 2319
QY 616 CCGGCGAGTGGGCGCTGCGGGTGTCTGCGGGGCGCTGCGGGGCGCGGCTGCTTA 675
DB 2320 CCGGCGAGTGGGCGCTGCGGGTGTCTGCGGGGCGCTGCGGGGCGCGGCTGCTTA 2379
QY 676 CGCGGCTGTTTCACTTCTGAGGCGCGCGGATACCATCTTCAATGGGCAACGTGTAC 735
DB 2380 CGCGGCTGTTTCACTTCTGAGGCGCGCGGATACCATCTTCAATGGGCAACGTGTAC 2439
QY 736 TACCTGCTTCTGCTGCTTTTCTGCGGGGCTGCTGAGATTTCAGCCGCGCGCG 795
DB 2440 TACCTGCTTCTGCTGCTTTTCTGCGGGGCTGCTGAGATTTCAGCCGCGCGCG 2499
QY 796 CCGGCTCCTGAGAGCTGCTTATTTTGGGCTTTTCACTGCTGTCGAGAACTG 855
DB 2500 CCGGCTCCTGAGAGCTGCTTATTTTGGGCTTTTCACTGCTGTCGAGAACTG 2559
QY 856 CGCAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915
DB 2560 CGCAGAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2619
QY 916 GCTCACTGAGAGAGGCTGCGGCTTCACTGCGCGAGCTGAGAGCAAGTGCAGCTTA 975
DB 2620 GCTCACTGAGAGAGGCTGCGGCTTCACTGCGCGAGCTGAGAGCAAGTGCAGCTTA 2679
QY 976 GTGAGCTTCACTGCTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1035
DB 2680 GTGAGCTTCACTGCTTCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2739
QY 1036 CTGGGCGGACAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 1095
DB 2740 CTGGGCGGACAGTCTCTGATGATGATGATGATGATGATGATGATGATGATGATG 2799
QY 1096 TTACAGGTCAACAAAGAGCTGGGAGCCAGAGTGTATGAGAGCAAGATGATGAGAG 1155
DB 2800 TTACAGGTCAACAAAGAGCTGGGAGCCAGAGTGTATGAGAGCAAGATGATGAGAG 2859
QY 1156 GTGTTCTTCTTCTTCTTCTTCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 1215
DB 2860 GTGTTCTTCTTCTTCTTCTTCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAG 2919
QY 1216 GGGCTCTGAGGCGACGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1275
DB 2920 GGGCTCTGAGGCGACGAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 2979
QY 1276 CCTTACTGAGATCTTCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1335
DB 2980 CCTTACTGAGATCTTCTGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3039
QY 1336 CACAGCAACTGTCTGTGAGAGCCGAGCTTCTGAGGACACCTCTGAGGAGCCAGGCG 1395
DB 3040 CACAGCAACTGTCTGTGAGAGCCGAGCTTCTGAGGACACCTCTGAGGAGCCAGGCG 3099
QY 1396 ACTGCTCTCCAGATGAGCAACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1455
DB 3100 ACTGCTCTCCAGATGAGCAACTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 3159
QY 1456 GTGGGCAACATCCGAGTGTGAGCACTGATGAGCACTGATGAGCACTGATGAGCA 1515
DB 3160 GTGGGCAACATCCGAGTGTGAGCACTGATGAGCACTGATGAGCACTGATGAGCA 3219
QY 1516 GTACAGGGCAACAGCATCTCTACTGAGAGCGCAGGTTACCGGCTCATCCGGAATT 1575
DB 3220 GTACAGGGCAACAGCATCTCTACTGAGAGCGCAGGTTACCGGCTCATCCGGAATT 3279

Chr	Start (kb)	End (kb)	Gene	Transcript	Accession	Length (bp)	GC (%)	GC3 (%)	GC4 (%)	GC5 (%)	GC6 (%)	GC7 (%)	GC8 (%)	GC9 (%)	GC10 (%)	GC11 (%)	GC12 (%)	GC13 (%)	GC14 (%)	GC15 (%)	GC16 (%)	GC17 (%)	GC18 (%)	GC19 (%)	GC20 (%)	GC21 (%)	GC22 (%)	GC23 (%)	GC24 (%)	GC25 (%)	GC26 (%)	GC27 (%)	GC28 (%)	GC29 (%)	GC30 (%)	GC31 (%)	GC32 (%)	GC33 (%)	GC34 (%)	GC35 (%)	GC36 (%)	GC37 (%)	GC38 (%)	GC39 (%)	GC40 (%)	GC41 (%)	GC42 (%)	GC43 (%)	GC44 (%)	GC45 (%)	GC46 (%)	GC47 (%)	GC48 (%)	GC49 (%)	GC50 (%)	GC51 (%)	GC52 (%)	GC53 (%)	GC54 (%)	GC55 (%)	GC56 (%)	GC57 (%)	GC58 (%)	GC59 (%)	GC60 (%)	GC61 (%)	GC62 (%)	GC63 (%)	GC64 (%)	GC65 (%)	GC66 (%)	GC67 (%)	GC68 (%)	GC69 (%)	GC70 (%)	GC71 (%)	GC72 (%)	GC73 (%)	GC74 (%)	GC75 (%)	GC76 (%)	GC77 (%)	GC78 (%)	GC79 (%)	GC80 (%)	GC81 (%)	GC82 (%)	GC83 (%)	GC84 (%)	GC85 (%)	GC86 (%)	GC87 (%)	GC88 (%)	GC89 (%)	GC90 (%)	GC91 (%)	GC92 (%)	GC93 (%)	GC94 (%)	GC95 (%)	GC96 (%)	GC97 (%)	GC98 (%)	GC99 (%)	GC100 (%)	GC101 (%)	GC102 (%)	GC103 (%)	GC104 (%)	GC105 (%)	GC106 (%)	GC107 (%)	GC108 (%)	GC109 (%)	GC110 (%)	GC111 (%)	GC112 (%)	GC113 (%)	GC114 (%)	GC115 (%)	GC116 (%)	GC117 (%)	GC118 (%)	GC119 (%)	GC120 (%)	GC121 (%)	GC122 (%)	GC123 (%)	GC124 (%)	GC125 (%)	GC126 (%)	GC127 (%)	GC128 (%)	GC129 (%)	GC130 (%)	GC131 (%)	GC132 (%)	GC133 (%)	GC134 (%)	GC135 (%)	GC136 (%)	GC137 (%)	GC138 (%)	GC139 (%)	GC140 (%)	GC141 (%)	GC142 (%)	GC143 (%)	GC144 (%)	GC145 (%)	GC146 (%)	GC147 (%)	GC148 (%)	GC149 (%)	GC150 (%)	GC151 (%)	GC152 (%)	GC153 (%)	GC154 (%)	GC155 (%)	GC156 (%)	GC157 (%)	GC158 (%)	GC159 (%)	GC160 (%)	GC161 (%)	GC162 (%)	GC163 (%)	GC164 (%)	GC165 (%)	GC166 (%)	GC167 (%)	GC168 (%)	GC169 (%)	GC170 (%)	GC171 (%)	GC172 (%)	GC173 (%)	GC174 (%)	GC175 (%)	GC176 (%)	GC177 (%)	GC178 (%)	GC179 (%)	GC180 (%)	GC181 (%)	GC182 (%)	GC183 (%)	GC184 (%)	GC185 (%)	GC186 (%)	GC187 (%)	GC188 (%)	GC189 (%)	GC190 (%)	GC191 (%)	GC192 (%)	GC193 (%)	GC194 (%)	GC195 (%)	GC196 (%)	GC197 (%)	GC198 (%)	GC199 (%)	GC200 (%)	GC201 (%)	GC202 (%)	GC203 (%)	GC204 (%)	GC205 (%)	GC206 (%)	GC207 (%)	GC208 (%)	GC209 (%)	GC210 (%)	GC211 (%)	GC212 (%)	GC213 (%)	GC214 (%)	GC215 (%)	GC216 (%)	GC217 (%)	GC218 (%)	GC219 (%)	GC220 (%)	GC221 (%)	GC222 (%)	GC223 (%)	GC224 (%)	GC225 (%)	GC226 (%)	GC227 (%)	GC228 (%)	GC229 (%)	GC230 (%)	GC231 (%)	GC232 (%)	GC233 (%)	GC234 (%)	GC235 (%)	GC236 (%)	GC237 (%)	GC238 (%)	GC239 (%)	GC240 (%)	GC241 (%)	GC242 (%)	GC243 (%)	GC244 (%)	GC245 (%)	GC246 (%)	GC247 (%)	GC248 (%)	GC249 (%)	GC250 (%)	GC251 (%)	GC252 (%)	GC253 (%)	GC254 (%)	GC255 (%)	GC256 (%)	GC257 (%)	GC258 (%)	GC259 (%)	GC260 (%)	GC261 (%)	GC262 (%)	GC263 (%)	GC264 (%)	GC265 (%)	GC266 (%)	GC267 (%)	GC268 (%)	GC269 (%)	GC270 (%)	GC271 (%)	GC272 (%)	GC273 (%)	GC274 (%)	GC275 (%)	GC276 (%)	GC277 (%)	GC278 (%)	GC279 (%)	GC280 (%)	GC281 (%)	GC282 (%)	GC283 (%)	GC284 (%)	GC285 (%)	GC286 (%)	GC287 (%)	GC288 (%)	GC289 (%)	GC290 (%)	GC291 (%)	GC292 (%)	GC293 (%)	GC294 (%)	GC295 (%)	GC296 (%)	GC297 (%)	GC298 (%)	GC299 (%)	GC300 (%)	GC301 (%)	GC302 (%)	GC303 (%)	GC304 (%)	GC305 (%)	GC306 (%)	GC307 (%)	GC308 (%)	GC309 (%)	GC310 (%)	GC311 (%)	GC312 (%)	GC313 (%)	GC314 (%)	GC315 (%)	GC316 (%)	GC317 (%)	GC318 (%)	GC319 (%)	GC320 (%)	GC321 (%)	GC322 (%)	GC323 (%)	GC324 (%)	GC325 (%)	GC326 (%)	GC327 (%)	GC328 (%)	GC329 (%)	GC330 (%)	GC331 (%)	GC332 (%)	GC333 (%)	GC334 (%)	GC335 (%)	GC336 (%)	GC337 (%)	GC338 (%)	GC339 (%)	GC340 (%)	GC341 (%)	GC342 (%)	GC343 (%)	GC344 (%)	GC345 (%)	GC346 (%)	GC347 (%)	GC348 (%)	GC349 (%)	GC350 (%)	GC351 (%)	GC352 (%)	GC353 (%)	GC354 (%)	GC355 (%)	GC356 (%)	GC357 (%)	GC358 (%)	GC359 (%)	GC360 (%)	GC361 (%)	GC362 (%)	GC363 (%)	GC364 (%)	GC365 (%)	GC366 (%)	GC367 (%)	GC368 (%)	GC369 (%)	GC370 (%)	GC371 (%)	GC372 (%)	GC373 (%)	GC374 (%)	GC375 (%)	GC376 (%)	GC377 (%)	GC378 (%)	GC379 (%)	GC380 (%)	GC381 (%)	GC382 (%)	GC383 (%)	GC384 (%)	GC385 (%)	GC386 (%)	GC387 (%)	GC388 (%)	GC389 (%)	GC390 (%)	GC391 (%)	GC392 (%)	GC393 (%)	GC394 (%)	GC395 (%)	GC396 (%)	GC397 (%)	GC398 (%)	GC399 (%)	GC400 (%)	GC401 (%)	GC402 (%)	GC403 (%)	GC404 (%)	GC405 (%)	GC406 (%)	GC407 (%)	GC408 (%)	GC409 (%)	GC410 (%)	GC411 (%)	GC412 (%)	GC413 (%)	GC414 (%)	GC415 (%)
-----	------------	----------	------	------------	-----------	-------------	--------	---------	---------	---------	---------	---------	---------	---------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------	-----------

FT		/note= "Calcium activated nonselective (CAN)
FT		transmembrane channel protein"
XX		
XX		
PN		US2003143557-A1.
PD		31-JUL-2003.
PX		
PF		08-MAY-2002; 2002US-00142649.
PR		25-JAN-2002; 2002US-0351938P.
PR		02-MAY-2002; 2002US-0377937P.
XX		
PA		(PENN/) PENNER R.
XX		
PI		Penner R;
XX		
DR		WPI; 2003-829785/77.
XX		P-PsDB; ADH62712.
PT		
PT		Screening for candidate bioactive agents involves contacting calcium-
PT		activated nonselective transmembrane channel polypeptide designated as
PT		TRPM4b with candidate agent, determining binding of candidate agent
PT		TRPM4b.
PS		Claim 5; SEQ ID NO 1; 25pp; English.
CC		
CC		The invention describes a method of screening (M1) for a candidate
CC		bioactive agent (CA) modulating monovalent cation (MC) permeability of
CC		the TRPM4b (I) channel. The method involves providing a recombinant cell
CC		(RC) with a nucleic acid encoding (I) and an inducible promoter operably
CC		linked to (I), capable of expressing (I), and comprises an MC indicator,
CC		inducing RC to express (I), contacting RC with MC and CA, and detecting
CC		intracellular levels of MC with an indicator. The method is useful for
CC		screening for a candidate bioactive agent capable of modulating monovalent
CC		cation permeability of a TRPM4b channel. This sequence encodes human
CC		calcium activated nonselective (CAN) transmembrane channel protein
CC		TRPM4b.
SQ		Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;
Query Match	90.8%; Score 1978.8; DB 10; Length 4061;	
Best Local Similarity	92.5%; Pred. No. 0;	
Matches 2157; Conservative	3; Mismatches 5; Indels 167; Gaps 1;	
OY	16	GCGCACGAGGGCTCTGGGACAGGCCCCCTGGAGCAGACTCTTTTGGGCATGTTCGTG 75
Db	1720	CTGATGCTGGCTCTGGGACAGGCCCCCTGGAGCAGACTCTTTTGGGCATGTTCGTG 1779
OY	76	AACAGGGCACAGATGGCCCATGTACTTCTGGAGATGGTGTTCCAATGCAGTTTCTCACT 135
Db	1780	AACAGGGCACAGATGGCCCATGTACTTCTGGAGATGGTGTTCCAATGCAGTTTCTCACT 1839
OY	136	CTTGGGGCTTTTGTCTGCTCCGGGTATGTGCACGCTTGGAGCCTGACGCTGAGAGGCA 195
Db	1840	CTTGGGGCTTTTGTCTGCTCCGGGTATGTGCACGCTTGGAGCCTGACGCTGAGAGGCA 1899
OY	196	GCACGAGGAAGAAGCTTGGCGCTTCAAGTTTATAGGGGATGGGCGTTTGAACCTCTTTGGCGAG 255
Db	1900	GCACGAGGAAGAAGCTTGGCGCTTCAAGTTTATAGGGGATGGGCGTTTGAACCTCTTTGGCGAG 1955S
OY	256	TGCTATGCGACAGTAGAGTGAAGGGGCTGCCGCTCTCTCCGTGCTGCGCGCTGTGG 315
Db	1960	TGCTATGCGACAGTAGAGTGAAGGGGCTGCCGCTCTCTCCGTGCTGCGCGCTGTGG 2019
OY	316	GGGATGCGCACTTGTGCTTCACTGAGCCATGTGAAGCTGACGCCGCTTCTTTGGCCAG 375
Db	2020	GGGATGCGCACTTGTGCTTCACTGAGCCATGTGAAGCTGACGCCGCTTCTTTGGCCAG 2079
OY	376	GATGGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGGAGATTAGGCAGACATAKACC 435
Db	2080	GATGGGGGTACAGTCTCTGCTGACACAGAAAGTGTGGGGAGATTAGGCAGACATAKACC 2139S
OY	436	ATCTGGGCGCTGTCTGCTCTTCTTTTGGCCCTCACTCACTAACAACCGGCTATCAC 495

Db 2140 ATCTGGGCGCTGGGTTCTGGCTTCTTTGGCCCTCCACTCATCTACACCCGCTCATCACC 2199
Qy 496 TTGAGAAATACAGAGAGAGAGCCACACGAGAGAGAGTAGAGTTGACATGATAGTGC 555
Db 2200 TTGAGAAATACAGAGAGAGAGCCACACGAGAGAGAGTAGAGTTGACATGATAGTGC 2259
Qy 556 ATTAATGAG 615
Db 2260 ATTAATGAG 2319
Qy 616 CCGCGGCAAGTCGGGCGCTGGGAGTTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
Db 2320 CCGCGCAAGTCGGGCGCTGGGAGTTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAG 2379
Qy 676 CCGCGCTGGTTCACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 735
Db 2380 CCGCGCTGGTTCACATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2439
Qy 736 TACCTGCTGTTCTGCTGCTTTTCTGCGGAGTGTCTGCTGATTCAGCGGAGAGAGAG 795
Db 2440 TACCTGCTGTTCTGCTGCTTTTCTGCGGAGTGTCTGCTGATTCAGCGGAGAGAGAG 2499
Qy 796 CCGGCTCCCTGAGAGCTGCTCTATTTCTGAGCTTTTCAAGCTGCTGAGAGAGAGAG 855
Db 2500 CCGGCTCCCTGAGAGCTGCTCTATTTCTGAGCTTTTCAAGCTGCTGAGAGAGAGAG 2559
Qy 856 CCGGAG 915
Db 2560 CCGGAG 2619
Qy 916 GCGCTCATGAG 975
Db 2620 GCGCTCATGAG 2679
Qy 976 GTGAGCTCTGAG 1035
Db 2680 GTGAGCTCTGAG 2739
Qy 1036 GTGAG 1095
Db 2740 GTGAG 2799
Qy 1096 TTACAGGTCAG 1155
Db 2800 TTACAGGTCAG 2859
Qy 1156 GTGAGCTCTGAG 1215
Db 2860 GTGAGCTCTGAG 2919
Qy 1216 GGGGCTCTGAG 1275
Db 2920 GGGGCTCTGAG 2979
Qy 1276 CCGTACCTGAG 1335
Db 2980 CCGTACCTGAG 3039
Qy 1336 CAGAGCAACTGAG 1395
Db 3040 CAGAGCAACTGAG 3099
Qy 1396 ACCTGCTGCTCCAGTAG 1455
Db 3100 ACCTGCTGCTCCAGTAG 3159
Qy 1456 GTGAGCAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1515
Db 3160 GTGAGCAACAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3219
Qy 1516 GTACAGGAG 1575

Db 3220 GTACAGGAG 3279
Qy 1576 CACTCTGAG 1635
Db 3280 CACTCTGAG 3339
Qy 1636 AGGCAATTTGAG 1695
Db 3340 AGGCAATTTGAG 3399
Qy 1696 CCGGTTTACCTTTCTTAAG 1755
Db 3400 CCGGTTTACCTTTCTTAAG 3459
Qy 1756 GAGAACTTTGCTGAG 1815
Db 3460 GAGAACTTTGCTGAG 3519
Qy 1816 CCGACGTCCTCAG 1875
Db 3520 CCGACGTCCTCAG 3579
Qy 1876 CAGCGCTGAG 1935
Db 3580 CAGCGCTGAG 3639
Qy 1936 CCGGAG 1995
Db 3640 CCGGAG 3699
Qy 1996 CCGGAG 2055
Db 3700 CCGGAG 2115
Qy 1916 CCGGAG 1975
Db 3760 TTGCTCTAG 3819
Qy 1949 AGGTGAG 2008
Db 3820 AGGTGAG 3879
Qy 2009 CAAACAG 2068
Db 3880 CAAACAG 3939
Qy 2069 GATTCGAG 2128
Db 3940 GATTCGAG 3999
Qy 2129 ACCCTTACAG 2180
Db 4000 ACCCTTACAG 4051

RESULT 11
ADR73511
ID ADR73511 standard; DNA; 4061 BP.
XX ADR73511;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX Human TRPM4, gene.
DE
XX Human TRPM4, gene.
KM
XX TRPM4; apoptosis; inhibitor; tumour; cytosolic; cancer; gene; ds.
OS
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 73..3717
FT CDS /*tag= a
FT /product= "Human TRPM4"


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Db      ||||| 2860 GTGTTCTTCTTCTTCTTCTTCTGCGGTGGAGCTTGGGTGGCCACGAG 2919
Qy      ||||| 1216 GGGCTCTGAGGCGGAGAGAGTACTTCCAGATCTCTGCGCCGGCTTCTTACCGT 1275
Db      ||||| 2920 GGGCTCTGAGGCGGAGAGAGTACTTCCAGATCTCTGCGCCGGCTTCTTACCGT 2979
Qy      ||||| 1276 CCTACCTGAGATCTTCTGCGGAGATTCCTCCAGAGACATGAGCGTGGCCCTCATGGAG 1335
Db      ||||| 2980 CCTACTGAGATCTTCTGCGGAGATTCCTCCAGAGACATGAGCGTGGCCCTCATGGAG 3039
Qy      ||||| 1336 CACAGCAACTGCTCTGTCGAGCCCGGCTTCTGAGCAGACCTCTCGGAGCCAGCGGAGC 1395
Db      ||||| 3040 CACAGCAACTGCTCTGTCGAGCCCGGCTTCTGAGCAGACCTCTCGGAGCCAGCGGAGC 3099
Qy      ||||| 1396 ACCTGCTCTCCAGATATGCCAATGCTGCTGCTCTCTCTGTCATCTTCTGCTC 1455
Db      ||||| 3100 ACCTGCTCTCCAGATATGCCAATGCTGCTGCTCTCTCTGTCATCTTCTGCTC 3159
Qy      ||||| 1456 GTGGCCAAACATCCGTCGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCAT 1515
Db      ||||| 3160 GTGGCCAAACATCCGTCGTCATCTGTCATCTGTCATCTGTCATCTGTCATCTGTCAT 3219
Qy      ||||| 1516 GTACAGGCGCAACAGCGATCTCTTCTGGAAGCGAGCGTTACCGCTCATCCGGAATTC 1575
Db      ||||| 3220 GTACAGGCGCAACAGCGATCTCTTCTGGAAGCGAGCGTTACCGCTCATCCGGAATTC 3279
Qy      ||||| 1576 CACTCTCGGCGCGGCTGGCCCGCCCTTATCTGTCATCTTCTGTCATCTTCTGCTC 1635
Db      ||||| 3280 CACTCTCGGCGCGGCTGGCCCGCCCTTATCTGTCATCTTCTGTCATCTTCTGCTC 3339
Qy      ||||| 1636 AGGCAATGTCAGGCGGAGCCCGGAGCCCGGAGCGTCTCCCGGCTCTGAGCATTC 1695
Db      ||||| 3340 AGGCAATGTCAGGCGGAGCCCGGAGCCCGGAGCGTCTCCCGGCTCTGAGCATTC 3399
Qy      ||||| 1696 CGGCTTACCTTCTTCTGGAAGCGAGCGGAGCTGTCATCTGTCATCTGTCATCTGTCAT 1755
Db      ||||| 3400 CGGCTTACCTTCTTCTGGAAGCGAGCGGAGCTGTCATCTGTCATCTGTCATCTGTCAT 3459
Qy      ||||| 1756 GAGAATCTTCTGTCGGAACGCGCTAGGAGCAAGCGGAGAGCGACTCCGAGMGTCTGAAG 1815
Db      ||||| 3460 GAGAATCTTCTGTCGGAACGCGCTAGGAGCAAGCGGAGAGCGACTCCGAGMGTCTGAAG 3519
Qy      ||||| 1816 CGCACTCTCCAGAGGTGACTTGGCACTGAAAGAGTGGGAGCACTCCGAGMGTCTGAAG 1875
Db      ||||| 3520 CGCACTCTCCAGAGGTGACTTGGCACTGAAAGAGTGGGAGCACTCCGAGMGTCTGAAG 3579
Qy      ||||| 1876 CAGGCTCTGAAAGTGTGAGCGGAGGAGTCCAGCAGTGTGTA----- 1915
Db      ||||| 3580 CAGGCTCTGAAAGTGTGAGCGGAGGAGTCCAGCAGTGTGTA----- 3639
Qy      ||||| 1916 ----- 1915
Db      ||||| 3640 GCCGAGCCCTGAGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3699
Qy      ||||| 1916 ----- 1915
Db      ||||| 3700 CTGGGCTCAAAAGCTGAGCCCTGCTGCGGACTTCAAGAGAAAGCCCCACAGGGAGTT 3759
Qy      ||||| 1916 ----- 1915
Db      ||||| 3760 TTGCTCTTAAGTAAGGCTATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGG 3819
Qy      ||||| 1949 AGGTGAGCCCGATGCTATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 2008
Db      ||||| 3820 AGGTGAGCCCGATGCTATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTGGGCT 3879
Qy      ||||| 2009 CAAAGCAGAGTCCCGGCTCTCCAGAAACAGTCCCAAGCTCTGGAGAGATCAAGGCT 2068
Db      ||||| 3880 CAAAGCAGAGTCCCGGCTCTCCAGAAACAGTCCCAAGCTCTGGAGAGATCAAGGCT 3939
Qy      ||||| 2069 GGATCCCGGAGCCGTTATCTGAGAGCTGAGGAGTCTTGGGAGTAAAGAGGAGCAAG 2128

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Db      3940 GGAATCCCGGCGGCTTATCATCTGAGGCTGACGGGCTCTTGGGTAACAGGACACAG 3999
Qy      2129 ACCCTACACATCAGATTCCTCAGACATGGGGAATAAGCATTTGAGA 2180
Db      4000 ACCCTACACATCAGATTCCTCAGACATGGGGAATAAGCATTTGAGA 4051

RESULT 12
ADSI2774
ID      ADSI2774 standard; cDNA; 4061 BP.
XX
XX      AC      ADSI2774;
XX
XX      DT      16-DEC-2004 (first entry)
XX
XX      DE      Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX
XX      KW      TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
XX      KW      prostate cancer; TRPM4b; gene; ss.
XX
XX      OS      Homo sapiens.
XX
XX      FT      Key Location/Qualifiers
XX      FT      CDS 73..3717
XX      FT      /tag= a
XX      FT      /product= "Human TRPM4b protein"
XX
XX      JP2004267118-A.
XX
XX      PD      30-SEP-2004.
XX
XX      PF      10-MAR-2003; 2003JP-00063578.
XX
XX      PR      10-MAR-2003; 2003JP-00063578.
XX
XX      PA      (SANY ) SANKYO CO LTD.
XX
XX      DR      WPI; 2004-693915/68.
XX      DR      P-PSDB; ADSI2775.
XX
XX      PT      Detecting prostatic cancer, comprises extracting RNA fractions from test
XX      PT      substance of subject and normal human, measuring and analyzing the
XX      PT      difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
XX      PT      expression levels.
XX
XX      PS      Claim 1; SEQ ID NO 1; 126bp; Japanese.
XX
XX      CC      The invention comprises a method for detecting prostatic cancer in a
XX      CC      subject. The method involves measuring the expression levels of specific
XX      CC      genes: transient receptor potential cation channel, subfamily M, member 4
XX      CC      (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
XX      CC      (BUCS1). The method of the invention is useful for the detection and
XX      CC      treatment of prostate cancer. The present cDNA sequence encodes the human
XX      CC      TRPM4b protein of the invention.
XX
XX      SQ      Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 90.8%; Score 1978.8; DB 13; Length 4061;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;

Qy      16 CGGACAGAGGCTCTGGGAGGCGCCCTGAGAGGAGCTGCTTCTTGGGCACTTGTCTG 75
Db      1720 CTGATGCTGAGCTCGGCGAGGCGCCCTGAGAGGAGCTGCTTCTTGGGCACTTGTCTG 1779
Qy      76 AACAGGCGACAGATGCGCATGTACTTCTGAGAGTGGGTTCCATGAGTTTCTCAGCT 135
Db      1780 AACAGGCGACAGATGCGCATGTACTTCTGAGAGTGGGTTCCATGAGTTTCTCAGCT 1839
Qy      136 CTGGGCGCTGTTTCTGCTCTCGGAGTATGCAAGCGCTGAGGCTGACGCTGAGAGGCA 195
Db      1840 CTGGGCGCTGTTTCTGCTCTCGGAGTATGCAAGCGCTGAGGCTGACGCTGAGAGGCA 1899

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OY	196	GACGGAGAAAGACCTGGCGTTCAAGTTTAGGGGAAAGGGCGTTGACCTCTTTGGCGAG	255
Db	1900	GCACGGAGAAAGACCTGGCGTTCAAGTTTAGGGGAAAGGGCGTTGACCTCTTTGGCGAG	1955
OY	256	TGCTATCCAGACAGTAGAGGTAGGGGCTGGCCGACCTCTCTCCGTCGGCGCCGCTGG	315
Db	1960	TGCTATCCAGACAGTAGAGGTAGGGGCTGGCCGACCTCTCTCTCCGTCGGCGCCGCTGG	2015
OY	316	GGGAGTGCACCTTGGCTCCAGCTGGCCATGCAAGCTGACGCCGTCCTTTTGGCCAG	375
Db	2020	GGGAGTGCACCTTGGCTCCAGCTGGCCATGCAAGCTGAGCCCGTCCTTTTGGCCAG	2075
OY	376	GATGGGGATACAGTCTCTGCTGACACAGAACTGTGTGGGAGATATATGGCCAGACTACACC	435
Db	2080	GATGGGGATACAGTCTCTGCTGACACAGAACTGTGTGGGAGATATATGGCCAGACTACACC	2135
OY	436	ATTGGGGCCCTGGTCTCTGCGCTCTCTTTTGGCCCTCCTCACTATCTACCCGCTCATCAC	495
Db	2140	ATTGGGGCCCTGGTCTCTGCGCTCTCTTTTGGCCCTCCTCACTATCTACCCGCTCATCAC	2195
OY	496	TTTCAAGAAATCAGAAAGAGAGGCCACACGGGAGAGAGCTAAGATTGACATGATATGTCTC	555
Db	2200	TTTCAAGAAATCAGAAAGAGAGGCCACACGGGAGAGAGCTAAGATTGACATGATATGTCTC	2255
OY	556	ATTATAGGGGAAAGGGCTGTGCGAGACGGCGGACCCAGCCGAGAAAGCCCGCTGGAGGGTC	615
Db	2260	ATTATAGGGGAAAGGGCTGTGCGAGACGGCGGACCCAGCCGAGAAAGCCCGCTGGAGGGTC	2315
OY	616	CCGCGCCAGTGGGGCGCTGCGGGGTTTCTGCGGGGGGCGCTGCGGGGGGCGCCGATGCTTA	675
Db	2320	CCGCGCCAGTGGGGCGCTGCGGGGTTTCTGCGGGGGGCGCTGCGGGGGGCGCCGATGCTTA	2375
OY	676	CGCGCGTGGTTCACCTTGGGGGGGCGCGGGTACATCTTCATGTGGGAAAGTGGTCAAGC	735
Db	2380	CGCGCGTGGTTCACCTTGGGGGGGCGCGGGTACATCTTCATGTGGGAAAGTGGTCAAGC	2435
OY	736	TACCTGTGTTTCTTGCTGCTGCTTTTCTGCGGGGTCTGCTGTGATTTTCCAGCCGAGCGCG	795
Db	2440	TACCTGTGTTTCTTGCTGCTGCTTTTCTGCGGGGTCTGCTGTGATTTTCCAGCCGAGCGCG	2495
OY	796	CCCGGCTCCCTGGAGCTGTGTCTAATTTTGTGGGCTTTCACGCTGCTGTGGAGAACTGG	855
Db	2500	CCCGGCTCCCTGGAGCTGTGTCTAATTTTGTGGGCTTTCACGCTGCTGTGGAGAACTGG	2555
OY	856	CGCACAAGGACTGAGAGGAGAGCGGGGAGAGCCTCGCACAGGGGGGCGCCGAGCCTTGGCAT	915
Db	2560	CGCACAAGGACTGAGAGGAGAGCGGGGAGAGCCTCGCACAGGGGGGCGCCGAGCCTTGGCAT	2615
OY	916	GCCTACCTGAGCTCAGCGGCTTGGCTCTAAGCTGCGGACAGCTGGAACGAGTGGACCTTA	975
Db	2620	GCCTACCTGAGCTCAGCGGCTTGGCTCTAAGCTGCGGACAGCTGGAACAGTGGACCTTA	2675
OY	976	GTTGGCTTCACCTGTGCTTCCTCGGAGCGTGGGCTGCGGCTGACCCCGGGTTTGTACAC	1035
Db	2680	GTTGGCTTCACCTGTGCTTCCTCGGAGCGTGGGCTGCGGCTGACCCCGGGTTTGTACAC	2735
OY	1036	CTGGGCGGCACTGTCTCTGACATGCACTTACATGATTTTACAGGTGCGGCTGCTTACATC	1095
Db	2740	CTGGGCGGCACTGTCTCTCTGACATGCACTTACATGATTTTACAGGTGCGGCTGCTTACATC	2795
OY	1096	TTTCAAGGTTCACAAACAGCTGGGGGCCAAAGATCTGCATCTGTAGAGAAATGATGAAGAC	1155
Db	2800	TTTCAAGGTTCACAAACAGCTGGGGGCCAAAGATCTGCATCTGTAGAGAAATGATGAAGAC	2855
OY	1156	GTGTTCTTCTTCTCTTCTTCTCTCGGCGCTGTGGCTGTAGCTATAGGCGTGGACCGAG	1215
Db	2860	GTGTTCTTCTTCTCTTCTTCTCTCGGCGCTGTGGCTGTAGCTATAGGCGTGGACCGAG	2915
OY	1216	GAGCTCTTGAAGCCACGGGACAGTACTTCCCAAGATATCTTGGCGCGCTTCTTACCGT	1275
Db	2920	GAGCTCTTGAAGCCACGGGACAGTACTTCCCAAGATATCTTGGCGCGCTTCTTACCGT	2975

QY	1216	CCCTACCTCGAGATCTTTCGGGCAATTTCCCCAGAGAGCAATGAGACGTGGCCCTCATGAG	1335
Db	2980	CCCTACCTCGAGATCTTTCGGGCAATTTCCCCAGAGAGCAATGAGACGTGGCCCTCATGAG	3039
QY	1336	CACAGCAACTCTCTGTGCGAGCCCGGCTTCTGGGCAACCTCTCGGGGCCCAAGCGGC	1395
Db	3040	CACAGCAACTCTCTGTGCGAGCCCGGCTTCTGGGCAACCTCTCGGGGCCCAAGCGGC	3099
QY	1396	ACCTGCGTCTCCAGATATGCCACTGGTGGTGTGCTGCTCTCTCATTTCTCTGTC	1455
Db	3100	ACCTGCGTCTCCAGATATGCCACTGGTGGTGTGCTGCTCTCTCATTTCTCTGTC	3159
QY	1456	GTGGCCAACTCCGCTGGTCAACTGTGCTCAATGTCATGTTCAGTTACACATTCGAGCAA	1515
Db	3160	GTGGCCAACTCCGCTGGTCAACTGTGCTCAATGTCATGTTCAGTTACACATTCGAGCAA	3219
QY	1516	GTACAGGGCAACAGGATCTTCTAGGAAGCGAGCGTATCCGCTTCATCCGGGAATTC	1575
Db	3220	GTACAGGGCAACAGGATCTTCTAGGAAGCGAGCGTATCCGCTTCATCCGGGAATTC	3279
QY	1576	CACCTCGGCGCGGCTGGGCCCGCCCTTTATTCGATATCTCCCATCTGGGCTCTGTC	1635
Db	3280	CACCTCGGCGCGGCTGGGCCCGCCCTTTATTCGATATCTCCCATCTGGGCTCTGTC	3339
QY	1636	AGGCATTTGTGTCAGGCGCACCCSSGAGCCCCAGCGCTCTCCCGGCGCTTCGACATTTTC	1695
Db	3340	AGGCATTTGTGTCAGGCGCACCCCGAGCCCCAGCGCTCTCCCGGCGCTTCGACATTTTC	3399
QY	1696	CGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGCTAATGTTGGAAATCGGTGCATTAAG	1755
Db	3400	CGGTTTACCTTTCTAAGAAAGCCGAGCGGAAGCTGCTAATGTTGGAAATCGGTGCATTAAG	3459
QY	1756	GAGAACTTTCGTCTGGCAACGCGCTAGGAGCAAGCGGGGAGAGCGACTCCGAGMTCTGAAG	1815
Db	3460	GAGAACTTTCGTCTGGCAACGCGCTAGGAGCAAGCGGGGAGAGCGACTCCGAGMTCTGAAG	3519
QY	1816	CGCAGTCCAGAAAGTGAAGCTTGGCACTGTAACAGCTGGGCAATTCGCGAGTACGAA	1875
Db	3520	CGCAGTCCAGAAAGTGAAGCTTGGCACTGTAACAGCTGGGCAATTCGCGAGTACGAA	3579
QY	1876	CAGGCGCTGAAAGTGTGTGAGAGCGGGAAGTCCAGAGTGA-----	1935
Db	3580	CAGGCGCTGAAAGTGTGTGAGAGCGGGAAGTCCAGAGTGA-----	3639
QY	1936	-----	1995
Db	3640	GCCGAGGCGCTGAGCGCGCTGTGCTGTGCCCCAGTGGGCGGCACCCCTGACCTG	3699
QY	1996	-----	2055
Db	3700	CCTGGGTCCAAAGACTGAGCCCTGCTGGCGACTTCAAGAGAAAGCCCCACAGGGGATT	3759
QY	1996	-----CCTGGGCGCCCGCACTGAGTGGCTTTGCTCTG	1948
Db	3760	TTTGCTCCTAGAGTAAAGGTCAATCTGGGCTGTGGCCCCCGACCTGTGTGGCTTGTCTTG	3819
QY	1949	AGGTGAGCCCATGTCTCACTCTGGGCACTGTCAAGAACCACTTTTGGAGTGTCACTTTA	2008
Db	3820	AGGTGAGCCCATGTCTCACTCTGGGCACTGTCAAGAACCACTTTTGGAGTGTCACTTTA	3879
QY	2009	CAAACCAAGAGATCCCGGCTCTCCAGAACCAAGTCCCAAGCTGGAGAGATCAAGGCT	2068
Db	3880	CAAACCAAGAGATCCCGGCTCTCCAGAACCAAGTCCCAAGCTGGAGAGATCAAGGCT	3939
QY	2069	GGATTCGCGGCGGTATTCATCTGAGAGCTGCAAGGCTCTTGGGGTAAACAGAGCAACAG	2128
Db	3940	GGATTCGCGGCGGTATTCATCTGAGAGCTGCAAGGCTCTTGGGGTAAACAGAGCAACAG	3999
QY	2129	ACCCTTCACTACAGATTCCTCACTGCGGGAATTAAGCATTTTCAGA	2180
Db	4000	ACCCTTCACTACAGATTCCTCACTGCGGGAATTAAGCATTTTCAGA	4051

RESULT 13
 ADN39239
 ID ADN39239 standard; CDNA; 4641 BP.
 XX
 AC ADN39239;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Cancer/angiogenesis/fibrosis-related nucleic acid. SEQ ID NO:557.
 XX
 KM Human; differential expression; cancer; angiogenic disorder;
 KM fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KM inflammatory disease; autoimmune disease;
 KM retinal neovascularisation syndrome; scarring; uterine fibroid;
 KM detection; diagnosis; prognosis; drug screening; drug targeting;
 KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;
 KM vlnereary; gene therapy; vaccine; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003042661-A2.
 XX
 PD 22-MAY-2003.
 XX
 PF 13-NOV-2002; 2002WO-US036810.
 XX
 PR 13-NOV-2001; 2001US-0350666P.
 PR 21-NOV-2001; 2001US-0332464P.
 PR 29-NOV-2001; 2001US-0334339P.
 PR 03-DEC-2001; 2001US-0335394P.
 PR 14-DEC-2001; 2001US-0340376P.
 PR 08-JAN-2002; 2002US-0347211P.
 PR 10-JAN-2002; 2002US-0347349P.
 PR 08-FEB-2002; 2002US-0355250P.
 PR 13-FEB-2002; 2002US-0356714P.
 PR 29-FEB-2002; 2002US-0359077P.
 PR 20-MAR-2002; 2002US-0368809P.
 PR 04-APR-2002; 2002US-0370110P.
 PR 12-APR-2002; 2002US-0372246P.
 PR 05-JUN-2002; 2002US-0386614P.
 PR 16-JUL-2002; 2002US-0396839P.
 PR 22-JUL-2002; 2002US-0397755P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
 PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
 XX
 DR WPI; 2003-468649/44.
 DR P-PDB; ADN39240.
 XX
 PT Determining the presence or absence of a pathological cell in a patient,
 PT useful for diagnosing, prognosing or treating cancer, comprises detecting
 PT a nucleic acid in a biological sample.
 XX
 PS Claim 8; SEQ ID NO 557; 1385bp; English.
 XX
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
 CC whose expression is upregulated or downregulated in specific cancers or
 CC other diseases such as angiogenic or fibrotic disorders, and to methods
 CC of determining the presence or absence of a pathological cell in a
 CC patient by detecting a nucleic acid at least 80% identical to those of
 CC the invention or by detecting a polypeptide of the invention. The
 CC invention also relates to expression vectors and host cells comprising a
 CC nucleic acid of the invention; antibodies which specifically bind a
 CC polypeptide of the invention; use of such antibodies for drug targeting;
 CC and methods of screening for modulators of activity or expression of the
 CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
 CC antibodies and methods are useful for diagnosing, prognosing and treating
 CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
 CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may
 CC also be useful in wound healing and in contraception. The present
 CC sequence represents a nucleic acid sequence of the invention.
 XX
 SQ Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;
 Query Match 90.8%; Score 1978.8; DB 11; Length 4641;
 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;
 QY 16 CGGCACAGAGGCGCTGGGACAGGCCCTGAGGAGCACTGCTTTGGGACATGTCG 75
 DB 2272 CTGAGTCTGCTGCTCGGACAGGCCCTGAGGAGCACTGCTTTGGGACATGTCG 2331
 QY 76 AACAGGCGAAGATGGCCATGTAATCTTGTGGAATGGTTCCAAATGAGTTTCTCGAGT 135
 DB 2332 AACAGGCGAAGATGGCCATGTAATCTTGTGGAATGGTTCCAAATGAGTTTCTCGAGT 2391
 QY 136 CTTGGGCGCTGTTTGTCTGCTCCGGGTGATGGACAGCCTGAGCCTGACGCTGAGAGGCA 195
 DB 2392 CTTGGGCGCTGTTTGTCTGCTCCGGGTGATGGACAGCCTGAGCCTGACGCTGAGAGGCA 2451
 QY 196 GCAAGGAGAAAGACCTGGCGTTCAAGTTTGAAGGGAATGGGCGTTGACCTTTGGCGAG 255
 DB 2452 GCAAGGAGAAAGACCTGGCGTTCAAGTTTGAAGGGAATGGGCGTTGACCTTTGGCGAG 2511
 QY 256 TGCATATGACAGAGTGAAGGTGAAGGCTGCCGCTCTCTCTCGTGGCTCCGCTTGG 315
 DB 2512 TGCATATGACAGAGTGAAGGTGAAGGCTGCCGCTCTCTCTCGTGGCTCCGCTTGG 2571
 QY 316 GGGGATGCCACTTGCTCCGACGTGAGCATGACAGCCGCGTGCCTTTTGGCCAG 375
 DB 2572 GGGGATGCCACTTGCTCCGACGTGAGCATGACAGCCGCGTGCCTTTTGGCCAG 2631
 QY 376 GATGGGATACAGTCTCTGTGACACAGAAATGGTGGAGATATGGCAGCACTACACC 435
 DB 2632 GATGGGATACAGTCTCTGTGACACAGAAATGGTGGAGATATGGCAGCACTACACC 2691
 QY 436 ATCTGGGCGCTGCTGCTGCTCTTTTGGCTCTCACTATCTACACCCGCTCATACC 495
 DB 2692 ATCTGGGCGCTGCTGCTGCTCTTTTGGCTCTCACTATCTACACCCGCTCATACC 2751
 QY 496 TTCAGGAATCAGAAAGAGAGCCACAGGAGAGAGCTAGATTGACATGATAGTGC 555
 DB 2752 TTCAGGAATCAGAAAGAGAGCCACAGGAGAGAGCTAGATTGACATGATAGTGC 2811
 QY 556 ATTATGAGGAAGGCGCTGTGAGACGAGCGGACCCAGCCGAGAAAGACGCGTGGGCTC 615
 DB 2812 ATTATGAGGAAGGCGCTGTGAGACGAGCGGACCCAGCCGAGAAAGACGCGTGGGCTC 2871
 QY 616 CGCGCCAGTCGGGCGCTCGGGTTGCTGCGGGGCGCGTGGGGGCGCGGTCCTA 675
 DB 2872 CGCGCCAGTCGGGCGCTCGGGTTGCTGCGGGGCGCGTGGGGGCGCGGTCCTA 2931
 QY 676 CGCGCGGTTTCACATTGAGGGGCGCGGTCACATCTTCAATGGGCAACGTCAGC 735
 DB 2932 CGCGCGGTTTCACATTGAGGGGCGCGGTCACATCTTCAATGGGCAACGTCAGC 2991
 QY 736 TACCTGCTGCTCTGCTGCTTTTCTCGGGGTCCTCTCGTGAATTTCCAGCCGCGCG 795
 DB 2992 TACCTGCTGCTCTGCTGCTTTTCTCGGGGTCCTCTCGTGAATTTCCAGCCGCGCG 3051
 QY 796 CCGGCTCCTGAGAGCTGCTCTTAATTTTGGGCTTTACGCTGCTGTCGAGAACTG 855
 DB 3052 CCGGCTCCTGAGAGCTGCTCTTAATTTTGGGCTTTACGCTGCTGTCGAGAACTG 3111
 QY 856 CGCAGAGGCTGAGGAGGCGGAGCGGAGCGCTGCGAGGCGGCGCGCGGCTGCGCAT 915
 DB 3112 CGCAGAGGCTGAGGAGGCGGAGCGGAGCGCTGCGAGGCGGCGCGCGGCTGCGCAT 3171
 QY 916 GCCTCACTAGAGCAGCGCTGCGCTTCACTTGCAGCAGCTGGAACAGAGTGCAGCTA 975
 DB 3172 GCCTCACTAGAGCAGCGCTGCGCTTCACTTGCAGCAGCTGGAACAGAGTGCAGCTA 3231

[illegible]

QY	1916	-----CTGCGGCCCGGACCCGTCGTGGCCCTTTCCTG	1948
Db	4312	TTGCTCTAGAGTAAGGCTCATCTGGGGCTTGCGCCCGACCTGGTGGCCTTGTCTTG	4371
QY	1949	AGGTAGAGCCCATGTGCATCTGGGCACTGTCAAGACCACTTTGGAGTGTCACTTA	2008
Db	4372	AGGTAGAGCCCATGTGCATCTGGGCACTGTCAAGACCACTTTGGAGTGTCACTTA	4431
QY	2009	CAAACCCANAGATCCCGGCTCCGCCAGAACCAAGTCCGACCTGGAGATCAAGGCT	2068
Db	4432	CAAACCCANAGATCCCGGCTCCGCCAGAACCAAGTCCGACCTGGAGATCAAGGCT	4491
QY	2069	GGATCCCGGCGCGTATTCATCTGAGGCTGCAGAGTCTTTGGGTAAACAGGACCAAG	2128
Db	4492	GGATCCCGGCGCGTATTCATCTGAGGCTGCAGAGTCTTTGGGTAAACAGGACCAAG	4551
QY	2129	ACCCCTCAACCACTCAAGATTCCTCACTAGGGGAATTAAGCCATTCCAGA	2180
Db	4552	ACCCCTCAACCACTCAAGATTCCTCACTAGGGGAATTAAGCCATTCCAGA	4603

RESULT 14

ID AAD32373 standard; cDNA; 2695 BP.

AC AAD32373

DT 18-JUN-2002 (first entry)

DE Human tryp9 splice variant cDNA.

KW Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;

KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; g

KW splice variant; ss.

OS Homo sapiens.

FH	Key	Location/Qualifiers

ET

[illegible]

XX

XX

XX

XX

XX

XX

DR P-PSDB; AAE20284.

PT Novel isolated nucleic acid encoding human prostate carcinoma associated

PT useful as molecular markers for diagnosing prostate cancer.

PS Claim 1; Fig 9B; 70pp; English.

CC The invention relates to human prostate carcinoma associated proteins

CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,

CC useful as molecular markers for diagnosing prostate cancer. Sequences of

CC useful for preventing, treating or ameliorating a prostate tumour,

CC cancer of the lung or melanoma. Polynucleotides of the invention are used
CC in antisense therapy. The present sequence is human Trp5 splice variant
CC cDNA

XX Sequence 2695 BP; 460 A; 873 C; 816 G; 546 T; 0 U; 0 Other;

Query Match 90.7%; Score 1977.2; DB 6; Length 2695;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2156; Conservative 3; Mismatches 6; Indels 167; Gaps 1;

```
QY 16 CGGACAGAGGGCTTCGGGACAGCCCCCTGGAGCACTGCTTCTTTGGGCACTTGCTG 75
DB 342 CTGGATCTGGCCCTCGGGACAGGCCCTCGAGCACTGCTTCTTTGGGCACTTGCTG 401
QY 76 AACGGGACAGAGGCGCATGTAATTTCTGGAGATGGGTTCCATGACATTTCTTCAAGT 135
DB 402 AACGGGACAGAGGCGCATGTAATTTCTGGAGATGGGTTCCATGACATTTCTTCAAGT 461
QY 136 CTGGGGCTCTGTTGCTGCTCCGGGTATGGCAGCCTGGAGCCTGACGCTGAGAGGCA 195
DB 462 CTGGGGCTCTGTTGCTGCTCCGGGTATGGCAGCCTGGAGCCTGACGCTGAGAGGCA 521
QY 196 GCACGAGAGAAAGACTGGCGCTTCAAGTTGAGGGGATGGCGTTGACCTTTTGGCGAG 255
DB 522 GCACGAGAGAAAGACTGGCGCTTCAAGTTGAGGGGATGGCGTTGACCTTTTGGCGAG 581
QY 256 TGCTATGCGACGATGAGGTGAGGGGCTGCCGCTCTCTCTCGGTGCTGCCGCTCTG 315
DB 582 TGCTATGCGACGATGAGGTGAGGGGCTGCCGCTCTCTCTCGGTGCTGCCGCTCTG 641
QY 316 GGGGATGCACTTGCCTCAGACTGGCCATGCAAGCTGACGCGCTGCTTTTGGCCAG 375
DB 642 GGGGATGCACTTGCCTCAGACTGGCCATGCAAGCTGACGCGCTGCTTTTGGCCAG 701
QY 376 GATGGGTACAGTCTGCTGACACAGAACTGTGGGAGATATGGCCAGCATACACC 435
DB 702 GATGGGTACAGTCTGCTGACACAGAACTGTGGGAGATATGGCCAGCATACACC 761
QY 436 ATCTGGGCTCTGTTCTCGCTTCTTTTGGCTCCTCATCTATCAACCCGCTCATACC 495
DB 762 ATCTGGGCTCTGTTCTCGCTTCTTTTGGCTCCTCATCTATCAACCCGCTCATACC 821
QY 496 TTCAGAAATCAGAAAGAGAGCCACACGAGGAGAGCTAGAGTTGACATGATAGTGC 555
DB 822 TTCAGAAATCAGAAAGAGAGCCACACGAGGAGAGCTAGAGTTGACATGATAGTGC 881
QY 556 ATTAAATGGGAAAGGCTGTTCGGGACGAGCCAGCCAGCGAAGAACGCGCTGGGGTC 615
DB 882 ATTAAATGGGAAAGGCTGTTCGGGACGAGCCAGCCAGCGAAGAACGCGCTGGGGTC 941
QY 616 CCGGCGCAGTCCGGGCTCGGAGTTGCTCGGGGGGCGCTGCGGGGGGCGCGCTGCTTA 675
DB 942 CCGGCGCAGTCCGGGCTCGGAGTTGCTCGGGGGGCGCTGCGGGGGGCGCGCTGCTTA 1001
QY 676 CGCGGCTGATTCACCTTCTGGGGGCGCGCGGTGACCACTTTCATGGGCAACGTGTGAGC 735
DB 1002 CGCGGCTGATTCACCTTCTGGGGGCGCGCGGTGACCACTTTCATGGGCAACGTGTGAGC 1061
QY 736 TACCTGCTGTTCTGCTGCTTTTCTCGGGGTGCTGCTGATGATTTTCAAGCCGCGCG 795
DB 1062 TACCTGCTGTTCTGCTGCTTTTCTCGGGGTGCTGCTGATGATTTTCAAGCCGCGCG 1121
QY 796 CCGGCTCTCCGAGAGCTGCTCTATTTCTGGGCTTTCAAGCTGCTGTGAGAGAACTG 855
DB 1122 CCGGCTCTCCGAGAGCTGCTCTATTTCTGGGCTTTCAAGCTGCTGTGAGAGAACTG 1181
QY 856 CGCAGAGGCTGAGCGAGGCGGGGAGAGCTGCGACGCGGGGCGCGGGGCTGGGCAAT 915
DB 1182 CGCAGAGGCTGAGCGAGGCGGGGAGAGCTGCGACGCGGGGCGCGGGGCTGGGCAAT 1241
QY 916 GCCTCACTGAGCAGCGCTGCGCTTACTCTGCGCAGCAGCTGGAACCAAGTGCAGCTTA 975
DB 1242 GCCTCACTGAGCAGCGCTGCGCTTACTCTGCGCAGCAGCTGGAACCAAGTGCAGCTTA 1301
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QY 976 GTGGCTCACTGCTTCTCTGGGCGTGGGCTGCCGGGTGACCCCGGGTTGTACAC 1035
DB 1302 GTGGCTCACTGCTTCTCTGGGCGTGGGCTGCCGGGTGACCCCGGGTTGTACAC 1361
QY 1036 CTGGGCGCACTGCTCTGATCAGCTTCAATGATTTTCAAGGTGCGGCTTCAATC 1095
DB 1362 CTGGGCGCACTGCTCTGATCAGCTTCAATGATTTTCAAGGTGCGGCTTCAATC 1421
QY 1096 TTCAAGGTCAACAAACAGCTGGGGCCCAAGATGCTATCTGAGCAAGATGATAAGAC 1155
DB 1422 TTCAAGGTCAACAAACAGCTGGGGCCCAAGATGCTATCTGAGCAAGATGATAAGAC 1481
QY 1156 GTGTTCTTCTTCTCTCTCTCTCGGGGTGAGCTGATGCTATGAGCGGCGCAGGAG 1215
DB 1482 GTGTTCTTCTTCTCTCTCTCTCGGGGTGAGCTGATGCTATGAGCGGCGCAGGAG 1541
QY 1216 GGGCTCTGAGGCGCACGGGACAGTACCTTCCAAATCTCTGCGCGCGCTTCTACCT 1275
DB 1542 GGGCTCTGAGGCGCACGGGACAGTACCTTCCAAATCTCTGCGCGCGCTTCTACCT 1601
QY 1276 CCTACTGCAAGATCTTTCGGGCAAGATTCACAGAGGACATGACGTGGCCCTCATAGAG 1335
DB 1602 CCTACTGCAAGATCTTTCGGGCAAGATTCACAGAGGACATGACGTGGCCCTCATAGAG 1661
QY 1336 CACAGCAACCTGCTGAGAGCCCGGCTTCTGGGCAACCTCTCGGGGGCCAGGCGGGC 1395
DB 1662 CACAGCAACCTGCTGAGAGCCCGGCTTCTGGGCAACCTCTCGGGGGCCAGGCGGGC 1721
QY 1396 ACCGTGCTCTCCAGTATGCAACATGCGTGGTGTGCTCTCTGATCTTCTGCTC 1455
DB 1722 ACCGTGCTCTCCAGTATGCAACATGCGTGGTGTGCTCTCTGATCTTCTGCTC 1781
QY 1456 GTGGCCAACTCTGCTGCTCAACTTGTCAATTTGCACTTCAACATTTGGCAAA 1515
DB 1782 GTGGCCAACTCTGCTGCTCAACTTGTCAATTTGCACTTCAACATTTGGCAAA 1841
QY 1516 GTACAGGGCAACAGCACTCTCTAGGAAGCCGAGGTTAACCGGCTCATCCGGGAATTC 1575
DB 1842 GTACAGGGCAACAGCACTCTCTAGGAAGCCGAGGTTAACCGGCTCATCCGGGAATTC 1901
QY 1576 CACTCTGGGCGCGCTGCGCGCCCTTATGCTCATCTCCCACTTGGCCCTGCTC 1635
DB 1902 CACTCTGGGCGCGCTGCGCGCCCTTATGCTCATCTCCCACTTGGCCCTGCTC 1961
QY 1636 AGGCAATTGTGACAGGCGACCCGAGAGCCCGACCGCTCTCCCGGCTTGAAGATTC 1695
DB 1962 AGGCAATTGTGACAGGCGACCCGAGAGCCCGACCGCTCTCCCGGCTTGAAGATTC 2021
QY 1696 CGGTTTAACTTTCTTAAGGAAGCCGAGCGGAGAGCTGTAACTGTGGAATGGTGCATTAAG 1755
DB 2022 CGGTTTAACTTTCTTAAGGAAGCCGAGCGGAGAGCTGTAACTGTGGAATGGTGCATTAAG 2081
QY 1756 GAGAACTTTCTGCTGGGACGCGCTAGGGAACAAGCGGAGAGCACTCCGAGMTCTAAG 1815
DB 2082 GAGAACTTTCTGCTGGGACGCGCTAGGGAACAAGCGGAGAGCACTCCGAGMTCTAAG 2141
QY 1816 CGCAGCTCCAGAGAGTGACTTGGCACTGAAACAGCTGGGACACATCCGAGTAGAA 1875
DB 2142 CGCAGCTCCAGAGAGTGACTTGGCACTGAAACAGCTGGGACACATCCGAGTAGAA 2201
QY 1876 CAGCGCTGAAAGTGTGAGCGGAGAGGTCAAGCAGTGA----- 1915
DB 2202 CAGCGCTGAAAGTGTGAGCGGAGAGGTCAAGCAGTGA----- 1915
QY 1916 ----- 1915
DB 2262 GCCGAGGCTTGAAGCGGCTTGTGCTGCTCCCGAGGTGGGCGGACCCCTTGACCTG 2321
QY 1916 ----- 1915
DB 2322 CTGGGTCAGAAAGCTGAGCCCTGTGCGGACTTCAAGAGAAAGCCCGACAGGGGATT 2381
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QY 1916 -----CCTGGCCCCCGCAGCTGTGGCTTGTCTTG 1948
DB 2382 TTGCTCTAGAGTAAGCTCATCTGGGCTCGGCCCGCACCTGTGGCTTGTCTTG 2441
QY 1949 AGGTAGAGCCCATGTCCATCTGGGCGCAGCTGTGAGACCACTTTGGAGTGTCACTTCA 2008
DB 2442 AGGTAGAGCCCATGTCCATCTGGGCGCAGCTGTGAGACCACTTTGGAGTGTCACTTCA 2501
QY 2009 CAATCAGACGATGCGCGGCTCTCCAGAACCACTCCAGCTGGAGAGATCAAGGCT 2068
DB 2502 CAATCAGACGATGCGCGGCTCTCCAGAACCACTCCAGCTGGAGAGATCAAGGCT 2561
QY 2069 GGATCCCGGCGCTTATCTCATCTGAGGCTGAGGCTCTTGGGCTAAAGGACCAAG 2128
DB 2562 GGATCCCGGCGCTTATCTCATCTGAGGCTGAGGCTCTTGGGCTAAAGGACCAAG 2621
QY 2129 ACCCTCAGCACTCAGATTCCTCACACTGGGGAATTAAGCCATTTCAGA 2180
DB 2622 ACCCTCAGCACTCAGATTCCTCACACTGGGGAATTAAGCCATTTCAGA 2673

RESULT 15

ADD32372
ID ADD32372 standard; cDNA; 4042 BP.

XX ADD32372;

DT 18-JUN-2002 (first entry)

XX Human Trp9 protein encoding cDNA.

XX Human; prostate carcinoma associated protein; Trp9, Trp10a; Trp10b;
XX transient receptor potential; calcium channel protein; Trp8a; Trp8b;
XX molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
XX tumour; chorion carcinoma; lung cancer; antisense therapy; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 42..3686

XX FT /tag=a

XX FT /product="Human Trp9 protein"

XX WO200210382-A2.

XX PD 07-FEB-2002.

XX PF 18-JUL-2001; 2001WO-EP008309.

XX PR 28-JUL-2000; 2000US-0221513P.

XX PA (WISS/) WISENBACH U.

XX PI Wisenbach U;

XX WP1: 2002-269013/31.

XX DR P-PSDB; AAE20283.

XX PT Novel isolated nucleic acid encoding human prostate carcinoma associated

XX protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,

XX useful as molecular markers for diagnosing prostate cancer.

XX Claim 1; Fig 9A; 70pp; English.

XX The invention relates to human prostate carcinoma associated proteins
XX such as transient receptor potential (Trp) 8a, Trp8b, Trp9, Trp10a and
XX Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
XX Trp10 are novel calcium channel proteins. Sequences of the invention are
XX useful as molecular markers for diagnosing prostate cancer. Sequences of
XX the invention, their antibodies, inhibitors and antisense molecules are
XX useful for preventing, treating or ameliorating a prostate tumour,
XX endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
XX cancer of the lung or melanoma. Polynucleotides of the invention are used

CC in antisense therapy. The present sequence is human Trp9 protein encoding
CC cDNA
XX
SQ Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;

Query Match 90.7%; Score 1977.2; DB 6; Length 4042;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2156; Conservative 3; Mismatches 6; Indels 167; Gaps 1;

QY 16 CGGACAGAGGCGCTCGGCGAGGCCCGCTGAGCGACCTCTTGGGACATGGCTG 75
DB 1689 CTGAGTGTGAGCTCTCGGCGAGGCCCGCTGAGCGACCTCTTGGGACATGGCTG 1748
QY 76 AACAGGCGACAGATGCGCATGTACTTCTGGAGATGGGTTTCAATGACGTTTCTAGCT 135
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	1974	90.6	3701	9	AT046396 Homo sapi
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ALIGNMENTS

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LOCUS Characterization of a calcium channel family.
DEFINITION BD270154.1 GI:33079922
ACCESSION BD270154
VERSION JP 2002536966-A/13
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Scharenberg A.M.
TITLE Characterization of a calcium channel family
JOURNAL Patent: JP 2002536966-A 13 05-NOV-2002;
BETH ISRAEL DEACONESS MEDICAL CENTER INC
OS Homo sapiens (human)
COMMENT
PN JP 2002536966-A/13
PD 05-NOV-2002
PF 20-DEC-1999 JP 2000592322
PR 30-DEC-1999 US 60/140415
PI ANDREW M SCHARENBERG
PC C12N15/09, A61K31/7115, A61K31/712, A61K31/7125, A61K35/76, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61P14/00, A61P43/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12Q1/48, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, G01N33/566, G01N33/577, C12N15/00, C12N5/00, A61K37/02
PC Characterization of a calcium channel family
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source

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DEFINITION Sequence 1 from Patent WO0162794.
ACCESSION AX235183
VERSION AX235183.1 GI:15593774
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS 1
TITLE Glucksmann, M.A., Curtis, R.A. and Lora, J.M.
JOURNAL Patent: WO 0162794-A 1 30-AUG-2001;
Millennium Pharmaceuticals, Inc. (US)
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1
Nilius, B., Prenen, J., Droogmans, G., Voets, T., Vennkens, R.,
Freichel, M., Wiesenbach, U. and Flockerzi, V.,
Voltage Dependence of the Ca²⁺-activated Cation Channel TRPM4
J. Biol. Chem. 278 (33), 30813-30820 (2003)
22791733
JOURNAL
PUBMED
12799367
2 (bases 1 to 4042)
Wiesenbach, U.
Direct Submission
Submitted (09-JUL-2003) Wiesenbach U., University of the Saarland,
Institute for Pharmacology and Toxicology, 66421 Homburg - Saar,
Saarland, GERMANY
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Db	1929	TGCTATGCGAGCACTGAGAGTGAAGGGCTGCCGCTCTCTCCGTCGTCGTCGCGCTCGG	1988
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Db	1989	GGGATGCGCACTTCTCTCAGCTGAGCCATGCAAGCTGACGCGCGTGCCTTTTGGCCAG	2048
QY	376	GATGGGGGTACAGTCTTGCTGACACAGAAGTGTGGGAGATATGGCCAGCATTACACC	435
Db	2049	GATGGGGGTACAGTCTTGCTGACACAGAAGTGTGGGAGATATGGCCAGCATTACACC	2108
QY	436	ATCTGGGCGCCGTGTTCTGCGCTTTCTTTGGCCTTCCACTATCTACACCCGCTCATACC	495
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QY	496	TTTCAGAGAAATCAGAAAGAGAGCCCAACAGGAGAGAGCTAGAGTTTGACATGATAGTGTG	555
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QY	556	ATTATATGGGAGAGGGCGCTGTGCGAGACGCGCGAGCCAGCCGAGAAAGACGCGCTGGGGGTG	615
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QY	616	CCGGCGCAAGTCGGGCGGTCGGGGTTGCTGCGGGGAGCGCTGCGGGGGCGCCGCTGCTTA	675
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QY	676	CGCGCGTGTTCACCTTCGGGGGGCGCGCGGTGACAAATCTTCAATGGGCAAGTGTGACG	735
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QY	796	CCGGGCTTCCGTGAGAGCTGCTCTATTTCTGGGCTTTACGCTGTGTGAGAGAACTG	855
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Db	2589	GCTTCACGTGAGCCACAGCGCTGCGCTCTTACCTCGCCGACACAGCTGAAACCAATGCGACTTA	2648
QY	976	GTGGCTCTGACCTGCTTCTCTGCGGCGTGAGGCTGCGGCTGACCCCGGGTTTGTACAC	1035
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QY	1036	CTGGGCGCGACATGTCTCTGCAATGACATTCAATGTGTTTCAAGGTGCGGCTGCTTCAATC	1095
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Db	2889	GGGCTCTTGAGGCCACGGGACAGTGACTTCCAAAGTATCTTGCGCCGCTCTTACCGT	2948
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Db	3129	GTGGCCAAACATCTCTGCTGTCAACTTGTCTCATTTGCCATGTTCACATTCATTCGGCAAA	3188
OY	1516	GTACAGGGCAACAGCGATCTCTAAGGCGCAGCGTATACCGCTCATTCGGGAATTC	1575
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Db	3789	AGGTGAGCCCCCATGTGTCATCTGGGACCATCTGAGGACCAACTTTGGGAGTGTCTATCTTAA	3848
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 DEFINITION Characterization of a calcium channel family.
 ACCESSION BD270156.1 GI:33079924
 VERSION JP 2002536966-A/15.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 4061)
 AUTHORS Scharenberg, A.M.
 TITLE Characterization of a calcium channel family
 JOURNAL Patent: JP 2002536966-A 15 05-NOV-2002;
 BETH ISRAEL DEACONESS MEDICAL CENTER INC
 COMMENT OS Homo sapiens (human)
 PN JP 2002536966-A/15
 PD 05-NOV-2002
 PF 20-DEC-1999 JP 2000592322
 PR 30-DEC-1998 US 60/114220, 29-JAN-1999 US 60/120018 PR
 22-JUN-1999 US 60/140415
 PI ANDREW M SCHARENBERG
 PC C12N15/09,A61K31/7115,A61K31/712,A61K31/7125,A61K35/76,A61K38/
 PC 00,
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 PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12Q1/48,C12Q1/
 PC 68,G01N33/15,
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 CC Characterization of a calcium channel family
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
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 Best Local Similarity 92.5%; Pred. No. 0;
 Matches 2157; Conservative 3; Mismatches 5; Indels 167; Gaps 1;
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 Db 1720 CTGATGCTGGCCCTCGGGAGAGGGCCCTGGAGCGAAGCTGCTTTGGGCACTGTGGTG 1779
 Qy 76 AAGAGGACAGATGGCCATGCTTGGAGATGGGTTCATGACGTTCCAGCT 135
 Db 1780 AAGAGGACAGATGGCCATGCTTGGAGATGGGTTCATGACGTTCCAGCT 1839
 Qy 136 CTTGGGGCTTTGCTGCTCCGGTGAATGGACGCTGAGCCTGAAGCTGAGAGCA 195
 Db 1840 CTTGGGGCTTTGCTGCTCCGGTGAATGGACGCTGAGCCTGAAGCTGAGAGCA 1899
 Qy 196 GCACGAGAGAAAGACTGGCGTTCAAGTTGAGGGGAGATGGCGTTGACCTTTGGCGAG 255
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 Qy 256 TGGTATGACAGAGTGAAGGCTGGCGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCG 315
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 Db 2140 ATCTGGGCGCTGTTCTCGCCTTTTGGCCCTCACTCATCTACACCCGCTCATCACC 2199
 Qy 496 TTACAGAAATCAGAGAGAGAGCCCAACGAGAGAGCTAGAGTTGACATGATAGTGC 555
 Db 2200 TTACAGAAATCAGAGAGAGAGCCCAACGAGAGAGCTAGAGTTGACATGATAGTGC 2259
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Dp	3700	CCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTAAAGAGAAAGCCCGCACAGGGGAT	37599
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Dp	3760	TTGCTCTTAAGATAAGCTCATCTGGAGGCTTGCGCCCGCACCTGGTGGCTTGTGCTTG	38119
Qy	1949	AGGTGAGCCCATGTCATCTGGGCGCACTGCAGGACACACCTTGGGAGTGTCACTCTTA	20081
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Dp	3880	CAAAACAAGCATGCCCGGCTCTTCCAGAAACAGTCCACGCTTGGAGATCAAGGCT	39399
Qy	2069	GGATTCCHGGCCGTTATCTCATCTGGAGGCTGAAGGTCCTTGGGGTAAACAGGACACAG	21281
Dp	3940	GGATTCCHGGCCGTTATCTCATCTGGAGGCTGAAGGTCCTTGGGGTAAACAGGACACAG	39999
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RESULT 5	AF497623	4061 bp	mRNA	linear	PRI 10-MAY-2002
LOCUS	AF497623				
DEFINITION	Homo sapiens caton channel TRPM4B (TRPM4B)				
ACCESSION	AF497623				
VERSION	AF497623.1	GI:20265878			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE AUTHORS	TITLE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 4061)	
Launay, P., Fleig, A., Perraud, A. L., Scharenberg, A. M., Penner, R. and Kline, J. P.	TRPM4 is a Ca2+-activated nonselective cation channel mediating cell membrane depolarization
JOURNAL MEDLINE	Cell 109 (3), 397-407 (2002)
PUBMED	12015988
REFERENCE AUTHORS	2 (bases 1 to 4061) Perraud, A.-L. and Scharenberg, A.
JOURNAL	Direct Submission
FEATURES	Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific Ave, Seattle, WA 98195-6120, USA Location/Qualifiers

ORIGIN	Query Match	Best Local Similarity	90.8%; 92.5%;	Score 1978.8;	DB 9;	Length 4061;
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QY	196	GCACGGAGGAAAGAACTCGGCGTTTCAAGTTTGAAGGGATAGGGCGGTGACCTCTTTGGCGAG				255
Db	1900	GCACGGAGGAAAGAACTCGGCGTTTCAAGTTTGAAGGGATAGGGCGGTGACCTCTTTGGCGAG				1959
QY	256	TGCTATCGAGCAGTAGAGGTGAAGGGCTGCCCGCTCTCTCTCGTGCAGTCCGCGCTTGG				315

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RESULT 6
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LOCUS AX443225
DEFINITION Sequence 7 from Patent W00210382.
ACCESSION AX443225
VERSION AX443225.1 GI:21690620

KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
Wissenbach, U.
Trp8, trp9 and trp10, markers for cancer
Patent: WO 0210382-A 7 07-FEB-2002;
Wissenbach, Ulrich (DE)
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ORIGIN

Query Match 90.7%; Score 1977.2; DB 6; Length 2695;
Best Local Similarity 92.5%; Pred. No. 0;
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RESULT 7
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LOCUS AX443227
DEFINITION Sequence 9 from Patent WO0210382.
ACCESSION AX443227
VERSION AX443227.1 GI:21690622
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Wiesenbach, U.
TITLE TrpB, trpB and trpD, markers for cancer
JOURNAL Patent: WO 0210382-A 9 07-FEB-2002;
Wiesenbach, Ulrich (DE)
FEATURES
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ORIGIN

Query Match 90.7%; Score 1977.2; DB 6; Length 4042;
Best Local Similarity 92.5%; Pred. No. 0;
Matches 2156; Conservative 3; Mismatches 6; Indels 167; Gaps 1;

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 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Primates; Catarrhini; Homnidae; Homo.
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Kawabata, A., Hiki, T., Kobatake, N., Inagaki, H., Ikema, Y.,
 Okamoto, S., Okitani, R., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T.,
 Shibahara, T., Tanaka, T., Nakamura, Y., Isegai, T. and Sugano, S.
 NEDO human cDNA sequencing project
 Unpublished
 2 (bases 1 to 3810)
 SUGANO, S., SUZUKI, Y., OTA, T., ODAYASHI, M., NISHI, T.,
 SHIBAHARA, T., TANAKA, T. and NAKAMURA, Y.
 Direct Submission
 Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,
 Minato-ku, Tokyo 108-8639, Japan (E-mail: f1cdna@ims.u-tokyo.ac.jp,
 Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan, cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing: Department of
 Virology and Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).

FEATURES
source

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CDS

ORIGIN

Query Match 90.6%; Score 1975.6; DB 9; Length 3810;
Best Local Similarity 92.4%; Pred. No. 0;
Matches 2155; Conservative 3; Mismatches 7; Indels 167; Gaps 1;

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Qy	1756	GAGAACTTTTCTGCTGACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG	1815
Db	3189	GAGAACTTTTCTGCTGACGCGCTAGGGACAAGCGGGAGAGCGACTCCGAGMGTCTGAAG	3248
Qy	1816	CGCAGCTCCGAGAGGTGGAATTGGCACTGAACAGCTGGGACATCCGCGAGTACGAA	1875
Db	3249	CGCAGCTCCGAGAGGTGGAATTGGCACTGAACAGCTGGGACATCCGCGAGTACGAA	3308
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Qy	1916	-----	1915
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Db	3489	TTGCTTTAGAGTAAGGCTCATGTGGGCTCTGGGCGCCCGCAGCTGTGGCTTGTCTTG	3548
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RESULT 9
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 VERSION AY046396.1 GI:15617228
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 3701)
 Xu, X.Z., Moebius, F., Gill, D.L. and Montell, C.
 Regulation of melastatin, a TRP-related protein, through
 interaction with a cytoplasmic isoform
 Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)
 JOURNAL MEDLINE
 PUBMED 21438010
 11535825
 2 (bases 1 to 3701)
 Xu, X.-Z., Moebius, F., Gill, D.L. and Montell, C.
 Direct Submission
 TITLE Submitted (17-JUL-2001) Biological Chemistry, Johns Hopkins Univ
 AUTHORS School of Medicine, 725 N. Wolfe Street, Baltimore, MD 21205, USA
 JOURNAL

FEATURES	location/Qualifiers
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ORIGIN

Query Match	90.6%; Score 1974; DB 9; Length 3701;	
Best Local Similarity	92.4%; Pred. No. 0;	
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Qy 556 ATTAATGAGGAAAGGAGCTGTCCGGAACGGGAGCCAGCCGAGAAAGACCCGCTGGGGGTC 615
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DEFINITION Sequence 88 from Patent WO198353.
ACCESSION AX402516
VERSION AX402516.1 GI:21387507
KEYWORDS
SOURCE
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Hillman,J.L., Tang,Y.T., Yue,H., Elliott,V.S., Tribouley,C.M.,
Lee,E.A., Ramkumar,J., Lal,P., Xu,Y., Warren,B.A., Hafalia,A.J.,
Baughn,M.R., Azimzai,Y., Batra,S., Burford,N., Yao,M.G.,
Nguyen,D.B., Lu,D.A., Walla,N.K., Au-Young,J. and Paterson,C.
Patent: WO 0198353-A 88 27-DEC-2001;
JOURNAL Incyte Genomics, Inc. (US)
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Location/Qualifiers
1..3599
source

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ORIGIN

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Best Local Similarity 92.4%; Pred. No. 0;  
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REFERENCE	1. Glucksmann, D., Leticia, J., Filanates, C., Catalina, J., Hernandez, R., Bond.
AUTHORS	Glucksmann, M. A., Curtis, R. A. and Lora, J. M.
TITLE	18607, a human calcium channel
JOURNAL	Patent: WO 0162794-A 3 30-AUG-2001, 1
FEATURES	Millennium Pharmaceuticals, Inc. (US)
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REFERENCE
1 (bases 1 to 3879)
Hofmann, T., Chubanov, V., Gudermann, T. and Montell, C.
TRPMs is a Voltage-Modulated and Ca(2+)-Activated Monovalent
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Curr. Biol. 13 (13), 1153-1158 (2003)
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LOCUS	2393 bp DNA linear
DEFINITION	BD082082 Reagents and methods useful for detecting diseases of the PAT 27-AUG-2002

PROSTATE, .
ACCESSION BD082082
VERSION BD082082.1 GI:22627692
KEYWORDS JP 2001523948-A/9.
SOURCE Zea mays

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 2393)

AUTHORS Cohen, M., Friedman, P.N., Gordon, J., Hodges, S.C., Klaas, M.R., Katochvili, J.D., Rapp, J.R., Russell, J.C. and Stroupe, S.D.
TITLE Reagents and methods useful for detecting diseases of the prostate
JOURNAL Patent: JP 2001523948-A 9 27-NOV-2001,
ABSTRACT LABORDIETICS

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		PR	08-OCT-1996	US 08/727688

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PI MICHAEL R KLAAS, JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C PI
RUSSELL,
PI STEVEN D STROUPE
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 1 (bases 1 to 4061)
 Launay, P., Fleig, A., Perraud, A.L., Scharenberg, A.M., Penner, R. and
 Kinet, J.P.
 TRPM4 is a Ca2+-activated nonselective cation channel mediating

cell membrane depolarization
Cell 109 (3), 397-407 (2002)
JOURNAL MEDLINE 22011788
PUBMED 12015988
REFERENCE 2 (bases 1 to 4061)
AUTHORS Perraud, A.-L. and Scharenberg, A.
TITLE Direct Submission
JOURNAL Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific
Ave, Seattle, WA 98195-6320, USA
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ORIGIN

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VERSION AJ575813.1 GI:32487283
KEYWORDS transient receptor potential ion channel melastatin subgroup member
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SOURCE Homo sapiens (human)
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REFERENCE 1 Nilius, B., Prenen, J., Droogmans, G., Voets, T., Vemkens, R.,
Freichel, M., Wissenbach, U. and Flockerzi, V.,
Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
J. Biol. Chem. 278 (33), 30813-30820 (2003)
PUBMED 1279367
MEDLINE 22791733
TITLE 2 (bases 1 to 4042)
AUTHORS Wissenbach, U.
TITLE Direct Substitution
SUBMITTED (09-JUL-2003) Wissenbach U., University of the Saarland,
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Saarland, GERMANY
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VERSION AX433227.1 GI:21690622
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
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 TITLE
 JOURNAL
 MEDLINE
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 Submitted (12-MAY-2003) Institut fuer Pharmakologie und
 Toxikologie, Phillips-Universitaet Marburg, Karl-von-Frisch-Strasse
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Db 61 GCCGGAAGAGAGAGAGCTGATCCCAAGATCTTCAAGAAAGAAAGACTTCAAGAGCTT 120
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VERSION	AK000048.1		
KEYWORDS	oligo capping; fls (full insert sequence).		
SOURCE	Homio sapiens (human)		
ORGANISM	Homio sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	1 Kawabata, A., Hiki, J. T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Ota, T., Suzuki, T., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.		
TITLE	NEBO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3810)		
AUTHORS	Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail: flichaa@ime.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)		
COMMENT	NEBO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).		
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Query Match	92.6%	Score 3759.6	DB 9	Length 3810
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AUTHORS Gluckemann, M.A., Curtie, R.A. and Lora, J.M.
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Millennium Pharmaceuticals, Inc. (US)
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AUTHORS									
Hillman, J. L., Tang, Y. T., Yue, H., Elliott, V. S., Tribouley, C. M., Lee, E. A., Raskumar, J., Lai, P., Xu, Y., Warren, B. A., Hatalita, A. J., Baughn, M. R., Azimzai, Y., Batrix, S., Burford, N., Yao, M. G., Nguyen, D. B., Lu, D. A., Walla, N. K., Au-Yang, J., and Patterson, C.									
JOURNAL									
Patent: WO 0198353-A8 27-DEC-2001;									
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REFERENCE
  1. (bases 1 to 3701)
  Xu, X.-Z., Moebius, F., Gill, D.L. and Montell, C.
  Regulation of melastatin, a TRP-related protein, through
  interaction with a cytoplasmic isoform
  Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)
  2. (bases 1 to 3701)
  Xu, X.-Z., Moebius, F., Gill, D.L. and Montell, C.
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alternatively spliced.
AY297044
VERSION AY297044.1 GI:31335330
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3523)
Hofmann, T., Chubpanov, V., Gudermann, T. and Montell, C.
TRPMs Is a Voltage-Modulated and Ca(2+)-Activated Monovalent
Selective Cation Channel
Curr. Biol. 13 (13), 1153-1158 (2003)

MEDLINE 22726392
PUBMED 12842017
REFERENCE 2 (bases 1 to 3523)
AUTHORS Chubpanov, V., Gudermann, T., Hofmann, T. and Montell, C.
TITLE Direct Submission
JOURNAL Submitted (12-MAY-2003) Institut fuer Pharmakologie und
Toxikologie, Phillips-Universitaet Marburg, Karl-von-Friesch-Strasse
1, Marburg D-35033, Germany
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REFERENCE 1
AUTHORS Gluckemann, M.A., Curtis, R.A. and Lora, J.M.

TITLE 18607, a human calcium channel
JOURNAL Patent: WO 0162794-A 3 30-AUG-2001;
Millemmium Pharmaceuticals, Inc. (US)
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Db	911	AGGCTCAGCCCTACCTGATGAGCTGTGCTTGTGGCTGTGTGGACCGCTGTGACATTG	970
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Qy	1418	TCAGCCTGTGGGACATTCTCTGACCCCGATGCGCTGTGGCCCAACTTAACAGCGCGGCGCT	1477
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Qy	1538	CAGGCTTAAAGGGGGAGCTGCGGAGCTCGGCGCCCGCGAATGAGGGGATGTGTGAGA	1597
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Qy	1658	CAGGCAAGGGCTTGGGGGAGACATGTATCTGCTCTGTGACCAAGGCCACTCTGCGCTCT	1717
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Qy	1718	CGCTGTGATGTGTGCTGTGGGAGAGCCCTCGTGAACGACCTGTCTTTTGGGCACTGTGTC	1777
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RESULT 12
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LOCUS CQ715325
DEFINITION Sequence 1259 from Patent WO02068579.
ACCESSION CQ715325
VERSION CQ715325.1 GI:42276182
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kites, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1259 06-SEP-2002;
FEATURES
SOURCE Location/Qualifiers
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ORIGIN

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Matches 3339; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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RESULT 13
AY297046

LOCUS AY297046

DEFINITION Homo sapiens transient receptor potential cation channel subfamily M member 4 splice variant C (TRPM4) mRNA, complete cds; alternatively spliced.

ACCESSION AY297046

VERSION AY297046.1 GI:31335334

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3444)
Hofmann, T., Chubakov, V., Gudermann, T. and Montell, C.
TRPM4 is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel
Curr. Biol. 13 (13), 1153-1158 (2003)

JOURNAL MEDLINE 22726392

PUBMED 12842017

REFERENCE 2 (bases 1 to 3444)
Chubakov, V., Hofmann, T., Gudermann, T. and Montell, C.
Direct Submision
Submitted (12-MAY-2003) Institut fuer Pharmakologie und Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse 1, Marburg D-35033, Germany

AUTHORS JOURNAL

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 73.8%; Score 2999; DB 9; Length 3444;
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DEFINITION Sequence 7 from Patent WO0210382.
ACCESSION AX443225
VERSION AX443225.1 GI:21690620
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Wiesenbach, U.
TITLE TP8, trp8 and trp10, markers for cancer
JOURNAL Patent: WO 0210382-A 7 07-FEB-2002;
Wiesenbach, Ulrich (DE)
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ORIGIN

Query Match 64.4%; Score 2616.4; DB 6; Length 2695;
Best local similarity 98.0%; Pred. No. 0;
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 DEFINITION AK000235
 ACCESSION AK000235.1 GI:7020185
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS
 1 Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Taahiro,H.,
 Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
 Nakamura,Y., Isonagi,T. and Sugano,S.

TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2981)
AUTHORS Sugano, S., Suzuki, Y., Ota, T., Ohayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
JOURNAL Direct Submission
Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
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Minato-ku, Tokyo 108-8639, Japan (E-mail: flicdha@ims.u-tokyo.ac.jp,
Tel: 81-3-5448-5286, Fax: 81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Biotechnology; cDNA library
construction: 5' - & 3' - end one pass sequencing: Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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/issue_type="colon mucosa"
/clone_lib="ColF"
/note="Cloning vector pME18SFL3"
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 04:57:16 ; Search time 1356.41 Seconds
(without alignment)
17723.356 Million cell updates/sec

Title: US-09-869-486B-29

Perfect score: 4061

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4061	100.0	4061	3	AAA49923 Human cal
2	4061	100.0	4061	10	Adh62711 Ca activa
3	4061	100.0	4061	13	ADR75511 Human TRP
4	4061	100.0	4061	13	ADSL1774 Transient
5	4028.4	99.2	4042	6	AA32372 Human Trp
6	3845	94.7	4641	11	Adh32329 Cancer/An
7	3812.2	93.9	3898	12	ADL06463 Human tum
8	3759.6	92.6	3810	6	Abk92167 Prostate
9	3759.6	92.6	3810	13	ADR66772 Human pro
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15	3579.8	88.2	3599	6	ABK28677 Human CDN
16	3542	87.2	3701	13	ADSL1776 Transient
17	3538.8	87.1	3676	12	ADQ8582 Human tum
18	3538.8	87.1	3676	13	ADQ85834 Human tum
19	3538.8	87.1	3676	13	ADQ86998 Human tum
20	3501	86.2	3501	6	ABK92224 Prostate

21	3501	86.2	3501	11	ADN39597 Cancer/an
22	3399	83.7	3583	11	ADL33391 Human tra
23	3376.8	83.2	3390	12	ADH51624 Human 186
24	3373.8	83.1	3387	5	AAH76384 Human TLC
25	2616.4	64.4	2695	5	AAAD32373 Human Trp
26	2412.4	59.4	2459	12	ADL06424 Human tum
27	2258	55.6	2393	3	AAV26656 Human PSI
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29	1978.8	48.7	2180	3	AAV46090 Consensus
30	1505	37.1	1524	2	AAV58585 Prostate
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ALIGNMENTS

RESULT 1	AAA49923	standard; CDN; 4061 BP.
ID	AAA49923	
XX	AAA49923;	
AC	10-0CT-2000	(first entry)
DT	10-0CT-2000	(first entry)
XX	Human calcium channel SOC-3/CRAC-2 CDNA.	
DE	SOC-2/CRAC-1; calcium channel; human; store operated channel;	
XX	calcium release activated channel; therapy; diagnosis;	
KW	lymphocyte proliferative disorder; ss.	
XX		
OS	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
FT	CDS	382..5979
FT		/*tag= a
XX		
XX	WO200040614-A2.	
XX	13-JUL-2000.	
PD	20-DEC-1999;	99WO-US029996.
XX		
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PR	22-JUN-1999;	99US-0140415P.
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XX	(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.	
PA		
XX		
XX	Scharenberg AM;	
FI	WPI; 2000-465957/40.	
XX		
DR	P-PSDB; AAY95436.	
XX		
PT	New SOC/CRAC calcium channel polynucleotides and polypeptides used to	
PT	diagnose and treat proliferative disorders associated with the channel,	
XX	and to screen for novel modulators of the channel.	
PS	Claim 1(a); Page 99-100; 108pp; English.	
XX		

CC The present sequence is a full-length nucleotide sequence of human SOC-
CC 3/CRAC-2 cDNA. It includes an open reading frame encoding SOC-3/CRAC-2
CC (see AY95436), a member of a novel family of store operated channel
CC (SOC) or calcium release activated channel (CRAC) polypeptides that
CC modulate Ca²⁺ flux into and out of a cell, and which may be activated
CC upon depletion of Ca²⁺ from intracellular calcium stores, allowing Ca²⁺
CC influx into a cell. SOC-3/CRAC-2 is expressed predominantly in kidney and
CC colon. Compositions for expressing SOC/CRAC calcium channel polypeptides
CC in cells may be useful for treating patients that have reduced
CC extracellular calcium influx into their SOC/CRAC-expressing cells. They
CC will also be useful for delivering therapeutic and/or imaging agents to
CC such cells to modulate proliferation and growth. SOC/CRAC polypeptides
CC also represent targets for designing and/or identifying inhibitors that
CC block lymphocyte proliferation and binding agents that selectively bind
CC to SOC/CRAC polypeptides to which drugs or toxins can be conjugated for
CC delivery to SOC/CRAC expressing cells. SOC/CRAC polynucleotides are used
CC as probes and primers to identify other members of the SOC/CRAC family of
CC calcium channels, as diagnostic reagents for identifying the presence of
CC SOC/CRAC polypeptides in biological samples, as agents for generating
CC SOC/CRAC binding polypeptides, and in gene therapy. Methods for
CC determining the level of SOC/CRAC expression in a subject can be used to
CC assess the presence, or absence, or stage of a proliferative disorder,
CC e.g. a lymphocyte proliferative disorder
XX

SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 4061; DB 3; Length 4061;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 601 AGCACTGGGGGCGCAAGGT 660

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DB 961 CCATGCTCTCTGT 1020
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DB 1381 CGGCTGAGT 1440
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QY 1561 GAGCTCCGGGCGCTGACGTGTGGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1620
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Qy 2581 GGGGGCAGCCTTGCAGCGGGGGGCCCGGGGCTGCGCACTGCTCACTAGGCGAGGCGCTG 2640
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Qy 2641 CGGCTTACCTTCCGCGAGAGCTGGAACGAGTCCGACCTAGTGGCTTCACTGCTCTCTC 2700
Db 2641 CGGCTTACCTTCCGCGAGAGCTGGAACGAGTCCGACCTAGTGGCTTCACTGCTCTCTC 2700
Qy 2701 CTGGGCGTGGGCTGCGGCTGACCCCGGGTTTGTACACCTGGGCGGACATGCTCTGCG 2760
Db 2701 CTGGGCGTGGGCTGCGGCTGACCCCGGGTTTGTACACCTGGGCGGACATGCTCTGCG 2760
Qy 2761 ATCGACTTCATGATGTTTCACGGTGCGGCTGCTTCACTTCTCACGGTCAACAAAGCTG 2820
Db 2761 ATCGACTTCATGATGTTTCACGGTGCGGCTGCTTCACTTCTCACGGTCAACAAAGCTG 2820
Qy 2821 GGGGCCAAGATGCTATGCTAGCAAGATGATGAAGAGCTGTCTTCTCTCTCTC 2880

Db 2821 GGGGCCAAGATGCTATGCTAGCAAGATGATGAAGACGTTCTTCTCTCTCTC 2880
Qy 2881 CTGGGCGTGGGCTGAGTACCTTATGAGGAGCAAGAGGGGCTCTGAGGCGACGGGAC 2940
Db 2881 CTGGGCGTGGGCTGAGTACCTTATGAGGAGCAAGAGGGGCTCTGAGGCGACGGGAC 2940
Qy 2941 AGTACTTCCCAAGTATCTGCGCGGCTCTTACCGCTCCCTACCTGACAGATCTTGGG 3000
Db 2941 AGTACTTCCCAAGTATCTGCGCGGCTCTTACCGCTCCCTACCTGACAGATCTTGGG 3000
Qy 3001 CAGATTTCCCAAGAGACATGAGAGTGGGCTCATGAGACACAGAACTGCTCTGAG 3060
Db 3001 CAGATTTCCCAAGAGACATGAGAGTGGGCTCATGAGAGACAGAACTGCTCTGAG 3060
Qy 3061 CCCGGCTTTGGGAGACACCTCTCGGGGGCCAGGGGGGCACTGCGTCTCCAGTATGCC 3120
Db 3061 CCCGGCTTTGGGAGACACCTCTCGGGGGCCAGGGGGGCACTGCGTCTCCAGTATGCC 3120
Qy 3121 AACTGGCTGGGTGCTGCTCTGCTCATCTTCTGCTCGTGGGCAACATCTGCTGGTC 3180
Db 3121 AACTGGCTGGGTGCTGCTCTGCTCATCTTCTGCTCGTGGGCAACATCTGCTGGTC 3180
Qy 3181 AACTGGCTCATTTGCCATGTTCAATTACATTCGAGCAAAAGTACAGGCAACAGGATCTC 3240
Db 3181 AACTGGCTCATTTGCCATGTTCAATTACATTCGAGCAAAAGTACAGGCAACAGGATCTC 3240
Qy 3241 TACTGGAAGGCGAGCGCTTACCGCTCATCCGGGAATCCACTCTGGGCGGCTGGCC 3300
Db 3241 TACTGGAAGGCGAGCGCTTACCGCTCATCCGGGAATCCACTCTGGGCGGCTGGCC 3300
Qy 3301 CCGGCTTTATCGATCTCTCCCATTTGGGCTCTGCTCAGGCAATGTGAGGCGAGCC 3360
Db 3301 CCGGCTTTATCGATCTCTCCCATTTGGGCTCTGCTCAGGCAATGTGAGGCGAGCC 3360
Qy 3361 CGGAGCCCGCAGCGCTCTCCCGGCGCTCGAGCAATTTCCGGATTTACCTTTCAAGGA 3420
Db 3361 CGGAGCCCGCAGCGCTCTCCCGGCGCTCGAGCAATTTCCGGATTTACCTTTCAAGGA 3420
Qy 3421 GCCGAGGGGAAGCTGCTAATCGTGGGAATCGGTGATTAAGAGAACTTTCTCTGCGACGC 3480
Db 3421 GCCGAGGGGAAGCTGCTAATCGTGGGAATCGGTGATTAAGAGAACTTTCTCTGCGACGC 3480
Qy 3481 GCTAGGGGACAAAGCGGGAAGGAGCACTCCGAGGCTGGAAGGCGACAGTCCAGAGGTGAC 3540
Db 3481 GCTAGGGGACAAAGCGGGAAGGAGCACTCCGAGGCTGGAAGGCGACAGTCCAGAGGTGAC 3540
Qy 3541 TTGGCACTGAAACAGCTGGGACATCGCGAGTACGAAACAGCGCTGAAAGTCTGAG 3600
Db 3541 TTGGCACTGAAACAGCTGGGACATCGCGAGTACGAAACAGCGCTGAAAGTCTGAG 3600
Qy 3601 CGGAGGCTCGACAGTGTAGCGCGTCTGGGGTGGGTGAGCCGAGGCGCTGAGCGCTCT 3660
Db 3601 CGGAGGCTCGACAGTGTAGCGCGTCTGGGGTGGGTGAGCCGAGGCGCTGAGCGCTCT 3660
Qy 3661 GCTTTGCTGCCCCCAGGTGGGCGGCAACCCCTTACCTGCTGGGTCCAAGACTGAGCC 3720
Db 3661 GCTTTGCTGCCCCCAGGTGGGCGGCAACCCCTTACCTGCTGGGTCCAAGACTGAGCC 3720
Qy 3721 CTGCTGGGGAATTCAGAGAAAGCCCAAGAGGGAATTTGTCTTGAAGTAAAGGCTCA 3780
Db 3721 CTGCTGGGGAATTCAGAGAAAGCCCAAGAGGGAATTTGTCTTGAAGTAAAGGCTCA 3780
Qy 3781 TCTGGGCTCTGGGCCCGGCACTGTGGCTTGTCTTGAAGTAAAGGCTCAATCT 3840
Db 3781 TCTGGGCTCTGGGCCCGGCACTGTGGCTTGTCTTGAAGTAAAGGCTCAATCT 3840
Qy 3841 GGGGCACTGTAGAGACCACTTTGGAGTGTATCTTAAACCAACAGCATGCGGCT 3900
Db 3841 GGGGCACTGTAGAGACCACTTTGGAGTGTATCTTAAACCAACAGCATGCGGCT 3900
Qy 3901 CCTCCAGAAACCAATCCAGGCTGGAGGATCAAGGCTGAGTCCGGGCGTTATCAT 3960

```
Db      3901 CCTCCAGAACCAAGTCCAGCTGGAGGATCAAGCCTTGATCCCGGCGCTTATCAT 3960
Qy      3961 CTGAGAGCTGACGAGGTCTTGGGGTAACAGAGCACAGACCCCTCACCTCACAGATT 4020
Db      3961 CTGAGAGCTGACGAGGTCTTGGGGTAACAGAGCACAGACCCCTCACCTCACAGATT 4020
Qy      4021 CCTCACACTGGGGAAATTAAGCCATTTCAGAGGAAAAAAA 4061
Db      4021 CCTCACACTGGGGAAATTAAGCCATTTCAGAGGAAAAAAA 4061

RESULT 2
ID      ADH62711 standard; cDNA; 4061 BP.
XX
AC      ADH62711;
XX
DT      25-MAR-2004 (first entry)
XX
DE      Ca activated nonselective transmembrane channel protein TRPM4b cDNA.
XX
KM      bioactive agent; monovalent cation permeability; TRPM4b channel; human;
XX      calcium activated nonselective transmembrane channel; gene; ss.
OS      Homo sapiens.
XX
FH      Key      Location/Qualifiers
FT      CDS      73..3717
FT              /tag= a
FT              /product= "TRPM4b"
FT              /note= "Calcium activated nonselective (CAN)
PN      US2003143557-A1.
XX
XX      31-JUL-2003.
XX
XX      08-MAY-2002; 2002US-00142649.
XX
XX      25-JAN-2002; 2002US-0351938P.
XX      PR      02-MAY-2002; 2002US-0377937P.
XX
XX      (PENN/) PENNER R.
XX
XX      Penner R;
XX
XX      MPI; 2003-829785/77.
XX      DR      P-PSDB; ADH62712.
XX
XX      Screening for candidate bioactive agents involves contacting calcium-
PT      activated nonselective transmembrane channel polypeptide designated as
PT      TRPM4b with candidate agent, determining binding of candidate agent
PT      TRPM4b.
XX
XX      Claim 5; SEQ ID NO 1; 25bp; English.
XX
XX      The invention describes a method of screening (M1) for a candidate
CC      bioactive agent (CA) modulating monovalent cation (MC) permeability of
CC      the TRPM4b (I) channel. The method involves providing a recombinant cell
CC      (RC) with a nucleic acid encoding (I) and an inducible promoter operably
CC      linked to (I), capable of expressing (I), and comprises an MC indicator,
CC      including RC to express (I), contacting RC with MC and CA, and detecting
CC      intracellular levels of MC with an indicator. The method is useful for
CC      screening for a candidate bioactive agent capable of modulating monovalent
CC      cation permeability of a TRPM4b channel. This sequence encodes human
CC      calcium activated nonselective (CAN) transmembrane channel protein
CC      TRPM4b.
XX
XX      Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;
SO
Query Match      100.0%; Score 4061; DB 10; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      1 GGTCTGGAAGCAGAGCCCGCGAGGAGCGCCCGGGCCCTGGGCTGCAGAGGTTGCGGC 60
Db      1 GGTCTGGAAGCAGAGCCCGCGAGGAGCGCCCGGGCCCTGGGCTGCAGAGGTTGCGGC 60
Qy      61 GGCCTGGGCGAGCATGTGTGTGCTCCGGAAGAGAGAGAGCTGATTCCTCAAGTCTTTCAAG 120
Db      61 GGCCTGGGCGAGCATGTGTGTGCTCCGGAAGAGAGAGAGCTGATTCCTCAAGTCTTTCAAG 120
Qy      121 AAGAAACCTGACAGACGTTTCATAGTTGATCTCAAGATCCGAGAGGAGACCTTGTGCCAG 180
Db      121 AAGAAACCTGACAGACGTTTCATAGTTGATCTCAAGATCCGAGAGGAGACCTTGTGCCAG 180
Qy      181 TGTGGGCGCCCGCGAGCCGCCACCCGCAAGTGGCCATGAGAGATGCTTCGGGGCAGGC 240
Db      181 TGTGGGCGCCCGCGAGCCGCCACCCGCAAGTGGCCATGAGAGATGCTTCGGGGCAGGC 240
Qy      241 GTGTGACCTGTGTGGGACAGCGATGCACACACACAGAGAAAGCCACCGATGCTTACGGA 300
Db      241 GTGTGACCTGTGTGGGACAGCGATGCACACACACAGAGAAAGCCACCGATGCTTACGGA 300
Qy      301 GAGCTGGAATTCAAGGGGGCGGGCGCAAGACAGCAATTTCTCCGGCTCTGAGCGGA 360
Db      301 GAGCTGGAATTCAAGGGGGCGGGCGCAAGACAGCAATTTCTCCGGCTCTGAGCGGA 360
Qy      361 ACGATCCAGCTGCAGTTTATAGTCTGTCAACAGCAGATGGGGCTTCGTGCCGGAAC 420
Db      361 ACGATCCAGCTGCAGTTTATAGTCTGTCAACAGCAGATGGGGCTTCGTGCCGGAAC 420
Qy      421 CTGTGTGTGTCACTGTCTGGGGGAGATCGGGGGGCCCCGCTCTCAAGACTGTGTGAGAGAC 480
Db      421 CTGTGTGTGTCACTGTCTGGGGGAGATCGGGGGGCCCCGCTCTCAAGACTGTGTGAGAGAC 480
Qy      481 CTGTGCGGTGCGGGCTGGGTGGCGGGCTGCCAGACACAGAGAGCTGATTTGTCACTGGG 540
Db      481 CTGTGCGGTGCGGGCTGGGTGGCGGGCTGCCAGACACAGAGAGCTGATTTGTCACTGGG 540
Qy      541 GGTCTGCACACGGGGCATCGGCCGAGCATGTGTGTGTGCTGTACGGAACCATCAGATGGCC 600
Db      541 GGTCTGCACACGGGGCATCGGCCGAGCATGTGTGTGTGCTGTACGGAACCATCAGATGGCC 600
Qy      601 AGCACTGGGGGAGCCAGAGGTGTGCTCATGGGTGTGGCCCCCTGGGGTGTGTCCGGAAAT 660
Db      601 AGCACTGGGGGAGCCAGAGGTGTGCTCATGGGTGTGGCCCCCTGGGGTGTGTCCGGAAAT 660
Qy      661 AGAGACACCTCATCAACCCCAAGGGCTGTTCCCTGGAGAGTACCGGTGGCGCGGTGAC 720
Db      661 AGAGACACCTCATCAACCCCAAGGGCTGTTCCCTGGAGAGTACCGGTGGCGCGGTGAC 720
Qy      721 CCGGAGGACGGGGTCAGTTTCCCTGGAATCAACATCTCGGCCCTTCTCTGTGTGAGAC 780
Db      721 CCGGAGGAGGGGGTCAAGTTTCCCTGGAATCAACATCTCGGCCCTTCTCTGTGTGAGAC 780
Qy      781 GACGGCAACACAGCGTCTGCTGGGGGGCGAAGAACCGCTTCCGCTTGGCGTGTCTTAC 840
Db      781 GACGGCAACACAGCGTCTGCTGGGGGGCGAAGAACCGCTTCCGCTTGGCGTGTCTTAC 840
Qy      841 ATCTACAGCGAAGAACCGGGCGTGGAGGAGATGGAATTGACATCCGTGCTGCTCCGC 900
Db      841 ATCTACAGCGAAGAACCGGGCGTGGAGGAGATGGAATTGACATCCGTGCTGCTCCGC 900
Qy      901 CTGATTTGATGTGATGAGAGATGTTTGAACGCGAATAGAGAACGCCACCGAGCTCAGGTC 960
Db      901 CTGATTTGATGTGATGAGAGATGTTTGAACGCGAATAGAGAACGCCACCGAGCTCAGGTC 960
Qy      961 CCATGTCTCTCTGTGGCTGTGCTCAGGGGAGAGTGTGCGGACTGTGCTGGCGAGACCTTGAA 1020
Db      961 CCATGTCTCTCTGTGGCTGTGCTCAGGGGAGAGTGTGCGGACTGTGCTGGCGAGACCTTGAA 1020
Qy      1021 GACACTCTGCGCCCGAGGAGTGGGGGAGCCAGGCAAGCGGAAGCCCGAGATGGAATCAGG 1080
Db      1021 GACACTCTGCGCCCGAGGAGTGGGGGAGCCAGGCAAGCGGAAGCCCGAGATGGAATCAGG 1080
```

QY 1081 CGTTTCTTCCCAAGGGAGCTTGAGGTCTGACAGGCCAGGTGAGAGATTATGACC 1140
Db 1081 CGTTTCTTCCCAAGGGAGCTTGAGGTCTGACAGGCCAGGTGAGAGATTATGACC 1140
QY 1141 CGGAAGAGAGCTCTGACAGTCTATTCTTCTGAGAGATGAGTCTGAGAAATTCAAGACATA 1200
Db 1141 CGGAAGAGAGCTCTGACAGTCTATTCTTCTGAGAGATGAGTCTGAGAAATTCAAGACATA 1200
QY 1201 GTTTGAAGAGCCCTGTGTAAGGCTGTGAGAGCTCGAAGGCTCAAGCTTACGTGATGAG 1260
Db 1201 GTTTGAAGAGCCCTGTGTAAGGCTGTGAGAGCTCGAAGGCTCAAGCTTACGTGATGAG 1260
QY 1261 CTGCGTTTGGCTGTGAGTGTGAACCGCTGAGCAATTGCCAGAGTAACTTTTCGAGGAG 1320
Db 1261 CTGCGTTTGGCTGTGAGTGTGAACCGCTGAGCAATTGCCAGAGTAACTTTTCGAGGAG 1320
QY 1321 GACATTCGAATGAGCGGTCTTTCATCTGAAAGCTTCCCTGATGAGACGCTGTGCTGAATGAC 1380
Db 1321 GACATTCGAATGAGCGGTCTTTCATCTGAAAGCTTCCCTGATGAGACGCTGTGCTGAATGAC 1380
QY 1381 CGGCGTGAAGTTGATGCGCTTGTGCTCAATTTCCCAAGGCTGAGCTGAGGCCACTTCTGAGC 1440
Db 1381 CGGCGTGAAGTTGATGCGCTTGTGCTCAATTTCCCAAGGCTGAGCTGAGGCCACTTCTGAGC 1440
QY 1441 CGGATGCGGCTGAGCCCACTTCAAGCGGCGGCCCTTCCCACTGCTCATCCGCAACCTT 1500
Db 1441 CGGATGCGGCTGAGCCCACTTCAAGCGGCGGCCCTTCCCACTGCTCATCCGCAACCTT 1500
QY 1501 TTGGAACAAGCGCTCCCAAGCGGCAAGGACCAAAAGCCCAAGCCCTTAAAGAGGAGAGCTGCG 1560
Db 1501 TTGGAACAAGCGCTCCCAAGCGGCAAGGACCAAAAGCCCAAGCCCTTAAAGAGGAGAGCTGCG 1560
QY 1561 GAGCTCCGCGCCCTGACGCTGGGAGCATGTGCTGAGAGATGCTGCTGGGAGAAATGTGCGCG 1620
Db 1561 GAGCTCCGCGCCCTGACGCTGGGAGCATGTGCTGAGAGATGCTGCTGGGAGAAATGTGCGCG 1620
QY 1621 CGAGAGTACCCCTCGAGGGGCGCTGAGAGCCCTCAACCCAGGCAAGGAGCTTTCGAGGAGAC 1680
Db 1621 CGAGAGTACCCCTCGAGGGGCGCTGAGAGCCCTCAACCCAGGCAAGGAGCTTTCGAGGAGAC 1680
QY 1681 ATGATCTGCTCTCGGACAAGGCAACTTGCGGCTTCTGCTGAGATGCTGAGCCTCGGCGAG 1740
Db 1681 ATGATCTGCTCTCGGACAAGGCAACTTGCGGCTTCTGCTGAGATGCTGAGCCTCGGCGAG 1740
QY 1741 GCGCCCTGAGGAGCACTGCTTTTGGGAGCACTGTTGCTGTAACAAGGCAAGATGCGCATG 1800
Db 1741 GCGCCCTGAGGAGCACTGCTTTTGGGAGCACTGTTGCTGTAACAAGGCAAGATGCGCATG 1800
QY 1801 TACTTCTGGGAGATGGGATTCGAATGAGTTTCTCAGACTTGGGGGCTGTTTGTGCTGTC 1860
Db 1801 TACTTCTGGGAGATGGGATTCGAATGAGTTTCTCAGACTTGGGGGCTGTTTGTGCTGTC 1860
QY 1861 CGGAGTATGAGCAGCGCTGAGAGCTGACGCTGAGAGGAGCAGCAGAGAAAGACCTGAGCG 1920
Db 1861 CGGAGTATGAGCAGCGCTGAGAGCTGACGCTGAGAGGAGCAGCAGAGAAAGACCTGAGCG 1920
QY 1921 TTCAAGTTTGAAGGGAGATGGGCGTTGACTTCTTGGGAGTGTCTATGCGACGATGAGGTG 1980
Db 1921 TTCAAGTTTGAAGGGAGATGGGCGTTGACTTCTTGGGAGTGTCTATGCGACGATGAGGTG 1980
QY 1981 AGGGCTGCGCGCTCTCTCTCGTGGCTGCGCGCTGAGGAGGAGTGGCCATTGCGCTCAG 2040
Db 1981 AGGGCTGCGCGCTCTCTCTCGTGGCTGCGCGCTGAGGAGGAGTGGCCATTGCGCTCAG 2040
QY 2041 CTGAGCATGCAAGCTGACGCGCTGAGCTTCTTGGCCAGAGATGGGATCAAGTCTGCTGCTG 2100
Db 2041 CTGAGCATGCAAGCTGACGCGCTGAGCTTCTTGGCCAGAGATGGGATCAAGTCTGCTGCTG 2100
QY 2101 ACAAGAAAGTGTGGGAGAGATGTGGCAGACACTTACCCATCTGGGCGCTGTGTTCTGCGC 2160
Db 2101 ACAAGAAAGTGTGGGAGAGATGTGGCAGACACTTACCCATCTGGGCGCTGTGTTCTGCGC 2160
QY 2161 TTCTTTTGGCCCTCACTATCAACCGGCGCTCATCACTTCAAGGAAATCAAGAGAGAG 2220

Db 2161 TTCTTTTGGCCCTCACTATCAACCGGCGCTCATCACTTCAAGGAAATCAAGAGAGAG 2220
QY 2221 CCCACAAGGAGAGACTTGAAGTTTGAATGGAATGATCTTATTAATGGGAAAGGCGCTGTC 2280
Db 2221 CCCACAAGGAGAGACTTGAAGTTTGAATGGAATGATCTTATTAATGGGAAAGGCGCTGTC 2280
QY 2281 GGGAGCGGAGAGCCGAGCGGAGAGAGCGCGCTGGGGGGTCCCGCGCAGTGGGCGGCTGCG 2340
Db 2281 GGGAGCGGAGAGCCGAGCGGAGAGAGCGCGCTGGGGGGTCCCGCGCAGTGGGCGGCTGCG 2340
QY 2341 GGTTCCTGCGGGGAGCGCTGCGGGGAGCGCGGCTGCTCAAGCGCGTGTTCACATCTTCTG 2400
Db 2341 GGTTCCTGCGGGGAGCGCTGCGGGGAGCGCGGCTGCTCAAGCGCGTGTTCACATCTTCTG 2400
QY 2401 GCGCGCGGCTGACCACTTCAATGAGGCAAGTGGCTGACCTTACCTGCTGCTGCTT 2460
Db 2401 GCGCGCGGCTGACCACTTCAATGAGGCAAGTGGCTGACCTTACCTGCTGCTGCTT 2460
QY 2461 TTCTGCGGGGCTGCTGCTGAGATTTCAAGCGGCGCGCGCGCTGCTGAGGCTGCTG 2520
Db 2461 TTCTGCGGGGCTGCTGCTGAGATTTCAAGCGGCGCGCGCGCTGCTGAGGCTGCTG 2520
QY 2521 CTCTATTTCTGAGGCTTTCAAGCTGCTGTGAGAGAACTGCGCAAGGAGCTGAGCGAGAGC 2580
Db 2521 CTCTATTTCTGAGGCTTTCAAGCTGCTGTGAGAGAACTGCGCAAGGAGCTGAGCGAGAGC 2580
QY 2581 GGGGCGAGCTGCGCAGCGGGGAGCCCGGAGCTGAGCAATGCTTCACTGAGCCAGGCTGCG 2640
Db 2581 GGGGCGAGCTGCGCAGCGGGGAGCCCGGAGCTGAGCAATGCTTCACTGAGCCAGGCTGCG 2640
QY 2641 GCGCTTCACTGCGCGGAGAGCTGGAACAGATGCGCACTGATGAGCTTCACTGCTTCTGCTG 2700
Db 2641 GCGCTTCACTGCGCGGAGAGCTGGAACAGATGCGCACTGATGAGCTTCACTGCTTCTGCTG 2700
QY 2701 CTGAGCGTGGAGCTGCGGCTGACCCCGGGTTTGTATCACTGAGGCGGCACTGCTCTGCG 2760
Db 2701 CTGAGCGTGGAGCTGCGGCTGACCCCGGGTTTGTATCACTGAGGCGGCACTGCTCTGCG 2760
QY 2761 ATGCACTTATGATTTTCAAGGTGCGGCTGCTTCACTGCTTCACTGCTTCACTGCTTCACTG 2820
Db 2761 ATGCACTTATGATTTTCAAGGTGCGGCTGCTTCACTGCTTCACTGCTTCACTGCTTCACTG 2820
QY 2821 GGGCCCAAGATGCTATGATGAGAGAAATGATGAGAGAGTGTCTTCTCTCTCTCTCTCTCT 2880
Db 2821 GGGCCCAAGATGCTATGATGAGAGAAATGATGAGAGAGTGTCTTCTCTCTCTCTCTCTCTCT 2880
QY 2881 CTGAGCGTGGAGCTGATGAGCTTATGAGCGTGGAGCAAGGAGGAGCTTCTGAGGCAAGGAGC 2940
Db 2881 CTGAGCGTGGAGCTGATGAGCTTATGAGCGTGGAGCAAGGAGGAGCTTCTGAGGCAAGGAGC 2940
QY 2941 AGTGACTTCCCAAGTATCTGCGCGGCTGCTTCTTCAAGCTGCTTCACTGCAAGTCTTCTGAG 3000
Db 2941 AGTGACTTCCCAAGTATCTGCGCGGCTGCTTCTTCTTCAAGCTGCTTCACTGCAAGTCTTCTGAG 3000
QY 3001 CAGATTTCCCAAGAGAGAAATGAGAGTGGAGCTTCAATGAGAGCAAGCAATGCTGCTGAGAG 3060
Db 3001 CAGATTTCCCAAGAGAGAAATGAGAGTGGAGCTTCAATGAGAGCAAGCAATGCTGCTGAGAG 3060
QY 3061 CCGGAGCTTCTGAGGAGCAAGCTTCTGAGGAGCCAGAGGAGGAGCACTGAGCTTCCCAAGTATG 3120
Db 3061 CCGGAGCTTCTGAGGAGCAAGCTTCTGAGGAGCCAGAGGAGGAGCACTGAGCTTCCCAAGTATG 3120
QY 3121 AACTGAGTGTGAGTGTGCTCTCTGCTATCTTCTGCTGCTGAGCCATCTGCTGCTG 3180
Db 3121 AACTGAGTGTGAGTGTGCTCTCTGCTATCTTCTGCTGCTGAGCCATCTGCTGCTG 3180
QY 3181 AACTGCTCATTTGCTATGATTTAGTTTACATTTGCGCAAAAGTACAGGAGCAAGGAGTCTC 3240
Db 3181 AACTGCTCATTTGCTATGATTTAGTTTACATTTGCGCAAAAGTACAGGAGCAAGGAGTCTC 3240
QY 3241 TACTGAGAGGAGAGGCTTACCGGCTCATCCGAGAAATTCACCTCTGCGGCGCGGCTGCGC 3300

```
Dh 3241 TACTGAGAGCGGACGGCTTACCGCCTCATCCGGGAAATTCACCTCTCGGCCCGCGCTGGCC 3300
Qy 3301 CGCCCTTATCGTCACTCTCCACTTGGCGCTCTGTGTCAGGCAATTGTGACGACGCC 3360
Dh 3301 CGCCCTTATCGTCACTCTCCACTTGGCGCTCTGTGTCAGGCAATTGTGACGACGCC 3360
Qy 3361 CGGAGCCCCCAGCGCTCTCCCGCGCTCTGAGCAATTTCCGGGTTTACCTTTCTAAGAA 3420
Dh 3361 CGGAGCCCCCAGCGCTCTCCCGCGCTCTGAGCAATTTCCGGGTTTACCTTTCTAAGAA 3420
Qy 3421 GCGGACGGAAGGCTGCTAAGCTGTGGAATCGGTGCAATTAAGAGAACTTTCTGCTGGAACCC 3480
Dh 3421 GCGGACGGAAGGCTGCTAAGCTGTGGAATCGGTGCAATTAAGAGAACTTTCTGCTGGAACCC 3480
Qy 3481 GCTAGGGAACAAGCGGAGAGCGACTCGAGCGCTCTGAGCGCGCTGAAAGGTGAGC 3540
Dh 3481 GCTAGGGAACAAGCGGAGAGCGACTCGAGCGCTCTGAGCGCGCTGAAAGGTGAGC 3540
Qy 3541 TTGGCACTGAAACAGCTGGGACACATCCGGAAGTACGAAACAGCGCTGAAAGGTGAGC 3600
Dh 3541 TTGGCACTGAAACAGCTGGGACACATCCGGAAGTACGAAACAGCGCTGAAAGGTGAGC 3600
Qy 3601 CGGAGGTCAGAGAGTGAAGCCCGCTCTGTGGGTGGTGGCCGAGGCCCTGAGCCCTCT 3660
Dh 3601 CGGAGGTCAGAGAGTGAAGCCCGCTCTGTGGGTGGTGGCCGAGGCCCTGAGCCCTCT 3660
Qy 3661 GCGTGTGCGCCCGGAGTGGGCGCCACCCCTGACCTGCGTGGGTGCAAAAGCTGAGCC 3720
Dh 3661 GCGTGTGCGCCCGGAGTGGGCGCCACCCCTGACCTGCGTGGGTGCAAAAGCTGAGCC 3720
Qy 3721 CTGCTGCGGAGCTTCAAGAGAAAGCCCGCAAGGGAATTTGCTCTAAGATGAGCTCA 3780
Dh 3721 CTGCTGCGGAGCTTCAAGAGAAAGCCCGCAAGGGAATTTGCTCTAAGATGAGCTCA 3780
Qy 3781 TCTGGGCTTGGGCGCCCGGACCTGTGTGCTCTTGAAGTGAAGCCCATATCTCATCT 3840
Dh 3781 TCTGGGCTTGGGCGCCCGGACCTGTGTGCTCTTGAAGTGAAGCCCATATCTCATCT 3840
Qy 3841 GGGGCACTGTCAAGAGCAACCTTTGGAGAGTGTCACTTCAAAACACAGATGCCGGCT 3900
Dh 3841 GGGGCACTGTCAAGAGCAACCTTTGGAGAGTGTCACTTCAAAACACAGATGCCGGCT 3900
Qy 3901 CTTCCAGAAACAGTCCAGCTCTGGAGAGATCAAGGCTGTGATCCGGGCGCTTATTCAT 3960
Dh 3901 CTTCCAGAAACAGTCCAGCTCTGGAGAGATCAAGGCTGTGATCCGGGCGCTTATTCAT 3960
Qy 3961 CTGAGAGCTGAGGCTCTTGGGTTAAGAGGACCAACAGCCCTTCAACCACTACAGATT 4020
Dh 3961 CTGAGAGCTGAGGCTCTTGGGTTAAGAGGACCAACAGCCCTTCAACCACTACAGATT 4020
Qy 4021 CCTCAGACTGGGAAATTAAGCAATTTCAAGAGAAAAAAA 4061
Dh 4021 CCTCAGACTGGGAAATTAAGCAATTTCAAGAGAAAAAAA 4061
Db 4021 CCTCAGACTGGGAAATTAAGCAATTTCAAGAGAAAAAAA 4061

RESULT 3
ID ADR73511 standard; DNA: 4061 BP.
XX ADR73511;
XX AC
XX AD
XX DT 02-DEC-2004 (first entry)
XX DE
XX Human TRPM4, gene.
XX TRPM4; apoptosis; inhibitor; tumour; cytosolic; cancer; gene; ds.
XX OS
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 73..3717
XX FT
XX /product= "Human TRPM4"
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XX XX
PN WO2004076682-A2.
XX 10-SEP-2004.
PD 26-FEB-2004; 2004MO-US006020.
XX 26-FEB-2003; 2003US-0450886P.
PR (SURR-) SURROMED INC.
XX (SURR-) SURROMED INC.
XX Axenovich SA, Scull R, Gelman M, Chui K, Ng D;
XX WPI; 2004-653428/63.
DR P-PSDB; ADR73512.
XX
PT Identifying a compound for inducing apoptosis, useful for diagnosing and
XX treating cancer, comprises identifying an inhibitor of a target.
XX
XX Example 1; SEQ ID NO 79; 255bp; English.
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The invention relates to a novel method for identifying a compound for inducing apoptosis comprising identifying an inhibitor of a target. Examples of an inhibitor of a target include: angio-associated, migratory cell protein (AAMP), disintegrin and metalloproteinase domain 8 (ADAM8), disintegrin-like and metalloprotease (repeats type) with thrombospondin type 1 motif, 17 (ADAMTS17), adenylate cyclase 3 (ADCY3), adrenergic beta receptor kinase 1 (ADRBK1), bladder cancer associated protein (BLCAP), chromosome 22 open reading frame 5 (C22orf5), CD81 antigen (target of antiproliferative antibody 1 (CD81), CD9 antigen (p24) (CD9), claudin 4 (CLDN4), chloride intracellular channel 1 (CLIC1), collagen, type VI, alpha 2 (COL6A2), CTL2, endothelin converting enzyme 1 (ECE1), ephrinB1 (EFNB1), flotillin 2 (FLOT2), intercellular adhesion molecule 3 (ICAM3), iduronate 2-sulfatase (Hunter syndrome) (IDS), jagged 2 (JAG2), junctional adhesion molecule 1 (JAM1), lectin, galactoside-binding soluble 3 binding protein (LGALS3BP), similar to possible G-protein receptor (LOC146330), CGI-78 protein (LOC51107), lipoprotein lipase (LPL), low density lipoprotein receptor-related protein 5 (LRP5), Lutheran blood group (Aubreyer b antigen included) (LU), membrane component, chromosome1, surface marker 1 (M1S1), serum constituent protein (MSE55), neuropathy target esterase (NTE), Homo sapiens CDNA FLJ1043 f1e, clone HSYR200248 (PLEXIN A1) or Homo sapiens CDNA FLJ44113 f1b, clone TEST14046487, highly similar to Mus musculus plexin A1 (PLXNA1), protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein) (liprin), alpha 3 (PFR13), Homo sapiens CC peptide-histidine transporter 4 (PTRA), mRNA (PTRA), solute carrier family 16 (monocarboxylic acid transporters) member 3 (SLC16A3), solute carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5), solute carrier family 39 (zinc transporter) member 3 (SLC39A1), serine protease inhibitor, Kunitz type 2 (SPINT2), stannocalcin 2 (STC2), tumour necrosis receptor superfamily member 21 (TNFRSF21), tumour rejection antigen (GP96) 1 (TRAI), or transient receptor potential cation channel, subfamily M member 4 (TRPM4), respectively comprising any of the 40 sequences of 87-1615 amino acids (the even numbers selected from SEQ ID:2-80), shown in the specification. The invention further comprises a method for inducing apoptosis and a method for diagnosing a tumour. The novel compounds have cytostatic activity. The method is useful for identifying a compound for inducing apoptosis. The methods and compounds are useful for diagnosing and treating cancer, and in determining the prognosis for cancer in the patient or the susceptibility of the patient to a therapeutic treatment. This polynucleotide sequence represents a gene encoding one of the 40 protein targets of the invention.

SO Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;
Query Match 100.0%; Score 4061; DB 13; Length 4061;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGTCTGAGAGCAGAGCCGCGGAGGAGGAGCGCCGCTGTGAGAGAGTTGCCGC 60
Dh 1 GGTCTGAGAGCAGAGCCGCGGAGGAGGAGCGCCGCTGTGAGAGAGTTGCCGC 60
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Qy 61 GCGCGCGCAGCATGTGTGTGTCGCGAGAGAGACAGACTGTGATCCCAAGATCTTCAAG 120
Db 61 GCGCGCGCAGCATGTGTGTGTCGCGAGAGAGAGACTGTGATCCCAAGATCTTCAAG 120
Qy 121 AAGAAAGCTGACAGACGTTCAATAGTTACTTCACAGATCCGGAGGGACCTTGTGCCAG 180
Db 121 AAGAAAGCTGACAGACGTTCAATAGTTACTTCACAGATCCGGAGGGACCTTGTGCCAG 180
Qy 181 TGTGGGCGCGCGCGAGCGCCACCGCGAGTGGCAATGAGAGATGCTTGGGGCAGACC 240
Db 181 TGTGGGCGCGCGCGAGCGCCACCGCGAGTGGCAATGAGAGATGCTTGGGGCAGACC 240
Qy 241 GTGTGACCTGTGTGGGACAGCGATGACACACACGAGAGAGCCACGATGCTTACGGA 300
Db 241 GTGTGACCTGTGTGGGACAGCGATGACACACACGAGAGAGCCACGATGCTTACGGA 300
Qy 301 GAGCTGACCTTACCGGGGGCGCGCGAGACACAGCAATTTCTCCGGCTCTGTAGCGGA 360
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Qy 361 ACGGATCCAGCTGACGTTATATGTGTGTCAACGCAATATGGGGCTTCCGTGCCCGAAC 420
Db 361 ACGGATCCAGCTGACGTTATATGTGTGTCAACGCAATATGGGGCTTCCGTGCCCGAAC 420
Qy 421 CTGTGTGTGTGACGTGTGGGGGATCGGGGGGCGCGCTCTCAAGACCTGTGCTGAGGAC 480
Db 421 CTGTGTGTGTGACGTGTGGGGGATCGGGGGGCGCGCTCTCTCAAGACCTGTGCTGAGGAC 480
Qy 481 CTGTGTGTGTGACGTGTGGGGGATCGGGGGGCGCGCTCTCAAGACCTGTGCTGAGGAC 540
Db 481 CTGTGTGTGTGACGTGTGGGGGATCGGGGGGCGCGCTCTCAAGACCTGTGCTGAGGAC 540
Qy 541 GGTCTGTGACAGGGGATGTGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 541 GGTCTGTGACAGGGGATGTGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Qy 601 AGCACTGGGGGACCAAGGT 660
Db 601 AGCACTGGGGGACCAAGGT 660
Qy 661 AGAGACACCTCATCAACCCCAAGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 AGAGACACCTCATCAACCCCAAGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 CCGAGAGACGGGGTCAAGTTTCCCTGTGACTTCAACTGTGTGTGTGTGTGTGTGTGT 780
Db 721 CCGAGAGACGGGGTCAAGTTTCCCTGTGACTTCAACTGTGTGTGTGTGTGTGTGTGT 780
Qy 781 GACGGACACACGGCTGTGTGGGGGCGAGAACGGCTTCCGCTTGTGCGCTGTGAGTCTTAC 840
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Db 841 ATCTCAGCAGAGAGACGGGGTGTGGAGGAGACTGTGAATTTGACATCCCTGTCTGCTC 900
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Qy 1381 CGGCTGTGATTTGT 1440
Db 1381 CGGCTGTGATTTGT 1440
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Db 1441 CCGATGGCGCTGTGGCGCAACTCTACAGGGCGGGCGCTTCCAACTGTGCTCATCGGACCTT 1500
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Db 1621 CCGAGGTAAACCCCTCGGGGGGGCGCTGGGAGCCCTACACAGGCGCAGGCTTGGGGAGAGC 1680
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Db 1681 ATGTATCTGTCTGTGAGCAAGAGGCACTGTGCGGCTCTGTGTGTGTGTGTGTGTGTGT 1740
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Db 1801 TACTTCTGTGAGATGGGTTCGAATGTGACATTTCTCACTCTTGGGGCTTGTGTGTGTGT 1860
Qy 1861 CCGGTGATGGGACGCTGTGAGGCTGTGACGCTGTGAGAGGACGACGAGAGAGAAAGCTTGGC 1920
Db 1861 CCGGTGATGGGACGCTGTGAGGCTGTGACGCTGTGAGAGGACGACGAGAGAGAAAGCTTGGC 1920
Qy 1921 TTCAAGTTTGAAGGGATGGGGTGTGACCTCTTTGGCGAGTGTATTCGACGAGTGTGAGTG 1980
Db 1921 TTCAAGTTTGAAGGGATGGGGTGTGACCTCTTTGGCGAGTGTATTCGACGAGTGTGAGTG 1980
Qy 1981 AGGGCTGCGGCTTCTTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2040
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Db 2161 TTCTTTTGGCTTCCATCTCATCTTACACCGGCTTATACCTTTCAGAAATCAGAAAGAGAG 2220
Qy 2221 CCGACAGGGAGGAGCTTGAAGTGTGATGTGTATTTATGAGGAGAGGCGCTGTG 2280

Db 2221 CCCACGCGGAGGAGCTAGAGTTTGAACATGAGATAGTGTCAATTATGAGGAAAGGCGCTGTGC 2280
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Db 2281 GGGACGCGGAGACCCAGCCGAGAGAGAGAGCGCGCTGAGGGATCCCGGCGAGTCCGAGCGCTCCG 2340
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Db 2341 GGTTCCTGCGGGGGGCGCTGCGGGGGGCGCGCGGTGCTTACAGCGCGTGTGTTCCATTCTG 2400
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Db 2521 CTCTATTTCTGGGCTTTTCAAGCTGTGTGTGAGGAACTGCGCCAGGGGCTTGAACGGAGGC 2580
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Db 2581 GGGGCGAGGCTGCGCAGCGGGGGGCGCGGGGCTGAGCTTCACTGAGCAGGCGGCTG 2640
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Db 2641 CGGCTTACCTCGCGCAGAGCTGGAACAGTGTGAGCTTGTGCTTCACTGCTTCTTCTC 2700
QY 2701 CTGGGCGTGGGCTGCGGCTGACCCCGGGTTGTACACCTGGGGCCGACCTGTCTTGC 2760
Db 2701 CTGGGCGTGGGCTGCGGCTGACCCCGGGTTGTACACCTGGGGCCGACCTGTCTTGC 2760
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Db 2761 ATCGACTTATGAGTTTCAAGGTCGGGCTTCACTGCTTCACTGCTTCACTGCTTCACTGCTT 2820
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Db 2821 GGGGCCAAGATCGTCACTGTGAGCAAGATGATGAAAGAGTGTCTTCTTCTTCTTCTTCT 2880
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Db 2881 CTGGGCGTGTGCTGTGATCTATGCGTGTGCGCAAGGAGGCTCTTGAAGCCACGAGAC 2940
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Db 2941 AGTGACTTCCCAAGTATCTGCGGCGGCTTCTTACGCTTCCCTGAGAGTCTTGGG 3000
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QY 3121 AACTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
Db 3121 AACTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3180
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Db 3181 AACTGCTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3240
QY 3241 TACTGAGAGGCGAGCTTACCGCTCATCCGGAATTCACCTTCTGCGCGCGCTGCGC 3300
Db 3241 TACTGAGAGGCGAGCTTACCGCTCATCCGGAATTCACCTTCTGCGCGCGCTGCGC 3300
QY 3301 CGGCGCTTATGCTATCTTCCCACTTGGCGCTTCTGCTGAGGCAATTGTGACGAGGAGCC 3360
Db 3301 CGGCGCTTATGCTATCTTCCCACTTGGCGCTTCTGCTGAGGCAATTGTGACGAGGAGCC 3360

QY 3361 CGGAGCGCCGAGCGCTTCTCCCGGCGCTGAGCATTTCCGGGTTTACCTTTCTAAGAA 3420
Db 3361 CGGAGCGCCGAGCGCTTCTCCCGGCGCTGAGCATTTCCGGGTTTACCTTTCTAAGAA 3420
QY 3421 GCGGAGCGGAGCTGTAACTGTGGAATCGGTGCTAAAGGAGAACTTTTGTCTGCGACGC 3480
Db 3421 GCGGAGCGGAGCTGTAACTGTGGAATCGGTGCTAAAGGAGAACTTTTGTCTGCGACGC 3480
QY 3481 GCTAGGAGCAAGCGGAGAGGAGCTCCGAGCGCTGGAAGCGCAGCTCCAGAAAGGTGAGC 3540
Db 3481 GCTAGGAGCAAGCGGAGAGGAGCTCCGAGCGCTGGAAGCGCAGCTCCAGAAAGGTGAGC 3540
QY 3541 TTGGCACTGAAACAGCTGAGACATCCGCGAGTACGAAACAGCGCTGAAAGTGTGAG 3600
Db 3541 TTGGCACTGAAACAGCTGAGACATCCGCGAGTACGAAACAGCGCTGAAAGTGTGAG 3600
QY 3601 CCGGAGGTTCAGCACTGTAGCCGCTCTGGGCTGTGAGCGGAGCGCTGAGCGCTCT 3660
Db 3601 CCGGAGGTTCAGCACTGTAGCCGCTCTGGGCTGTGAGCGGAGCGCTGAGCGCTCT 3660
QY 3661 GCTTGTGCGCCCGAGGTGAGCGCGCACCCCGTGAACCTGCTGGTCCAAAGACTGAGGC 3720
Db 3661 GCTTGTGCGCCCGAGGTGAGCGCGCACCCCGTGAACCTGCTGGTCCAAAGACTGAGGC 3720
QY 3721 CTGCTGCGGAGCTTCAAGAGAGAGAGCGCCACAGGGGATTTTGTCTTGAAGTAAAGCTCA 3780
Db 3721 CTGCTGCGGAGCTTCAAGAGAGAGAGCGCCACAGGGGATTTTGTCTTGAAGTAAAGCTCA 3780
QY 3781 TTTGGGCTCTGGGCGCCCGGACCTGTGTGCTTGTCTTGAAGTAAAGCTTCACTT 3840
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QY 3841 GGGGCACTGTGAGCAACCTTTGGGAGTGTGATCTTCAAAACAGACAGATGCCGCT 3900
Db 3841 GGGGCACTGTGAGCAACCTTTGGGAGTGTGATCTTCAAAACAGACAGATGCCGCT 3900
QY 3901 CCTCCAGAACAGTCCAGCGCTGAGAGATCAAGGCTGTGATCCCGGCGCTTATCAT 3960
Db 3901 CCTCCAGAACAGTCCAGCGCTGAGAGATCAAGGCTGTGATCCCGGCGCTTATCAT 3960
QY 3961 CTGAGGCTGCAAGGCTCTTGGGTTAAAGGAGCCACAGACCTTCACTACAGATT 4020
Db 3961 CTGAGGCTGCAAGGCTCTTGGGTTAAAGGAGCCACAGACCTTCACTACAGATT 4020
QY 4021 CCTCACTGGGGAATTAAGCATTTCAAGGAAAAAA 4061
Db 4021 CCTCACTGGGGAATTAAGCATTTCAAGGAAAAAA 4061

RESULT 4
ADSI2774
ID ADSI2774 standard; cDNA; 4061 BP.
XX
XX ADSI2774;
XX
XX 16-DEC-2004 (first entry)
XX
XX
DE Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX
KW transient receptor potential cation channel, subfamily M; member 4;
KW TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW prostate cancer; TRPM4b; gene; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 73..3717
FT /*tag= a
FT /product= "Human TRPM4b protein"
XX
XX JP2004267118-A.

PD	30-SEP-2004.
XX	
PE	10-MAR-2003; 2003JP-00063578.
XX	
PR	10-MAR-2003; 2003JP-00063578.
XX	
PA	(SANY) SANKYO CO LTD.
XX	
DR	WPI; 2004-693915/68.
XX	
DR	P-PSDB; ADS12775.
XX	
PT	Detecting prostatic cancer, comprises extracting RNA fractions from test
PT	substance of subject and normal human, measuring and analyzing the
PT	difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT	expression levels.
XX	
PS	Claim 1; SEQ ID NO 1; 126bp; Japanese.
XX	
CC	The invention comprises a method for detecting prostatic cancer in a
CC	subject. The method involves measuring the expression levels of specific
CC	genes: transient receptor potential cation channel, subfamily M, member 4
CC	(TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC	(BUCS1). The method of the invention is useful for the detection and
CC	treatment of prostate cancer. The present cDNA sequence encodes the human
CC	TRPM4b protein of the invention.
XX	
SEQ	Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;
	Query Match 100.0%; Score 4061; DB 13; Length 4061;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 4061; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGTCTGGAAGCAGACCCGCGGAGAGCGCCGGGCCCTTGCGCTGCAGAGAGTTGGCG 60
DB	1 GGTCTGGAAGCAGACCCGCGGAGAGCGCCGGGCCCTTGCGCTGCAGAGAGTTGGCG 60
QY	61 GGCCGCGGCGAGCATGTGTGTGTCGCCGAGAAAGAGCGAGTGGATCCCAAGATCTTCAAG 120
DB	61 GGCCGCGGCGAGCATGTGTGTGTCGCCGAGAAAGAGCGAGTGGATCCCAAGATCTTCAAG 120
QY	121 AAGAAAGACTTGACAGACGTTACTAGTTGACTCCACAGATCCGGAGGGAGCCTTGTGCCAG 180
DB	121 AAGAAAGACTTGACAGACGTTACTAGTTGACTCCACAGATCCGGAGGGAGCCTTGTGCCAG 180
QY	181 TGTGGGCGCCCCCGGAGCCGCCACCCCGCAGTGGCCATGAGAGATGCTTTCGGGCGAGCC 240
DB	181 TGTGGGCGCCCCCGGAGCCGCCACCCCGCAGTGGCCATGAGAGATGCTTTCGGGCGAGCC 240
QY	241 GTGTGATCCGTGTGTGGGACAGCGATGCACACACACGAGAGAGGCCACCGATGCTTACGGA 300
DB	241 GTGTGATCCGTGTGTGGGACAGCGATGCACACACACGAGAGAGGCCACCGATGCTTACGGA 300
QY	301 GAGCTGGACTTCACGGGGGCGGCGCGGAAGCAGACAAATTCCTCCGGCTCTGTACCGGA 360
DB	301 GAGCTGGACTTCACGGGGGCGGCGCGGAAGCAGACAAATTCCTCCGGCTCTGTACCGGA 360
QY	361 ACGATCCAGCTGCAAGTTATAGTCTGTGTCACACGACAGATGGGGCTTCGTCGCCGAAC 420
DB	361 ACGATCCAGCTGCAAGTTATAGTCTGTGTCACACGACAGATGGGGCTTCGTCGCCGAAC 420
QY	421 CTGGTGTGTCAAGTCTGAGGGGAGATCGGGGGGCCCTTCCTTCAGACTTGTGTGAGAGAC 480
DB	421 CTGGTGTGTCAAGTCTGAGGGGAGATCGGGGGGCCCTTCCTTCAGACTTGTGTGAGAGAC 480
QY	481 CTGGTGTGTGTGAGTCTGAGGGGAGATCGGGGGGCCCTTCCTTCAGACTTGTGTGAGAGAC 540
DB	481 CTGGTGTGTGTGAGTCTGAGGGGAGATCGGGGGGCCCTTCCTTCAGACTTGTGTGAGAGAC 540
QY	541 GGTCTGCACACGGGGAGATGGCCCGGAGATGTGGTGTGTGACGGGACCATTAAGATGGCC 600
DB	541 GGTCTGCACACGGGGAGATGGCCCGGAGATGTGGTGTGTGACGGGACCATTAAGATGGCC 600
QY	601 AGCACTGGGGGACCAAGATGTGGCCATGGGTGTGGCCCTTCGGGGTGTGTGTCGGAGAT 660

Db	601	AGCATGGGGGACCCAAAGGTGTGTGCATGTGGTGTGGCCCTTGGGGTGTGGTCCGGAAT	660
Qy	661	AGAGACACCTTCATCAACCCCAAGGGCTGTTCCTCTGGAGGTACCGTGGCGCGTGC	720
Db	661	AGAGACACCTTCATCAACCCCAAGGGCTGTTCCTCTGGAGGTACCGGGTGGCGGGTGC	720
Qy	721	CCGAGAGACGGGGTCAAGTTTCCCTGGACTACAACTACTGCGCTTCTTCTGTGTGAC	780
Db	721	CCGAGAGACGGGGTCAAGTTTCCCTGGACTACAACTACTGCGCTTCTTCTGTGTGAC	780
Qy	781	GACGSGACAACAACGCTGTGCTGGGGGGGAGAAACCGCTTCCGCTTGCGCTGTGAGTCTAC	840
Db	781	GACGSGACAACAACGCTGTGCTGGGGGGGAGAAACCGCTTCCGCTTGCGCTGTGAGTCTAC	840
Qy	841	ATCTCACAGACAGAAAGACGGGCGTGGGAGAGACTGGAATTTGACATCCCTGTCCCTCTC	900
Db	841	ATCTCACAGACAGAAAGACGGGCGTGGGAGAGACTGGAATTTGACATCCCTGTCCCTCTC	900
Qy	901	CTGATTTAGTGTGATGAGAGATGTTGACGCGAATAGAGAACGCCAACCCAGGCTCAAGCTC	960
Db	901	CTGATTTAGTGTGATGAGAGATGTTGACGCGAATAGAGAACGCCAACCCAGGCTCAAGCTC	960
Qy	961	CCATGTCTCTCTGTGGCTGTGAGGGGAGCTGTGGACTGTGCGTGGCGGAGACCCCTGGAA	1020
Db	961	CCATGTCTCTCTGTGGCTGTGAGGGGAGCTGTGGACTGTGCGTGGCGGAGACCCCTGGAA	1020
Qy	1021	GACACTCTGGGCCCCAGGGAGTGGGGGAGCCAGGCAAGCGAAGCCGAGATGTGAATCAGG	1081
Db	1021	GACACTCTGGGCCCCAGGGAGTGGGGGAGCCAGGCAAGCGAAGCCGAGATGTGAATCAGG	1081
Qy	1081	CGTTTCTTCCCAAAGGGGACCTTGAGGTCTCTGACGGCCCAAGTGTGAGAGATTTATGACC	1141
Db	1081	CGTTTCTTCCCAAAGGGGACCTTGAGGTCTCTGACGGCCCAAGTGTGAGAGATTTATGACC	1141
Qy	1141	CGGAAGAGTCTCTGACAGTCTATTTCTTGAGATGTGGTCTGAAGAAATTCGAGACATA	1201
Db	1141	CGGAAGAGTCTCTGACAGTCTATTTCTTGAGATGTGGTCTGAAGAAATTCGAGACATA	1201
Qy	1201	GTTTGAAGAGCCCTTGTGAAGGCGCTGTGGAGTCTGAGGCGCTCAGGCTTACTGTGATGAG	1261
Db	1201	GTTTGAAGAGCCCTTGTGAAGGCGCTGTGGAGTCTGAGGCGCTCAGGCTTACTGTGATGAG	1261
Qy	1261	CTGCGTTTGGCTGTGGCTTGGAAACCGCGTGAACATTTGCCAGAGTAACTCTTTGGGGG	1321
Db	1261	CTGCGTTTGGCTGTGGCTTGGAAACCGCGTGAACATTTGCCAGAGTAACTCTTTGGGGG	1321
Qy	1321	GACATCCAAATGGCGGTCTTTCATCTTCMAAGTCTCCATAGGAAGCCCTGTGTGAATGAC	1381
Db	1321	GACATCCAAATGGCGGTCTTTCATCTTCMAAGTCTCCATAGGAAGCCCTGTGTGAATGAC	1381
Qy	1381	CGGCGTGAAGTCTGTGCGCTTGCTCATTTTCCACGGGCTCAGGCTGGGGCACTTCTGTGAC	1441
Db	1381	CGGCGTGAAGTCTGTGCGCTTGCTCATTTTCCACGGGCTCAGGCTGGGGCACTTCTGTGAC	1441
Qy	1441	CCGATGTGCGCTGTGCGCCAACTCTACAGCGCGGCGCTTCCAACTGCTCATCCGCAACTT	1501
Db	1441	CCGATGTGCGCTGTGCGCCAACTCTACAGCGCGGCGCTTCCAACTGCTCATCCGCAACTT	1501
Qy	1501	TTTGAACCAAGGCGTCTCCACAGCGCAGGCAACAAAGCTTAAAGGGGGAGCTGCG	1561
Db	1501	TTTGAACCAAGGCGTCTCCACAGCGCAGGCAACAAAGCTTAAAGGGGGAGCTGCG	1561
Qy	1561	GAGCTCCGAGCCCCCTGACGTGAGGAGATGTGCTGAGAGAGTGTGCGCG	1621
Db	1561	GAGCTCCGAGCCCCCTGACGTGAGGAGATGTGCTGAGAGAGTGTGCGCG	1621
Qy	1621	CCGAGGTACCCCTCCGGGGGCGCTGGAGCCCTCAACCGAGGCAAGGGCTTGGGGAGAGC	1681
Db	1621	CCGAGGTACCCCTCCGGGGGCGCTGGAGCCCTCAACCGAGGCAAGGGCTTGGGGAGAGC	1681
Qy	1681	ATGTATCTGCTCTGTGAGACAGGCCACTTGGCCGCTTGTGCTGATGCTGGCTGGGCAAG	1741
Db	1681	ATGTATCTGCTCTGTGAGACAGGCCACTTGGCCGCTTGTGCTGATGCTGGCTGGGCAAG	1741

Db 1681 AAGTATCTGCTCGGACAAAGCCACCTGCGGCTCTCGTGGATGTCGGCTCGGGCAG 1740
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QY 1861 CCGGTATATGAGAGCCTGAGAGCTGACGCTGAGAGAGCAGACAGAGAGAAAGACTGGG 1920
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Db 1921 TTCAGATTGAGAGGAGATGGGCGTTGACCTTTTGGAGAGTGTATGCGAGCTGAGTGGT 1980
QY 1981 AAGGCTGCGGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 AAGGCTGCGGCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
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QY 2281 GGGAGCGGGAGAGCCAGCCGAGAGAGAGCGCGCTGGGGTCCCGGCGAGTCCGGCTGCG 2340
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QY 2401 GGGCGCGCGGTGACATCTTCAATGGGCAAGTGTGACGCTACTGCTGCTGCTGCTT 2460
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Db 2461 TTTCTGCGGGGTGCTGCTCGTGAATTTCCAGCGCGCGCGCGCTCCCTGAGACTGCTG 2520
QY 2521 CTCTATTTCTGGGCTTTCAAGCTGCTGAGAGAACTGCGCAGGGGCTGAGCGAGG 2580
Db 2521 CTCTATTTCTGGGCTTTCAAGCTGCTGAGAGAACTGCGCAGGGGCTGAGCGAGG 2580
QY 2581 GGGGAGAGCTGCGCAGCGGGGCGCGGCGCTGAGCATGAGCTCACTGAGAGCGGCTG 2640
Db 2581 GGGGAGAGCTGCGCAGCGGGGCGCGGCGCTGAGCATGAGCTCACTGAGAGCGGCTG 2640
QY 2641 CCGCTTACTCTGCGCAGAGCTGAGAACAGTGTGAGCTAGTGGCTTCACTGCTTCTG 2700
Db 2641 CCGCTTACTCTGCGCAGAGCTGAGAACAGTGTGAGCTAGTGGCTTCACTGCTTCTG 2700
QY 2701 CTGGGAGTGGGCTGCGGCTGAGACCGGGTTTGTACCACTGGGCGGCACTGTCTCTG 2760
Db 2701 CTGGGAGTGGGCTGCGGCTGAGACCGGGTTTGTACCACTGGGCGGCACTGTCTCTG 2760
QY 2761 ATGCACTTATGTTTCAAGGTGCGGCTTCACTCTTCAAGGTGCAAAAGAGCTG 2820
Db 2761 ATGCACTTATGTTTCAAGGTGCGGCTTCACTCTTCAAGGTGCAAAAGAGCTG 2820

QY 2821 GGGCCCAAGATGCTATCGTGAAGAAATGATGAAGAGCTGTTCTTCTTCTTCTTCTT 2880
Db 2821 GGGCCCAAGATGCTATCGTGAAGAAATGATGAAGAGCTGTTCTTCTTCTTCTTCTT 2880
QY 2881 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
Db 2881 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940
QY 2941 AGTGAATTCAGAGTATCCCTGCGCGGCTTCTACCGCTTCTACCTGAGATCTTCCGG 3000
Db 2941 AGTGAATTCAGAGTATCCCTGCGCGGCTTCTACCGCTTCTACCTGAGATCTTCCGG 3000
QY 3001 CAGATTCCCAAGAGACATGAGAGCTGAGCTCATGAGACAGAGCAATGCTGCTGAG 3060
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QY 3301 CCGCCCTTATGCTATCTCCCACTTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
Db 3301 CCGCCCTTATGCTATCTCCCACTTGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 3360
QY 3361 CCGAGCGGCGCAGCGCTCTCCCGGCGCTGAGCAATTCGCGGTTTACTTCTTAAGAA 3420
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QY 3421 GCGAGCGGGAAGCTGTAACGTGGGAATCGTGAATTAAGAGAACTTCTGCTGAGCAG 3480
Db 3421 GCGAGCGGGAAGCTGTAACGTGGGAATCGTGAATTAAGAGAACTTCTGCTGAGCAG 3480
QY 3481 GCTAGGAGACAGCGGAGAGGCACTCCGAGCTTGAAGCGCACTCCAGAAAGTGGAG 3540
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Db 3541 TTGGCACTGAACAGCTGGGACACATCCGCGAGTACGAACAGCGCTGAAGTGGAG 3600
QY 3601 CCGGAGGTTCAGACAGTGTAGCCGCTGCTGAGGTGGTGGCCGAGGCTTGAAGCGCTT 3660
Db 3601 CCGGAGGTTCAGACAGTGTAGCCGCTGCTGAGGTGGTGGCCGAGGCTTGAAGCGCTT 3660
QY 3661 GCTTGTGCTGCGCCAGGTGGGCGGCAACCTCTGACCTGCTGCTGCTGCTGCTGCTG 3720
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QY 3781 TCTGGGCTCTGCGCCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
Db 3781 TCTGGGCTCTGCGCCCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3840
QY 3841 GGGGCACTGTCAAGACCACTTTGGAGTGTATCTTACAAACAGCATGCTGCTGCTG 3900
Db 3841 GGGGCACTGTCAAGACCACTTTGGAGTGTATCTTACAAACAGCATGCTGCTGCTG 3900

QY 3901 CCTCCAGAACGATCCAGCCTGGAGGATCAAGGCTGTATCCCGGCGCTTATCCAT 3960
DB 3901 CCTCCAGAACGATCCAGCCTGGAGGATCAAGGCTGTATCCCGGCGCTTATCCAT 3960
QY 3961 CTGGAGGCTGCGAGGCTCTTGGGGTAAACAGGACCAAGACCCCTACCACTCAGAGATT 4020
DB 3961 CTGGAGGCTGCGAGGCTCTTGGGGTAAACAGGACCAAGACCCCTACCACTCAGAGATT 4020
QY 4021 CCTCAGCTGGGGAATTAAGCATTTTCAGAGAAAAAAA 4061
DB 4021 CCTCAGCTGGGGAATTAAGCATTTTCAGAGAAAAAAA 4061

RESULT 5
AAD32372
ID AAD32372 standard; cDNA; 4042 BP.
XX AAD32372;
XX
XX AAD32372 (first entry)
XX
XX 18-JUN-2002
XX
XX Human Trp9 protein encoding cDNA.
XX
XX Human; prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
XX transient receptor potential; calcium channel protein; Trp8a; Trp8b;
XX molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
XX tumour; chorion carcinoma; lung cancer; antisense therapy; ss.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX CDS 42..3686
XX /tag= a
XX /product= "Human Trp9 protein"
XX
XX MO200210382-A2.
XX
XX 07-FEB-2002.
XX
XX 18-JUN-2001; 2001WO-EP008309.
XX
XX 28-JUN-2000; 2000US-0221513P.
XX
XX (WISS/) WISSENBACH U.
XX
XX Wissebach U;
XX
XX MPI; 2002-269013/31.
XX
XX P-PSDB; AAE20283.
XX
XX Novel isolated nucleic acid encoding human prostate carcinoma associated
XX protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
XX useful as molecular markers for diagnosing prostate cancer.
XX
XX Claim 1; Fig 9A; 70pp; English.
XX
XX The invention relates to human prostate carcinoma associated proteins
XX such as transient receptor potential (Trp)8a, Trp8b, Trp9, Trp10a and
XX Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
XX Trp10 are novel calcium channel proteins. Sequences of the invention are
XX useful as molecular markers for diagnosing prostate cancer. Sequences of
XX the invention, their antibodies, inhibitors and antisense molecules are
XX useful for preventing, treating or ameliorating a prostate tumour,
XX endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
XX cancer of the lung or melanoma. Polynucleotides of the invention are used
XX in antisense therapy. The present sequence is human Trp9 protein encoding
XX cDNA
XX
SQ Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;

Query Match 99.2%; Score 4028.4; DB 6; Length 4042;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4029; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 32 CGGGGCGCTGGCTGCAAGAGTTGCGGGCGCGGAGAGATGGTGGCCCGAAGG 91
DB 1 CGGGGCGCTGGCTGCAAGAGTTGCGGGCGCGGAGAGATGGTGGCCCGAAGG 60
QY 92 AGCAGAGCTGATCCCAAGATCTTCAAGAAAGACCTGACAGAGCTTCAATAGTTGA 151
DB 61 AGCAGAGCTGATCCCAAGATCTTCAAGAAAGACCTGACAGAGCTTCAATAGTTGA 120
QY 152 CCAAGATCCGGAGAGGACCTTGTGCAAGTGGGCGCCCGGAGCCGCGAG 211
DB 121 CCAAGATCCGGAGAGGACCTTGTGCAAGTGGGCGCCCGGAGCCGCGAG 180
QY 212 TGGCCATGAGAGATGCTTGGGGGAGCGGTGTGACCGGTGGGACAGGATGACACA 271
DB 181 TGGCCATGAGAGATGCTTGGGGGAGCGGTGTGACCGGTGGGACAGGATGACACA 240
QY 272 CCAAGAGAGAGCCGAGATGCTTGAAGAGAGCTTGAAGAGAGAGCCGAGAGC 331
DB 241 CCAAGAGAGAGCCGAGATGCTTGAAGAGAGCTTGAAGAGAGAGCCGAGAGC 300
QY 332 AAGCAATTTCTCCGAGCTCTGACCGAAGATCCAGCTGAGTTATAGTCTGTCA 391
DB 301 AAGCAATTTCTCCGAGCTCTGACCGAAGATCCAGCTGAGTTATAGTCTGTCA 360
QY 392 CACGACATGGGGCTTCCGTCGACCCGGAACCTGTGTGTCAAGTGTGGGGGATGGGG 451
DB 361 CACGACATGGGGCTTCCGTCGACCCGGAACCTGTGTGTCAAGTGTGGGGGATGGGG 420
QY 452 GCCCGCTCTCAGACCTGAGCTGAGAGAGCTGTGCGTGTGGGCTGTGGCGTGGCC 511
DB 421 GCCCGCTCTCAGACCTGAGCTGAGAGAGCTGTGCGTGTGGGCTGTGGCGTGGCC 480
QY 512 AAGACAGAGAGCTGATGTCACTGGGGGTCTGACACGAGCATCGGCGCATGTGG 571
DB 481 AAGACAGAGAGCTGATGTCACTGGGGGTCTGACACGAGCATCGGCGCATGTGG 540
QY 572 GTGTGGCTGTACGGGACCATAGATGGGACACCTGGGGGACCAAGTGTGGGATAG 631
DB 541 GTGTGGCTGTACGGGACCATAGATGGGACACCTGGGGGACCAAGTGTGGGATAG 600
QY 632 GTGTGGCCCTGGGGGTGTGTCGGGAATGAGACACCTGATCAACCCCAAGGCTGT 691
DB 601 GTGTGGCCCTGGGGGTGTGTCGGGAATGAGACACCTGATCAACCCCAAGGCTGT 660
QY 692 TCCCTGCGAGGTACCGGTGGCGGCTGACCCGAGAGAGCGGGTCCAGTTTCCCTGAG 751
DB 661 TCCCTGCGAGGTACCGGTGGCGGCTGACCCGAGAGAGCGGGTCCAGTTTCCCTGAG 720
QY 752 ACAACTATCGGCGCTTCTCTGTGTGACAGCGGACACAGGCTGCTGGGGGCGAGA 811
DB 721 ACAACTATCGGCGCTTCTCTGTGTGACAGCGGACACAGGCTGCTGGGGGCGAGA 780
QY 812 ACCGCTTCGCTTGGGCGCTGAGTCTTCACTCAAGCAGAGAGCGGCGTGGAGGGA 871
DB 781 ACCGCTTCGCTTGGGCGCTGAGTCTTCACTCAAGCAGAGAGCGGCGTGGAGGGA 840
QY 872 CTGGAATGACATCCCTGTCTGTCTCTGATTTGATGATGAGAGATGTTGAGC 931
DB 841 CTGGAATGACATCCCTGTCTGTCTCTGATTTGATGATGAGAGATGTTGAGC 900
QY 932 GAATGAGAGAGCCAGGCTCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 991
DB 901 GAATGAGAGAGCCAGGCTCAGTCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
QY 992 CTGGGAGTGGCTGGGAGAGCCCTGGAAGACATCTGGGCGCCAGGAGTGGGGAGGCA 1051
DB 961 CTGGGAGTGGCTGGGAGAGCCCTGGAAGACATCTGGGCGCCAGGAGTGGGGAGGCA 1020
QY 1052 GGCAAGGGAAGCCGAGATGAATCAAGCGTTTCTTCCAAAGGGAGCTTGAAGTCC 1111
DB 1021 GGCAAGGGAAGCCGAGATGAATCAAGCGTTTCTTCCAAAGGGAGCTTGAAGTCC 1080

1112 TGCAGGCCAGGTGAGAGATTATGACCCGGAGAGGCTCTGACAGTCTATTCTTCTG 1171
1081 TTGAGGCCAGAGGTGAGAGATTATGACCCGGAGAGGCTCTGACAGTCTATTCTTCTG 1140
1172 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTGAAGGCTTGTGAAGGCTGTGGGA 1231
1141 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTGAAGGCTTGTGAAGGCTGTGGGA 1200
1232 GCTCGAGGCTCAGGCTACCTGAGATGAGTGGTTTGGCTGTGGTGAAGCCGGTGG 1291
1201 GCTCGAGGCTCAGGCTACCTGAGATGAGTGGTTTGGCTGTGGTGAAGCCGGTGG 1260
1292 ACAATTGCCAGAGTGAATCTTTTCGGGGGAGCATCCAAATGGCGTCTTTCATCTCGAAG 1351
1261 ACAATTGCCAGAGTGAATCTTTTCGGGGGAGCATCCAAATGGCGTCTTTCATCTCGAAG 1320
1352 CTTTCCCTCATGAGCGCCCTGCTGATGACCGGCTGAGTTCTGTGGCTTGTCTATTCCC 1411
1321 CTTTCCCTCATGAGCGCCCTGCTGAAATGACCGGCTGAGTTCTGTGGCTTGTCTATTCCC 1380
1412 AGGAGCTCAGGCTGAGGCACTTCTGACCCCGATGGCGTGGCCAACTCTACAGGCGG 1471
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1472 CGGCTCTCAAATCTGCTCATCCGCAACTTTTGGACAGGCGTCTCCACAGCGAGGACCA 1531
1441 CGGCTCTCAAATCTGCTCATCCGCAACTTTTGGACAGGCGTCTCCACAGCGAGGACCA 1500
1532 AAGCCCTCAGGCTTAAAGGGGGAGCTGCGAGTCTCCGGCCCTCTGACGTGGGGCATGTGC 1591
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1652 CTCACCCAGGCAAGGCTTTCGGGAGAGCATGTATCTGCTCTCGACAAAGGCCACTCTGC 1711
1621 CTCACCCAGGCAAGGCTTTCGGGAGAGCATGTATCTGCTCTCGACAAAGGCCACTCTGC 1680
1712 CGCTCTGCTGATGCTGGGCTTTCGGGAGAGGCCCCCTGAGCGACCTGTCTTTGGGCAAC 1771
1681 CGCTCTGCTGATGCTGGGCTTTCGGGAGAGGCCCCCTGAGCGACCTGTCTTTGGGCAAC 1740
1772 TGTGCTGAACAGGCGACAGATGGGCATGTACTTCTGGGAGATGGGTTCCATGCACTT 1831
1741 TGTGCTGAACAGGCGACAGATGGGCATGTACTTCTGGGAGATGGGTTCCATGCACTT 1800
1832 CCTCAGCTCTTGGGCGCTGTGTGCTCTCCGGTGAATGGACGCTGAGCGCTG 1891
1801 CCTCAGCTCTTGGGCGCTGTGTGCTCTCCGGTGAATGGACGCTGAGCGCTG 1860
1892 AGGAGGACAGCAGGAGGAAAGACTTGGCGTTCAAGTTGAGGGGATGGGCTTGACCTCT 1951
1861 AGGAGGACAGCAGGAGGAAAGACTTGGCGTTCAAGTTGAGGGGATGGGCTTGACCTCT 1920
1952 TTGGCAGAGTCTATGCGAGAGTGAAGGCTGCGCGCTCTCCCTCCGCTGGTGGC 2011
1921 TTGGCAGAGTCTATGCGAGAGTGAAGGCTGCGCGCTCTCCCTCCGCTGGTGGC 1980
2012 CGCTCTGAGGGGAGTGCACCTTGGCTCAGCTGGCCATGCAAGCTGAACGCCGTGCTTCT 2071
1981 CGCTCTGAGGGGAGTGCACCTTGGCTCAGCTGGCCATGCAAGCTGAACGCCGTGCTTCT 2040
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2192 TCATCACCCTTCAGGAATCAGAGAGAGCCACAGGGAGGAGTGAAGTTGACATGG 2251

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2372 GGTGCTTACGCGCTGTGTTCACTTCTGGGGGCGCGCGGTGACATCTTATGGGCAAG 2431
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2492 CGGCGCGCGCGGCTCCCTGAGAGCTGCTCTATTCTGGGCTTTCACAGCTGTGGC 2551
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2552 AGGAATGCGCGCAGGCGCTGAGCGGAGCGGGGCAAGCTTGCCAGCGGGGCGCCGGGC 2611
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2792 TTCAATCTTCAACGCTCAACAAACAGCTGGGGCCCAAGATCGTCATCGGAGCAAGATGA 2851
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2852 TGAAGAGCTGTCTTCTTCTCTTCTCTGCGGTGGTGGCTGAGCTATGGCGTGG 2911
2821 TGAAGAGCTGTCTTCTTCTCTTCTCTGCGGTGGTGGCTGAGCTATGGCGTGG 2880
2912 CCACGAGGGGCTCTGAGGCGACGAGACATGACTTCCCAAGTATCTGCGCGCTCT 2971
2881 CCACGAGGGGCTCTGAGGCGACGAGACATGACTTCCCAAGTATCTGCGCGCTCT 2940
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3092 AGGCGGGACCTGCTTCTCCAGTATGCCAACTGGCTGGTGGTGTCTCTGTCTATCT 3151
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3272 GGGAAATTCACCTCTGCGCGCGGCTGGCCCGCTTTATCGTCACTTCCACTTGGCGC 3331


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Db 3241 GGGAAATCCACTCTGCGCCCGCGCTGCGCCCGCCCTTATCGTCACTTCCACTTGCGCC 3300
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Db 3301 TCTCTGCTAGGCAATTTGTCAGGCGACCCCGGAGGCCCGGAGCCCTCTCCCGGCGCTG 3360
Oy 3392 AGCATTTCCGGGTTTACCTTTTCTAAGAAAGCCGAGCGGAAAGTGTCTTAAGCTGGGAATCG 3451
Db 3361 AGCATTTCCGGGTTTACCTTTTCTAAGAAAGCCGAGCGGAAAGTGTCTTAAGCTGGGAATCG 3420
Oy 3452 TGCATTAAGAGAACTTTTCTGCTGCGACCGCGCTAGGAGCAAGCGGAGAGCACTCCGAGC 3511
Db 3421 TGCATTAAGAGAACTTTTCTGCTGCGACCGCGCTAGGAGCAAGCGGAGAGCACTCCGAGC 3480
Oy 3512 GTCTGAACCGCAGCTTCCCGAGAAAGTGTGACTTGGCACTGAAACAAGCTGGAGCACTCCGCG 3571
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Oy 3572 AGTACGAACAGCGCCCTGAAAGTGTGAGCGGAGAGGTCCAGAGCTGTAAGCGCGCTCTG 3631
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Oy 3872 CATCTTTACAAACCAAGCATGCGCGCTCTCCCAAGCAAGTCCAGCTGGAGAGAT 3931
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Oy 3932 CAAGGCTGGATCCCGGCGCGTATTCATCTGGAAGCTGCGAGGCTTGGGCTTAACAG 3991
Db 3901 CAAGGCTGGATCCCGGCGCGTATTCATCTGGAAGCTGCGAGGCTTGGGCTTAACAG 3960
Oy 3992 GACCAAGAGCCCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4051
Db 3961 GACCAAGAGCCCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4020
Oy 4052 GGAAGAAAAA 4061
Db 4021 GGAAGAAAAA 4030

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RESULT 6
ADN39239
ID ADN39239 standard; cDNA; 4641 BP.

ADN39239;
17-JUN-2004 (first entry)
Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:57.
Human: differential expression; cancer; angiogenic disorder;
fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
inflammatory disease; autoimmune disease;
retinal neovascularisation syndrome; scarring; uterine fibroid;
detection; diagnosis; prognosis; drug screening; drug targeting;
wound healing; contraception; cytostatic; cardiant; immunomodulatory;
vulnerary; gene therapy; vaccine; gene; ss.

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OS Homo sapiens.
XX
XX MO2003042661-A2.
XX
XX 22-MAY-2003.
XX
XX 13-NOV-2002; 2002MO-US036810.
XX
XX 13-NOV-2001; 2001US-0350666P.
XX
XX 21-NOV-2001; 2001US-0332464P.
XX
XX 29-NOV-2001; 2001US-0334393P.
XX
XX 03-DEC-2001; 2001US-0335394P.
XX
XX 14-DEC-2001; 2001US-0340376P.
XX
XX 08-JAN-2002; 2002US-0347211P.
XX
XX 10-JAN-2002; 2002US-0347349P.
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XX 08-FEB-2002; 2002US-0355250P.
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XX 13-FEB-2002; 2002US-0356714P.
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XX 20-FEB-2002; 2002US-0359077P.
XX
XX 29-MAR-2002; 2002US-0368809P.
XX
XX 04-APR-2002; 2002US-0370110P.
XX
XX 12-APR-2002; 2002US-0372246P.
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XX 05-JUN-2002; 2002US-0386614P.
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XX 16-JUL-2002; 2002US-0396839P.
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XX 22-JUL-2002; 2002US-0397775P.
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XX 22-JUL-2002; 2002US-0397845P.
XX
XX 09-SEP-2002; 2002US-0409450P.
XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glyne R, Hevezi PA;
XX Mack DH, Murray R, Watson SR, Wilson KE, Ziortnik A;
XX WPI; 2003-468649/44.
XX
XX P-PSDB; ADN39240.
XX
XX Determining the presence or absence of a pathological cell in a patient,
XX useful for diagnosing, prognosing or treating cancer, comprises detecting
XX a nucleic acid in a biological sample.
XX
XX Claim 8; SEQ ID NO 557; 1385bp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX whose expression is upregulated or downregulated in specific cancers or
XX other diseases such as angiogenic or fibrotic disorders, and to methods
XX of determining the presence or absence of a pathological cell in a
XX patient by detecting a nucleic acid at least 80% identical to those of
XX the invention or by detecting a polypeptide of the invention. The
XX invention also relates to expression vectors and host cells comprising a
XX nucleic acid of the invention; antibodies which specifically bind a
XX polypeptide of the invention; use of such antibodies for drug targeting;
XX and methods of screening for modulators of activity or expression of the
XX polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX antibodies and methods are useful for diagnosing, prognosing and treating
XX cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX neovascularisation syndromes, scarring and uterine fibroids. They may
XX also be useful in wound healing and in contraception. The present
XX sequence represents a nucleic acid sequence of the invention.
XX
XX Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;
XX
XX Query Match 94.7%; Score 3845; DB 11; Length 4641;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3845; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 217 ATGAGAGATGCTTCTGCGGCGCGCTGTCACCGTGGGACAGAGAGCAACACACAG 276
Db 769 ATGAGAGATGCTTCTGCGGCGCGCTGTCACCGTGGGACAGAGAGCAACACACAG 828
Oy 277 GAGAAGCCCAACGATGCTTACGAGAGAGCTGATCTTCAAGCGGCGCGGCGCAACACAGC 336
Db 829 GAGAAGCCCAACGATGCTTACGAGAGAGCTGATCTTCAAGCGGCGCGGCGCAACACAGC 888

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QY	337	AATTTCCCTCCGGCTCTCTGACCCGAACGGATCCAGCTGACGTTTATGCTGTGTCAACGC	396
Db	889	AATTTCCCTCCGGCTCTCTGACCCGAACGGATCCAGCTGACGTTTATGCTGTGTCAACGC	948
QY	397	ACATGGGGCTTCCGCGCCCGCAACTCGTGGTGTCAAGCTGGGGGGATCGGGGGGCC	456
Db	949	ACATGGGGCTTCCGCGCCCGCAACTCGTGGTGTCAAGCTGGGGGGATCGGGGGGCC	1008
QY	457	GTCTCCAGACCTGGCTGCAGAGCCTGCTGCGTGGGCTGGTGCAGGCTGCCAAGC	516
Db	1009	GTCTCCAGACCTGGCTGCAGAGCCTGCTGCGTGGGCTGGTGGCGGCTGCCAAGC	1068
QY	517	ACAGAGCCTGATTTGTACTGTGGGGGTCTGCACACGGGCATCCGCGCGGCATGTTGGTGTG	576
Db	1069	ACAGAGCCTGATTTGTACTGTGGGGGTCTGCACACGGGCATCCGCGCGGCATGTTGGTGTG	1128
QY	577	GCTGACGGAGCAATCAGATGGCCAGCACTGGGGGCAACAAGGTGGTGGCCATGGGTGTG	636
Db	1129	GCTGACGGAGCAATCAGATGGCCAGCACTGGGGGCAACAAGGTGGTGGCCATGGGTGTG	1188
QY	637	GCCCCCTGGGGTGTGGTCCGGAAATAGACACCCCTCATCAACCCCAAGGGCTGTTCCCT	696
Db	1189	GCCCCCTGGGGTGTGGTCCGGAAATAGACACCCCTCATCAACCCCAAGGGCTGTTCCCT	1248
QY	697	GCGAGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCTTGGACTACAC	756
Db	1249	GCGAGTACCGGTGGCGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCTTGGACTACAC	1308
QY	757	TACTGGGCTTCTTCTGTGTGAGCAGCGGCAACAACGGCTGCTGGGGGGGAGAAACGC	816
Db	1309	TACTGGGCTTCTTCTGTGTGAGCAGCGGCAACAACGGCTGCTGGGGGGGAGAAACGC	1368
QY	817	TTCCGCTTGCCTGTGAGTCTCTACATCTCACAGCAAGAACGGGCGTGGAGGGACTGGA	876
Db	1369	TTCCGCTTGCCTGTGAGTCTCTACATCTCACAGCAAGAACGGGCGTGGAGGGACTGGA	1428
QY	877	ATTGACATCCCTGTCTCTCTCTCTCTGATTGATGTGATGAAAGATGTTGACCGCAATA	936
Db	1429	ATTGACATCCCTGTCTCTCTCTCTCTGATTGATGTGATGAAAGATGTTGACCGCAATA	1488
QY	937	GAGAACGCGACCCAGGGCTCAGCTCCCATGTCCTCGTGGGCTGGCTCAGGGGGAGCTGCG	996
Db	1489	GAGAACGCGACCCAGGGCTCAGCTCCCATGTCCTCGTGGGCTGGCTCAGGGGGAGCTGCG	1548
QY	997	GACTGCTGGGGGAGACCCCTGAGAACACTCTGCGCCCAAGGAGTGGGGGAGCCAGGCCAA	1056
Db	1549	GACTGCTGGGGGAGACCCCTGAGAACACTCTGCGCCCAAGGAGTGGGGGAGCCAGGCCAA	1608
QY	1057	GGCGAAGCCCGAGATCGAATCAGCGGCTTTCTTCCCAAGGGGACTTGAAGCTCTGACG	1116
Db	1609	GGCGAAGCCCGAGATCGAATCAGCGGCTTTCTTCCCAAGGGGACTTGAAGCTCTGACG	1668
QY	1117	GCCCGGTGGAGAGGATATGACCCCGGAAGAGCTCCGACAGTCAATCTTCTGAGAT	1176
Db	1669	GCCCGGTGGAGAGGATATGACCCCGGAAGAGCTCCGACAGTCAATCTTCTGAGAT	1728
QY	1177	GGGTCTGAGAAATTGAGACCAATGTTTGAAGGCCCTTGTGAAGGCCCTGTGGAGCTCG	1236
Db	1729	GGGTCTGAGAAATTGAGACCAATGTTTGAAGGCCCTTGTGAAGGCCCTGTGGAGCTCG	1788
QY	1237	GAGGCTCAGCCTACCTGATGATGAGCTGCGTTTGTGTGCTGTGGAAACCGCGTGGACATT	1296
Db	1789	GAGGCTCAGCCTACCTGATGATGAGCTGCGTTTGTGTGCTGTGGAAACCGCGTGGACATT	1848
QY	1297	GCCCGAATGAACTTTTCGGGGGAGATCCAAATGGCGGTCTTCCATCTCGAAGCTTCC	1356
Db	1849	GCCCGAATGAACTTTTCGGGGGAGATCCAAATGGCGGTCTTCCATCTCGAAGCTTCC	1908
QY	1357	CTCATGAGACGCTCTGATATGACCGGGCTGAGTTCTGCGCTTGGCTCATTTTCCACGGC	1416
Db	1909	CTCATGAGACGCTCTGATATGACCGGGCTGAGTTCTGCGCTTGGCTCATTTTCCACGGC	1968
QY	1417	CTGACGCTGGGCACTTCTCTGACCCCGATGCGCTGGGCCCTGACCACTTACAGCGCGCGCC	1476

Db	1969	CTCAGCCTGGGCCACTTCTCTGACCCCGATGCGCCTGGCCCACTTACAGCGGGCGCC	2028
QY	1477	TCCAACTGCTCATCCGCAACCTTTTGGACCGAGCGTCCACAGCGAGGACCAAAACC	1536
Db	2029	TCCAACTGCTCATCCGCAACCTTTTGGACCGAGCGTCCACAGCGAGGACCAAAACC	2088
QY	1537	CCAGCCCTAAAAGGGGAGCTGCGGAGCTCGGCGCCCTTGACTGTGGGCACTGTCTAGG	1596
Db	2089	CCAGCCCTAAAAGGGGAGCTGCGGAGCTCGGCGCCCTTGACTGTGGGCACTGTCTAGG	2148
QY	1597	ATGCGCTGGGGAAAGATGTGCGCGCCGAGGATACCCCTCCGGGGGCGCGTGGAACTCTAC	1656
Db	2149	ATGCGCTGGGGAAAGATGTGCGCGCCGAGGATACCCCTCCGGGGGCGCGTGGAACTCTAC	2208
QY	1657	CCAGGCGAGGCTTCCGGGAGAGCATGTATCTGCTCCGACAGAGGCACCTCGCGCTC	1716
Db	2209	CCAGGCGAGGCTTCCGGGAGAGCATGTATCTGCTCCGACAGAGGCACCTCGCGCTC	2268
QY	1717	TCGCTGATGCTGCGCTTCGGGACGAGCCCTCGAGGCACTGCTTTTGGGCACTGTG	1776
Db	2269	TCGCTGATGCTGCGCTTCGGGACGAGCCCTCGAGGCACTGCTTTTGGGCACTGTG	2328
QY	1777	CTGAACAGGGGACAGATGCGCATCTTCCGGGAGATGGGTTCCATGCAATGTTCCTCA	1836
Db	2329	CTGAACAGGGGACAGATGCGCATCTTCCGGGAGATGGGTTCCATGCAATGTTCCTCA	2388
QY	1837	GCTCTTGGGGGCTCTTTTGTGCTGCTCCGGGTGATGACAGCCTGAGCCTGACGCTGAGAG	1896
Db	2389	GCTCTTGGGGGCTCTTTTGTGCTGCTCCGGGTGATGACAGCCTGAGCCTGAGGAGAG	2448
QY	1897	GCAGACGAGAGAAAGACCTGGCCTTCAAGTTTGAGGGGATGGGCGTTTGACTTTTGGC	1956
Db	2449	GCAGACGAGAGAAAGACCTGGCCTTCAAGTTTGAGGGGATGGGCGTTTGACTTTTGGC	2508
QY	1957	GAGTGCATTCGCACAGATGAGATGAGGGCTGGCCGCTCCCTCCGATCGCTGCGCGCTC	2016
Db	2509	GAGTGCATTCGCACAGATGAGATGAGGGCTGGCCGCTCCCTCCGATCGCTGCGCGCTC	2568
QY	2017	TGGGGGGGATGSCACTTTGGCCTCACACTGGGACATGACAAGCTGACGCGCTGCTTTTGGC	2076
Db	2569	TGGGGGGGATGSCACTTTGGCCTCACACTGGGACATGACAAGCTGACGCGCTTCTTTGGC	2628
QY	2077	CAGATGAGGATACAGTCTTCTGCTGACACAGAAATGGTGGGAGATATGGCCAGACTACA	2136
Db	2629	CAGATGAGGATACAGTCTTCTGCTGACACAGAAATGGTGGGAGATATGGCCAGACTACA	2688
QY	2137	CCCATCTGGGCGCTGTGCTTCTGCTTCTTTGGCCCTCATCATCTTACACCCGCTCATC	2196
Db	2689	CCCATCTGGGCGCTGTGCTTCTGCTTCTTTGGCCCTCATCATCTTACACCCGCTCATC	2748
QY	2197	ACCTTCAGGAATCAGAAAGAGAGCCCAACGAGAGAGCTAGATTTGACATGATAGT	2256
Db	2749	ACCTTCAGGAATCAGAAAGAGAGCCCAACGAGAGAGCTAGATTTGACATGATAGT	2808
QY	2257	GTCATTAATGAGGAAGGGCTGTGCGGACCGCGGACCCAGCCGAAAGACGCGCTGAGG	2316
Db	2809	GTCATTAATGAGGAAGGGCTGTGCGGACCGCGGACCCAGCCGAAAGACGCGCTGAGG	2868
QY	2317	GTCGCGGCGCAGTGGGCGCTTCGCGGTTGCTGCGGGGGCGCTTCGGGGGGCGCGGTGC	2376
Db	2869	GTCGCGGCGCAGTGGGCGCTTCGCGGTTGCTGCGGGGGCGCTTCGGGGGGCGCGGTGC	2928
QY	2377	CTAGCGCGCTGGTTCAACTTTCGGGGGGCGCGGATGACATCTTCATGGGCAAGTGTTC	2436
Db	2929	CTAGCGCGCTGGTTCAACTTTCGGGGGGCGCGGATGACATCTTCATGGGCAAGTGTTC	2988
QY	2437	AGCTACCTGCTGTTCTGTGCTTTTCTCGCGGATGCTGCTGCGAATTTCCAGCCGCG	2496
Db	2989	AGCTACCTGCTGTTCTGTGCTTTTCTCGCGGATGCTGCTGCGAATTTCCAGCCGCG	3048
QY	2497	CCGCCCGGCTCCCTGAGCTGCTGCTCATTTTCTGGCGTTTCAACGCTGTGTGCGAGAA	2556

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Db      3049  CCGCCGCGCTCCCTGAGAGCTGCTCTAATTTCTGCGCTTTTCAACGCTGCTGTGCGAGGAA 3108
Qy      2557  CTGGCCGAGAGGCTGAGGGAGGGGGGAGCCCTGCGACGCGGGGGGCCCGGGGCTGGC 2616
Db      3109  CTGGCCGAGAGGCTGAGGGAGGGGGGAGCCCTGCGACGCGGGGGGCCCGGGGCTGGC 3168
Qy      2617  CATGCTCACTGAGCAGCAGCGCTGCGCTCTACCTGCGGAGAGCTGGAACAGTGGCAGC 2676
Db      3169  CATGCTCACTGAGCAGCAGCGCTGCGCTCTACCTGCGGAGAGCTGGAACAGTGGCAGC 3228
Qy      2677  CTAGTGGCTCTACCTGCTTCTCTGCGCGTGGCGTGGCGCTGACCCCGGGTTTGTAC 2736
Db      3229  CTAGTGGCTCTACCTGCTTCTCTGCGCGTGGCGTGGCGCTGACCCCGGGTTTGTAC 3288
Qy      2737  CACCTGGGCGGCACTGTCTCTGCGATCGACTTCAATGTTTTCAACGCTGCGGTGTTTAC 2796
Db      3289  CACCTGGGCGGCACTGTCTCTGCGATCGACTTCAATGTTTTCAACGCTGCGGTGTTTAC 3348
Qy      2797  ATCTTCAAGGTCAACAAACAGCTGGGGGCCAAGATCGTCACTGAGCAAGATGATGAAG 2856
Db      3349  ATCTTCAAGGTCAACAAACAGCTGGGGGCCAAGATCGTCACTGAGCAAGATGATGAAG 3408
Qy      2857  GACGTGTTCTTCTCTCTCTTCTCTGCGCGTGGCGTGGTACGCTATGCGTGGCCACG 2916
Db      3409  GACGTGTTCTTCTCTCTCTTCTCTGCGCGTGGCGTGGTACGCTATGCGTGGCCACG 3468
Qy      2917  GAGGGGCTCTGAGGGCCACGGGACAGTACTTCCCAATCTCTGCGCGCTCTTCTTAC 2976
Db      3469  GAGGGGCTCTGAGGGCCACGGGACAGTACTTCCCAATCTCTGCGCGCTCTTCTTAC 3528
Qy      2977  CGTCCCTCACTGAGATCTTGGGCGAGATTCCCGAGAGACATGGAAGCTGGCCCTCAG 3036
Db      3529  CGTCCCTCACTGAGATCTTGGGCGAGATTCCCGAGAGACATGGAAGCTGGCCCTCAG 3588
Qy      3037  GAGCAGACCAACTGCTGCTGCGAGGCCGCGCTTCTGAGGACACCTCTGCGGGCCAGGCG 3096
Db      3589  GAGCAGACCAACTGCTGCTGCGAGGCCGCGCTTCTGAGGACACCTCTGCGGGCCAGGCG 3648
Qy      3097  GGCACTGCTGCTCTCCAGTATGCGCACTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3156
Db      3649  GGCACTGCTGCTCTCCAGTATGCGCACTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGG 3708
Qy      3157  CTCGCGGCAACATCTGCTGCTGCTCAACTGCTCATTTGCAATGTTAAGTTAATTCGCGC 3216
Db      3709  CTCGCGGCAACATCTGCTGCTGCTCAACTGCTCATTTGCAATGTTAAGTTAATTCGCGC 3768
Qy      3217  AAAGTACAGGGGCAACAGCGATCTCTAATGGAAGGCGCAGCGTTACCGGCTCATCCGGGAA 3276
Db      3769  AAAGTACAGGGGCAACAGCGATCTCTAATGGAAGGCGCAGCGTTACCGGCTCATCCGGGAA 3828
Qy      3277  TTCCACTCTCGGCGCGCGCTGGCCCGGCTTTATGCTCATTTCCCACTTGGGCTCTCTG 3336
Db      3829  TTCCACTCTCGGCGCGCGCTGGCCCGGCTTTATGCTCATTTCCCACTTGGGCTCTCTG 3888
Qy      3337  CTACAGCAATTGTGAGGCAACCCGGAAGCCCGGAGCCGCTCTCCCGGCGCTCGAGCAT 3396
Db      3889  CTACAGCAATTGTGAGGCAACCCGGAAGCCCGGAGCCGCTCTCCCGGCGCTCGAGCAT 3948
Qy      3397  TTCCGGGTTTACTTTCTTAAGGAAGCCGAGCGGAAGTGTCTAACTGGGAATCGGTGAT 3456
Db      3949  TTCCGGGTTTACTTTCTTAAGGAAGCCGAGCGGAAGTGTCTAACTGGGAATCGGTGAT 4008
Qy      3457  AAGGAGAACTTTCTGCTGCGACGCGCTTAGGAGCAAGCGGAGAGCGACTCCGAGGCTGTG 3516
Db      4009  AAGGAGAACTTTCTGCTGCGACGCGCTTAGGAGCAAGCGGAGAGCGACTCCGAGGCTGTG 4068
Qy      3517  AAGCGACAGTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 3576
Db      4069  AAGCGACAGTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGCGAGTAC 4128
Qy      3577  GAACAGCGCTGAAAGTCTGAGCGGAGAGGTCCAGCAGTGTAGCGCGCTCTGCGGGTGG 3636
Db      4129  GAACAGCGCTGAAAGTCTGAGCGGAGAGGTCCAGCAGTGTAGCGCGCGCTCTGCGGGTGG 4188

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Qy      3637  GTGGCCGAGGCGCTGAGCGGCTGTGCTTGTGCGCCCGGAGTGGGCGGCCACCCCTGAC 3696
Db      4189  GTGGCCGAGGCGCTGAGCGGCTGTGCTTGTGCGCCCGGAGTGGGCGGCCACCCCTGAC 4248
Qy      3697  CTGGCTGGGTTCAAAGACTGAGCCCTGTGCGGACTTCAAGAGAGAACCCCGACAGGGG 3756
Db      4249  CTGGCTGGGTTCAAAGACTGAGCCCTGTGCGGACTTCAAGAGAGAACCCCGACAGGGG 4308
Qy      3757  ATTTTGCTCTAAGTAAAGGCTCATCTGAGGCTTGGGCGCCCGGCACTGTGGGCTTGTCC 3816
Db      4309  ATTTTGCTCTAAGTAAAGGCTCATCTGAGGCTTGGGCGCCCGGCACTGTGGGCTTGTCC 4368
Qy      3817  TTGAGTGAAGCCCAATGCTCATCTGAGGCACTGTGAGGACCACTTTTGGAGTGCATCC 3876
Db      4369  TTGAGTGAAGCCCAATGCTCATCTGAGGCACTGTGAGGACCACTTTTGGAGTGCATCC 4428
Qy      3877  TTACAAACCAAGCATGCGCGCTCTCTCCAGAAACCACTGCCAGCTGGAGATCAAG 3936
Db      4429  TTACAAACCAAGCATGCGCGCTCTCTCCAGAAACCACTGCCAGCTGGAGATCAAG 4488
Qy      3937  CCTGGATCCCGGCGCGTTATCATCTGAGGCTGAGGCTCTTGGGGTAAACAGGACCA 3996
Db      4489  CCTGGATCCCGGCGCGTTATCATCTGAGGCTGAGGCTCTTGGGGTAAACAGGACCA 4548
Qy      3997  CAGACCCCTCACTCACTCAAGATTCTCTCACTGCGGGAATTAAGCCATTTCAGAGAAA 4056
Db      4549  CAGACCCCTCACTCACTCAAGATTCTCTCACTGCGGGAATTAAGCCATTTCAGAGAAA 4608
Qy      4057  AAAAA 4061
Db      4609  AAAAA 4613

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RESULT 7
ADL06463
ID ADL06463 standard; cDNA; 3898 BP.
XX
AC ADL06463;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #43.
XX
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
  cancer; cytosolic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GENTECH ) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V,
  Spencer SD, Wu TD, Zhang Z;
XX
DR WPI: 2004-257144/24.
DR P-PsDB; ADL06543.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
  polypeptide, useful for preparing a composition for diagnosing or
  treating cancer.
PT

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XX Claim 1; SEQ ID NO 43; 319pp; English.
PS
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAR) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAR polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAR cDNA sequence of the invention.
XX
SQ Sequence 3898 BP; 685 A; 1207 C; 1235 G; 771 T; 0 U; 0 Other;
Query Match 93.9%; Score 3812.2; DB 12; Length 3898;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3848; Conservative 0; Mismatches 23; Indels 2; Gaps 2;
QY 190 CCCCAGACCGCCACCCCGCAGTGGCCATGAGAGATGCCCTTCGCGGACGCGTGTGACC 249
DB 7 CCCCCGAGCGCCACCCCGCAGTGGCCATGGA-GAAGCCTTCGCGGACGCGTGTGACC 65
QY 250 GTGTGGGACAGCGATGCAC-AACCAAGGAAAGCCACCGATGCTTAGAGAGCTGGA 308
DB 66 GTGTGGGACAGCGATGCACACACAGAGAAAGCCACCGATGCTTAGAGAGCTGGA 125
QY 309 CTTCAAGGGGGCGGCGGAGACAGCAATTTCTCCGCGCTCTGAACGAGATCC 368
DB 126 CTTCAAGGGGGCGGCGGAGACAGCAATTTCTCCGCGCTCTGAACGAGATCC 185
QY 369 AGCTGAGTTTATAGTCTGTCAACGCAATGGGGCTTCGTCGCCGAACCTGTGTGT 428
DB 186 AGCTGAGTTTATAGTCTGTCAACGCAATGGGGCTTCGTCGCCGAACCTGTGTGT 245
QY 429 GTCAAGTCTGGGGGGATCGGGGGGCCCGTCTTCCAGACTGTGCTCAAGACTGTGCTG 488
DB 246 GTCAAGTCTGGGGGGATCGGGGGGCCCGTCTTCCAGACTGTGCTCAAGACTGTGCTG 305
QY 489 TCGTGGGCTGGTGGCGGCTGCCAGAGACAGAGAGCTGGAATTGTACTGGGGGTCTGCA 548
DB 306 TCGTGGGCTGGTGGCGGCTGCCAGAGACAGAGAGCTGGAATTGTACTGGGGGTCTGCA 365
QY 549 CAGGGGCAATCGGCGGCAATGTTGTGTGTGCTGTACCGGACCAATGAGACTGCG 608
DB 366 CAGGGGCAATCGGCGGCAATGTTGTGTGTGCTGTACCGGACCAATGAGACTGCG 425
QY 609 GGGGACCAAGGTGTGGCCATGGGTGTGGCCCCCTGGGGTGTGTCCGAAATGAGACAC 668
DB 426 GGGGACCAAGGTGTGGCCATGGGTGTGGCCCCCTGGGGTGTGTCCGAAATGAGACAC 485
QY 669 CCTCATCAACCCCAAGGGCTCGTTCCCTGAGGTTACCGGTGGCGGGTGAACCCGAGGA 728
DB 486 CCTCATCAACCCCAAGGGCTCGTTCCCTGAGGTTACCGGTGGCGGGTGAACCCGAGGA 545
QY 729 CGGGGTCAAGTTTCCCTGAGCTACCAATCTACGCGCTTCTTCTGTGTGACGACG 788
DB 546 CGGGGTCAAGTTTCCCTGAGCTACCAATCTACGCGCTTCTTCTGTGTGACGACG 605
QY 789 ACAAGGCTGCTGGGGGGGAGAGAACGCTTCGCTGGCGCTGGAATCTTCAATCTACA 848
DB 606 ACAAGGCTGCTGGGGGGGAGAGAACGCTTCGCTGGCGCTGGAATCTTCAATCTACA 665
QY 849 GCAGAAAGAGGGGGTGGGAGGAGCTGGAATTGACCTCGTCTGCTCTCTGATTTGA 908
DB 666 GCAGAAAGAGGGGGTGGGAGGAGCTGGAATTGACCTCGTCTGCTCTCTGATTTGA 725
QY 909 TGGTGAATGAAGATTTGACGCGAATAGAGAACGACCAAGGCTCAGCTCCATGCT 968
DB 726 TGGTGAATGAAGATTTGACGCGAATAGAGAACGACCAAGGCTCAGCTCCATGCT 785
QY 969 CCTCGTGGCTGCTCAGGGGGAGCTGCGACTGCTGGCGGAGACCTTGAAAGACCTCT 1028

DB 786 CCTCGTGGCTGCTCAGGGGGAGCTGCGGACTGCTTGGCGAGACCTTGAAAGACCTCT 845
QY 1029 GGCCCCAGGAGATGGGGGGAGCCAGGCAAGCCGAAATCGAATCAGCGTTCTT 1088
DB 846 GGCCCCAGGAGATGGGGGGAGCCAGGCAAGCCGAAATCGAATCAGCGTTCTT 905
QY 1089 TCCCAAGGGGACCTTTAGGTCCTTCAGGCGCCAGGTGAGAGATTTATGACCCGAGGA 1148
DB 906 TCCCAAGGGGACCTTTAGGTCCTTCAGGCGCCAGGTGAGAGATTTATGACCCGAGGA 965
QY 1149 GCTTCGACAGCTATTTCTTCTGAGAGTGGCTGAGAAATTCGAGCCATAGTTTGA 1208
DB 966 GCTTCGACAGCTATTTCTTCTGAGAGTGGCTGAGAAATTCGAGCCATAGTTTGA 1025
QY 1209 GGCCCTTGGAAGGCTGTGGAGCTCGGAGGCTCAGCGCTACCTGATGAGCTCGTTT 1268
DB 1026 GGCCCTTGGAAGGCTGTGGAGGCTCGGAGGCTCAGCGCTACCTGATGAGCTCGTTT 1085
QY 1269 GGCCTGTGGAACCGGCTGGAGCAATTGCCAGATGAATCTTTTGGGGGACATCCA 1328
DB 1086 GGCCTGTGGAACCGGCTGGAGCAATTGCCAGATGAATCTTTTGGGGGACATCCA 1145
QY 1329 ATGGCGGTCTTCCATCTTGAAGCTTCCCTCATGAGCGCCCTGCTGAATGAGCCGCTGA 1388
DB 1146 ATGGCGGTCTTCCATCTTGAAGCTTCCCTCATGAGCGCCCTGCTGAATGAGCCGCTGA 1205
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DB 1206 GTTCGTGCGCTTGTCTCATTTTCCAGGCGCTCAGCCTGGGCACTTCTTGAACCCGATGCG 1265
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DB 1386 GCCCCTGACGTGGGGACATGTCTGAGATGCTGCTGGGAGAGATGTGCGCCGAGATTA 1445
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DB 1626 GAGAGATGGGTTCCAAATGACGTTTCTCAAGCTTTTGGGGCTGTGTGCTCGGGTGTAT 1685
QY 1869 GGCAGCGCTGAGAGCTGAGGCTGAGAGGACAGACGAGAGAAAGACTGTGCTTCAAGTT 1928
DB 1686 GGCAGCGCTGAGAGCTGAGGCTGAGAGGACAGACGAGAGAAAGACTGTGCTTCAAGTT 1745
QY 1929 TGAAGGAGATGGGCGTTGACCTTTTGGGAGGCTATCGACAGTGAAGGTGAGGCTGTC 1988
DB 1746 TGAAGGAGATGGGCGTTGACCTTTTGGGAGGCTATCGACAGTGAAGGTGAGGCTGTC 1805
QY 1989 CCGCTCTCTCTCCGTGCTGCGCTCGCTGCGGGAGATGCACTTTCAGACTGAGCAT 2048
DB 1806 CCGCTCTCTCTCCGTGCTGCGCTCGCTGCGGGAGATGCACTTTCAGACTGAGCAT 1865
QY 2049 GCAAGCTGACGCGCGCTCTTTTGGCCAGGATGGGGTACAGTCTGTGCTGACACAGAA 2108
DB 1866 GCAAGCTGACGCGCGCTCTTTTGGCCAGGATGGGGTACAGTCTGTGCTGACACAGAA 1925

QY 2109 GTGGTGGAGATATAGCCAGCACTACACCATCTGGCCCTGGTTCTGGCTTCTTTG 2168
DB 1926 GTGGTGGAGATATAGCCAGCACTACACCATCTGGCCCTGGTTCTGGCTTCTTTG 1985
QY 2169 CCTTCACATCTATCAACCCGCTCATCACTTCAGAAATCAGAAAGAGACCCACAAG 2228
DB 1986 CCTTCACATCTATCAACCCGCTCATCACTTCAGAAATCAGAAAGAGACCCACAAG 2045
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QY 2349 CGGGGGCCGCTGGGGGGGGCGCGGTGCCTACGCCGCTGGTTCACTTCGGGGCGCGC 2408
DB 2166 CGGGGGCCGCTGGGGGGGGCGCGGTGCCTACGCCGCTGGTTCACTTCGGGGCGCGC 2225
QY 2409 GGTGACATCTTCATATGGGCAAGTGTGACCTGCTGTCTGGCTGCTTTTCTCGCG 2468
DB 2226 GGTGACATCTTCATATGGGCAAGTGTGACCTGCTGTCTGGCTGCTTTTCTCGCG 2285
QY 2469 GGTGCTGCTCGTGAATTTCAAGCGGGCGCGCGGCTCCCTGGAGCTGCTGCTATTT 2528
DB 2286 GGTGCTGCTCGTGAATTTCAAGCGGGCGCGCGGCTCCCTGGAGCTGCTGCTATTT 2345
QY 2529 CTGGCTTTTCAAGCTGTGTGAGAGAACTGGCCAGAGGCTGAGCGAGCGGGGAG 2588
DB 2346 CTGGCTTTTCAAGCTGTGTGAGAGAACTGGCCAGAGGCTGAGCGAGCGGGGAG 2405
QY 2589 CCTGCCAGCGGGGGGCCCGGGGCTGGCCATGCTCTCACTGAGCCAGCGCTGCTCTA 2648
DB 2406 CCTGCCAGCGGGGGGCCCGGGGCTGGCCATGCTCTCACTGAGCCAGCGCTGCTCTA 2465
QY 2649 CCTGCCAGCGCTGGAACTAGTGGAGCTAGTGGCTCTCACTGCTCTCTCTGGGGGT 2708
DB 2466 CCTGCCAGCGCTGGAACTAGTGGAGCTAGTGGCTCTCACTGCTCTCTCTGGGGGT 2525
QY 2709 GGGCTGCCGCTGACCCCGGGTTTGTACCACTGGGGCGCACTGCTCTGATGACTT 2768
DB 2526 GGGCTGCCGCTGACCCCGGGTTTGTACCACTGGGGCGCACTGCTCTGATGACTT 2585
QY 2769 CATGTTTTTCAAGGTGCGGCTGCTTCACTTTCAGGTCAACAAACAGCTGGGGCCAA 2828
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DB 2646 GATGCTCATCGTGGAGAGATGATGAAGAGCTGTTCTTCTCTCTCTCTCTGGGGGT 2705
QY 2889 GTGGCTGTATGCTTATGAGCTGGCCAGAGAGGCTCTGAGAGCCACGGGACAGTGACTT 2948
DB 2706 GTGGCTGTATGCTTATGAGCTGGCCAGAGAGGCTCTGAGAGCCACGGGACAGTGACTT 2765
QY 2949 CCAAGATATCTTGGCGCGCTGTTCTTACCTGCTCTTACCTGAGATCTTTCGGGACAGTTCC 3008
DB 2766 CCAAGATATCTTGGCGCGCTGTTCTTACCTGCTCTTACCTGAGATCTTTCGGGACAGTTCC 2825
QY 3009 CCAGAGAGACATGAGAGCTGGCCCTCATATGAGACAGAGCACTGCTGTGGAGCCGGGCTT 3068
DB 2826 CCAGAGAGACATGAGAGCTGGCCCTCATATGAGACAGAGCACTGCTGTGGAGCCGGGCTT 2885
QY 3069 CTGGGACACACCTCTCTGGGGCCAGCGGGGACCTGCTCTCCAGTATGCAACTGGCT 3128
DB 2886 CTGGGACACACCTCTCTGGGGCCAGCGGGGACCTGCTCTCCAGTATGCAACTGGCT 2945
QY 3129 GGTGGTGTGCTCTCTGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3188
DB 2946 GGTGGTGTGCTCTCTGCTATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005

QY 3189 CATTCAGTGTTCAGTTACATATTCGAGCAAGTACAGGGCAACAGCGATCTCTACGAA 3248
DB 3006 CATTCAGTGTTCAGTTACATATTCGAGCAAGTACAGGGCAACAGCGATCTCTACGAA 3065
QY 3249 GGGCAGCGTTAACCGCTCATTCGGGAAATTCACCTTGGGCCCGGCTGGCCCGCTT 3308
DB 3066 GGGCAGCGTTAACCGCTCATTCGGGAAATTCACCTTGGGCCCGGCTGGCCCGCTT 3125
QY 3309 TATGCTATCTTCCACTTGGCTCTGCTCAAGCAATTTGTGACAGCGACCCCGAGCC 3368
DB 3126 TATGCTATCTTCCACTTGGCTCTGCTCAAGCAATTTGTGACAGCGACCCCGAGCC 3185
QY 3369 CGAGCGCTCTCCCGGCGCTCGAGCAATTCGGGTTTACCTTTTAAGAAAGCGAGCG 3428
DB 3186 CGAGCGCTCTCCCGGCGCTCGAGCAATTCGGGTTTACCTTTTAAGAAAGCGAGCG 3245
QY 3429 GAAGCTGTAACTGTGGAAATCGGTGACATTAAGAGAACTTTCTGCTGGACGCTAGGGA 3488
DB 3246 GAAGCTGTAACTGTGGAAATCGGTGACATTAAGAGAACTTTCTGCTGGACGCTAGGGA 3305
QY 3489 CAGCGGAGAGCCGACTCGAGCTGTGAAGCGACCTCCAGAAAGTGTGACTTGGCACT 3548
DB 3306 CAGCGGAGAGCCGACTCGAGCTGTGAAGCGACCTCCAGAAAGTGTGACTTGGCACT 3365
QY 3549 GAACAGCTGGGACATCCGCGAGTACGAAACAGGCGCTGAAGGTGAGCGGGAGGT 3608
DB 3366 GAACAGCTGGGACATCCGCGAGTACGAAACAGGCGCTGAAGGTGAGCGGGAGGT 3425
QY 3609 CCAGAGTGTAGCGCGCTCTGGGGTGGGTGGCGGAGGCTGAGCCGCTGCTGCTTGT 3668
DB 3426 CCAGAGTGTAGCGCGCTCTGGGGTGGGTGGCGGAGGCTGAGCCGCTGCTGCTTGT 3485
QY 3669 GCCCCAGGTGGGCCGCCACCCCTGACCTGCTGGTCTCAAGACTGAGCCCTGTGGC 3728
DB 3486 GCCCCAGGTGGGCCGCCACCCCTGACCTGCTGGTCTCAAGACTGAGCCCTGTGGC 3545
QY 3729 GGACTTCAAGAGAAAGCCCCCAAGGGATTTTCTCTTAAGTAAAGCTCATGCGGGC 3788
DB 3546 GGACTTCAAGAGAAAGCCCCCAAGGGATTTTCTCTTAAGTAAAGCTCATGCGGGC 3605
QY 3789 TGGCCCCCGACAGCTGTGGCTTGTCTTGGAGTGAAGCCCATGCTCATGCGGCACT 3848
DB 3606 TGGCCCCCGACAGCTGTGGCTTGTCTTGGAGTGAAGCCCATGCTCATGCGGCACT 3665
QY 3849 GTCAAGACACCTTTGGAGTGTATCTTCAACAAACACAGACATGCCCCGCTCTCCAG 3908
DB 3666 GTCAAGACACACCTTTGGAGTGTATCTTCAACAAACACAGACATGCCCCGCTCTCCAG 3725
QY 3909 AACCAATCCCAAGCTGGAGAGATGAAGGCTGGATCCCGGGCGCTTAATCCATTCGAGGC 3968
DB 3726 AACCAATCCCAAGCTGGAGAGATGAAGGCTGGATCCCGGGCGCTTAATCCATTCGAGGC 3785
QY 3969 TGCAGGCTCTTGGGGTTAAACAGAGACACAGACCCCTACACATCAAGATTCCTCAAC 4028
DB 3786 TGCAGGCTCTTGGGGTTAAACAGAGACACAGACCCCTCAACATCAAGATTCCTCAAC 3845
QY 4029 TGGGAAATTAAGCCATTTTCAGAGAAAAAAA 4061
DB 3846 TGGGAAATTAAGCCATTTTCAGAGAAAAAAA 3878

RESULT 8
ABK92167
ID ABK92167 standard; DNA; 3810 BP.
XX ABK92167;
XX AC
XX 15-AUG-2002 (first entry)
DT
XX Prostate cancer-associated DNA sequence #53.
DE
XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

Db 1321 TGAGATCTCTGGGGAAAGTGCAGCGCCGAGGTACCCCTCCGAGGCGCTGAGACC 1380
Qy 1652 CTCACCCAGGCGAGGGCTTTCGGGGAGAGCATGTATCTGCTCGGACAAGGCACTCGC 1711
Db 1381 CTCACCCAGGCGAGGGCTTTCGGGGAGAGCATGTATCTGCTCGGACAAGGCACTCGC 1440
Qy 1712 CGCTCTCGCTGGATGCTGGCCCTCGGGCAGGCCCTCGAGCGACCTGCTTCTTTGGGAC 1771
Db 1441 CGCTCTCGCTGGATGCTGGCCCTCGGGCAGGCCCTCGAGCGACCTGCTTCTTTGGGAC 1500
Qy 1772 TGTTCCTGAACAGGGCAAGATGGCTATGTACTTCTGGAGATGGGTTCCAATGCAATTT 1831
Db 1501 TGTTCCTGAACAGGGCAAGATGGCTATGTACTTCTGGAGATGGGTTCCAATGCAATTT 1560
Qy 1832 CCTGAGCTCTTGGGGGCTGTTTGGCTCCGGGATGAGCAAGCCTGAGCCTGACGCTG 1891
Db 1561 CCTGAGCTCTTGGGGGCTGTTTGGCTCCGGGATGAGCAAGCCTGAGCCTGACGCTG 1620
Qy 1892 AGGAGGCAAGCAGAGAAAGACTGGGCTTCAAGTTTGAAGGAGATGGGCTTGAAGCTT 1951
Db 1621 AGGAGGCAAGCAGAGAAAGACTGGGCTTCAAGTTTGAAGGAGATGGGCTTGAAGCTT 1680
Qy 1952 TTGGGAGTGTATGAGCAGAGTGAAGGCTGCGGCTCTCTCTCGCTCGCTG 2011
Db 1681 TTGGGAGTGTATGAGCAGAGTGAAGGCTGCGGCTCTCTCTCGCTCGCTG 1740
Qy 2012 CGCTCTGGGGGAGTCCCACTTGCTCCAGCTGAGCCATGCAAGCTACCGCCGCTTCT 2071
Db 1741 CGCTCTGGGGGAGTCCCACTTGCTCCAGCTGAGCCATGCAAGCTACCGCCGCTTCT 1800
Qy 2072 TTGCCAGATGGGGTGAAGTCTGTGTCAGACAGAGTGGTGGGAGATATGACAGA 2131
Db 1801 TTGCCAGATGGGGTGAAGTCTGTGTCAGACAGAGTGGTGGGAGATATGACAGA 1860
Qy 2132 CTACACCCATCTGGGCTCTGGTCTCGCTTCTTTGCTCTCACTCACTACACCGCC 2191
Db 1861 CTACACCCATCTGGGCTCTGGTCTCGCTTCTTTGCTCTCACTCACTACACCGCC 1920
Qy 2192 TCATCACTTTCAGAAATCAGAAAGAGGCCACACCGGAGAGCTTAAGTTTGACATGG 2251
Db 1921 TCATCACTTTCAGAAATCAGAAAGAGGCCACACCGGAGAGCTTAAGTTTGACATGG 1980
Qy 2252 ATAGTGTCAATTAATGGGAGAGGCTGTGCGGAGCGGAGCCAGCCGAGAGAGCGCCG 2311
Db 1981 ATAGTGTCAATTAATGGGAGAGGCTGTGCGGAGCGGAGCCAGCCGAGAGAGCGCCG 2040
Qy 2312 TGGGGTCCCGCGCAGTCCGGCCGTCCGGTGTGCTGCGGGGCGCTGCGGGGCGCC 2371
Db 2041 TGGGGTCCCGCGCAGTCCGGCCGTCCGGTGTGCTGCGGGGCGCTGCGGGGCGCC 2100
Qy 2372 GGTGCTTAGCGCGCTGTTTCACTTTCGGGGCGCGCGGTGACATCTTTCATGGGCAAG 2431
Db 2101 GGTGCTTAGCGCGCTGTTTCACTTTCGGGGCGCGCGGTGACATCTTTCATGGGCAAG 2160
Qy 2432 TGTGAGCTACCTGCTGTTCCGCTGCTTTCGCGGGGTGTGTCGTGATTTCCAGC 2491
Db 2161 TGTGAGCTACCTGCTGTTCCGCTGCTTTCGCGGGGTGTGTCGTGATTTCCAGC 2220
Qy 2492 CGGGCGCGCGCGCTTTCGAGAGCTGCTTAATTTCTGGGCTTTCAGCGCTGCTGCG 2551
Db 2221 CGGGCGCGCGCGCTTTCGAGAGCTGCTTAATTTCTGGGCTTTCAGCGCTGCTGCG 2280
Qy 2552 AGGAACTGCGCAGGGCTTGAAGCGGAGCGGGGAGCTTTCGACGAGGGGCGCGGGC 2611
Db 2281 AGGAACTGCGCAGGGCTTGAAGCGGAGCGGGGAGCTTTCGACGAGGGGCGCGGGC 2340
Qy 2612 CTGAGCAATGCTCACTGAGCAGGCGCTGCTTCACTGCGCAAGCTGGAACAGT 2671
Db 2341 CTGAGCAATGCTCACTGAGCAGGCGCTGCTTCACTGCGCAAGCTGGAACAGT 2400
Qy 2672 GCGACCTAGGCTCTCACTGCTTCTCTGAGGCTGAGGCTGACCCCGGCTT 2731

Db 2401 GCGACCTAGGCTCTCACTGCTTCTCTGAGGCGTGGGCTGCGGCTGACCCCGGCTT 2460
Qy 2732 TGTACCACTTGGGCGCAGCTGCTCTGATCGACTTCAATGATTTTCAAGGCGGCTG 2791
Db 2461 TGTACCACTTGGGCGCAGCTGCTCTGATCGACTTCAATGATTTTCAAGGCGGCTG 2520
Qy 2792 TTCACTTTCACGGTCAACAAACAGCTGGGCGCCAGATGCTCATCTGAGCAAGATGA 2851
Db 2521 TTCACTTTCACGGTCAACAAACAGCTGGGCGCCAGATGCTCATCTGAGCAAGATGA 2580
Qy 2852 TGAAGAGCTGTTCTTCT 2911
Db 2581 TGAAGAGCTGTTCTTCT 2640
Qy 2912 CCAGGAGGGGCTCTGAGGCGACGAGGACAGTGACTTCCCAAGTATCCCTGGCGCGCT 2971
Db 2641 CCAGGAGGGGCTCTGAGGCGACGAGGACAGTGACTTCCCAAGTATCCCTGGCGCGCT 2700
Qy 2972 TCTACCGTCCCTACCTGAGATCTTCCGGCAGATTTCCCAAGAGACATGACGTGCGC 3031
Db 2701 TCTACCGTCCCTACCTGAGATCTTCCGGCAGATTTCCCAAGAGACATGACGTGCGC 2760
Qy 3032 TCATGAGCAGCAAGCACTGCTGTGAGGCCCGGCTTGGGACACCTCTCGGGGCGC 3091
Db 2761 TCATGAGCAGCAGCAAGCACTGCTGTGAGGCCCGGCTTGGGACACCTCTCGGGGCGC 2820
Qy 3092 AGCGGGGACCTGGCTCTCCCAAGTATGCACTGGGCTGCTGCTCTCTCTCTCTCTCT 3151
Db 2821 AGCGGGGACCTGGCTCTCCCAAGTATGCACTGGGCTGCTGCTCTCTCTCTCTCTCT 2880
Qy 3152 TCTGCTGTGGGCAACATCTGCTGTCGTCATCTTGTCACTTTCAGTTTCAAGAT 3211
Db 2881 TCTGCTGTGGGCAACATCTGCTGTCGTCATCTTGTCACTTTCAGTTTCAAGAT 2940
Qy 3212 TCGGCAAGTACAGGGCAACGCAATCTTACGAGAGCGCAGGTTTACCGCTCATCC 3271
Db 2941 TCGGCAAGTACAGGGCAACGCAATCTTACGAGAGCGCAGGTTTACCGCTCATCC 3000
Qy 3272 GGGAAATTCACATCTTCGGCGCGCGCTGGCGCCCTTTATGTATCTTCCCATTTGGCC 3331
Db 3001 GGGAAATTCACATCTTCGGCGCGCGCTGGCGCCCTTTATGTATCTTCCCATTTGGCC 3060
Qy 3332 TCTGCTCAGGCAATTTGTCAGGCGACCCCGGAGCCCGCAGCTCTCCCGGCGCTCG 3391
Db 3061 TCTGCTCAGGCAATTTGTCAGGCGACCCCGGAGCCCGCAGCTCTCCCGGCGCTCG 3120
Qy 3392 AGCATTTCCGGGTTTACCTTTCTAAGAGAGCGGAGCTGTAAGTGGGATTCG 3451
Db 3121 AGCATTTCCGGGTTTACCTTTCTAAGAGAGCGGAGCTGTAAGTGGGATTCG 3180
Qy 3452 TGCATTAAGAGAACTTTTCTGCTGGACGCGCTTAGGACAGCGGAGAGCGACTCCGAGC 3511
Db 3181 TGCATTAAGAGAACTTTTCTGCTGGACGCGCTTAGGACAGCGGAGAGCGACTCCGAGC 3240
Qy 3512 GTCTGAAGCGCAGCTCCAGAGGTGACCTTGGACAGTGAACACCTGGGACACATCCGCG 3571
Db 3241 GTCTGAAGCGCAGCTCCAGAGGTGACCTTGGACAGTGAACACCTGGGACACATCCGCG 3300
Qy 3572 AGTACGAACAGCGCTGTAAGTGTGAGAGCGGAGGTTCAGACAGTGAAGCCGCTCTCG 3631
Db 3301 AGTACGAACAGCGCTGTAAGTGTGAGAGCGGAGGTTCAGACAGTGAAGCCGCTCTCG 3360
Qy 3632 GGTGGGTGCGGAGCGCTGAGCGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 3691
Db 3361 GGTGGGTGCGGAGCGCTGAGCGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 3420
Qy 3692 CTGACCTGCTGGTTCAGAGACAGGACCTGCTGGGAGATTCAGAGAGAGGCGCCAC 3751
Db 3421 TTGACCTGATGGTTCAGAGAGTGAAGCATGTGAGGAGATTTTAAAGAGAGGCGCCAC 3480
Qy 3752 AGGGATTTTGTCTCTAGAGTGAAGCTCATCTGGGCTCTGGCGCCCGCAGCTTGTGGCT 3811
Db 3481 AGGGATTTTGTCTCTAGAGTGAAGCTCATGTGGGCTCTGGCGCCCGCAGCTTGTGGCT 3540

Db 661 GAATAGAGAACGCCACCCAGGCTCAGACTCCATGTCTCTCGTGGCTCAGGGGAG 720
Qy 992 CTGGCGGACTGGCTGGCGGAGACCCCTGGAGAACACTTGGCCCCCAGGAGATGGGGAGCCA 1051
Db 721 CTGGCGGACTGGCTGGCGGAGACCCCTGGAGAACACTTGGCCCCCAGGAGATGGGGAGCCA 780
Qy 1052 GGCAAGGCGAAGCCGAGATCGAATCAGGCTGTTCTTCCCAAGGGGAGCTTGAAGTCC 1111
Db 781 GGCAAGGCGAAGCCGAGATCGAATCAGGCTGTTCTTCCCAAGGGGAGCTTGAAGTCC 840
Qy 1112 TGCAGGCCAGGTGAGAGAGATTATGACCCGGAAGAGCTCCTGACAGTCTATTCTTCTG 1171
Db 841 TGCAGGCCAGGTGAGAGAGATTATGACCCGGAAGAGCTCCTGACAGTCTATTCTTCTG 900
Qy 1172 AGGATGGCTCTGAGGAATTCGAGACCATAGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 1231
Db 901 AGGATGGCTCTGAGGAATTCGAGACCATAGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 960
Qy 1232 GCTCGGAGGCTCAGGCTTACCTGGAATGAGCTGGTGGCTGGCTTGGGAACCGCTGG 1291
Db 961 GCTCGGAGGCTCAGGCTTACCTGGAATGAGCTGGTGGCTGGCTTGGGAACCGCTGG 1020
Qy 1292 ACATTGCCAGAGTGAACCTTTTCGGGGGAGCATCCAAATGGGGGTCTTCCATCTCGAAG 1351
Db 1021 ACATTGCCAGAGTGAACCTTTTCGGGGGAGCATCCAAATGGGGGTCTTCCATCTCGAAG 1080
Qy 1352 CTTCCTCTATGGACGCTCTGTGAATGACCGGCTGAGATTGGTGGCTTGCATATTTCC 1411
Db 1081 CTTCCTCTATGGACGCTCTGTGAATGACCGGCTGAGATTGGTGGCTTGCATATTTCC 1140
Qy 1412 ACGGCTCAGGCTGGGGCACTTCTGACCCCGATGGGCTGGGCCCAACTCTACGGCGG 1471
Db 1141 ACGGCTCAGGCTGGGGCACTTCTGACCCCGATGGGCTGGGCCCAACTCTACGGCGG 1200
Qy 1472 CGCCCTCCAACTCGCTACCTCCGCAACTTTTGGACGAGCGTCCCAAGCGAGGACCA 1531
Db 1201 CGCCCTCCAACTCGCTACCTCCGCAACTTTTGGACGAGCGTCCCAAGCGAGGACCA 1260
Qy 1532 AAGCCCGACCTTAAAGGGGAGGCTGGGAGCTCCGGCCCCCTTGAAGCTGGGGAGTGGC 1591
Db 1261 AAGCCCGACCTTAAAGGGGAGGCTGGGAGCTCCGGCCCCCTTGAAGCTGGGGAGTGGC 1320
Qy 1592 TGAAGAATGCTGCTGGGGAGAGATGTGCGCGCGAGTACCCCTCCGGGGGCGCTGGAGC 1651
Db 1321 TGAAGAATGCTGCTGGGGAGAGATGTGCGCGCGAGTACCCCTCCGGGGGCGCTGGAGC 1380
Qy 1652 CTCAACCGAGGCGAGGCTTCGGGGAGAGCATGTATCTGCTCTCGACAAGGCGACCTCGC 1711
Db 1381 CTCAACCGAGGCGAGGCTTCGGGGAGAGCATGTATCTGCTCTCGACAAGGCGACCTCGC 1440
Qy 1712 CGCTCTCGCTGAGTCTGTGGCTCGGGCAGGCCCCCTGAGCGACCTGCTTTTGGGAC 1771
Db 1441 CGCTCTCGCTGAGTCTGTGGCTCGGGCAGGCCCCCTGAGCGACCTGCTTTTGGGAC 1500
Qy 1772 TGTGCTGAACAGGGGACAGATGGGCAATGTACTTCTGGGAGATGGGATTCCAATGAGTTT 1831
Db 1501 TGTGCTGAACAGGGGACAGATGGGCAATGTACTTCTGGGAGATGGGATTCCAATGAGTTT 1560
Qy 1832 CTTCAAGCTTTTGGGGCTGTGTTGCTGCTCCGGGTATGGGACGCTGAGGCTGACGCTG 1891
Db 1561 CTTCAAGCTTTTGGGGCTGTGTTGCTGCTCCGGGTATGGGACGCTGAGGCTGACGCTG 1620
Qy 1892 AGGAGGCGACGCGAGGAAAGACTTGGCGTTCAAGTTTGAAGGAGATGGCGTTGACTCT 1951
Db 1621 AGGAGGCGACGCGAGGAAAGACTTGGCGTTCAAGTTTGAAGGAGATGGCGTTGACTCT 1680
Qy 1952 TTGGGAGTGTATGCGACGAGTGAAGTGAAGGCGCGGCTCTCTCTCGCTCGCTGCG 2011
Db 1681 TTGGGAGTGTATGCGACGAGTGAAGTGAAGGCGCGGCTCTCTCTCGCTCGCTGCG 1740
Qy 2012 CGCTCTGGGGGATGCCACTTGGCTCTCAGCTGGCATGCAAGCTGACGCGCTGCTCT 2071

Db 1741 CGCTCTGGGGGATGCCACTTGGCTCTCAGCTGGCATGCAAGCTGACGCGCGCTCT 1800
Qy 2072 TTGCCCAAGATGGGGTACAGTCTTGTCTGACACAGAAAGTGTGGGGAGATTAGGCCAGA 2131
Db 1801 TTGCCCAAGATGGGGTACAGTCTTGTCTGACACAGAAAGTGTGGGGAGATTAGGCCAGA 1860
Qy 2132 CTACACCACTGGGCGCTGGTCTCGGCTTCTTGTGCGCTCACTCATCTACCGCGC 2191
Db 1861 CTACACCACTGGGCGCTGGTCTCGGCTTCTTGTGCGCTCACTCATCTACCGCGC 1920
Qy 2192 TCATCACTTCAGAAATCAGAAAGAGAGCCACACGAGAGAGCTGAGATTGACATG 2251
Db 1921 TCATCACTTCAGAAATCAGAAAGAGAGCCACACGAGAGAGCTGAGATTGACATG 1980
Qy 2252 ATAGTGTCTTATGGGGAAGGGCTGTGCGGACGCGGACCCAGCCGAGAAAGCGCGC 2311
Db 1981 ATAGTGTCTTATGGGGAAGGGCTGTGCGGACGCGGACCCAGCCGAGAAAGCGCGC 2040
Qy 2312 TGGGGGTCCCGGCGAGTCGGGCGTCCGGGTTGCTGGGGGGGCGCTGGGGGGCGCC 2371
Db 2041 TGGGGGTCCCGGCGAGTCGGGCGTCCGGGTTGCTGGGGGGGCGCTGGGGGGCGCC 2100
Qy 2372 GGTGCTACGCGCGTGTTCACATTTGSGGCGCGCGGTGACCATCTTCATGGGCAAG 2431
Db 2101 GGTGCTACGCGCGTGTTCACATTTGSGGCGCGCGGTGACCATCTTCATGGGCAAG 2160
Qy 2432 TGGTACGCTACTGCTGTGTTCTGTGCTGTTTCTCGCGGGTGTCTCGTGAATTTCCAGC 2491
Db 2161 TGGTACGCTACTGCTGTGTTCTGTGCTGTTTCTCGCGGGTGTCTCGTGAATTTCCAGC 2220
Qy 2492 CGGGCGCGCGGGCTCCCGGAGCTGCTGCTATTTCTGGGCTTTCAGCGCTGTGG 2551
Db 2221 CGGGCGCGCGGGCTCCCGGAGCTGCTGCTATTTCTGGGCTTTCAGCGCTGTGG 2280
Qy 2552 AGGAATCGCGCGAGGGCTGAGCGAGGCGGGGAGAGCTCGCACGGGGGCGCCGGGCG 2611
Db 2281 AGGAATCGCGCGAGGGCTGAGCGAGGCGGGGAGAGCTCGCACGGGGGCGCCGGGCG 2340
Qy 2612 CTGGGCAATGCTCTACTGAGCCAGCGGCTGCGCTTCACTTGCGGACAGCTGGAACGAT 2671
Db 2341 CTGGGCAATGCTCTACTGAGCCAGCGGCTGCGCTTCACTTGCGGACAGCTGGAACGAT 2400
Qy 2672 GCGACCTAGTGGCTCTACCTGCTTCCTCGGGGGTGGGCTGGCGGCGTACCCGGGCT 2731
Db 2401 GCGACCTAGTGGCTCTACCTGCTTCCTCGGGGGTGGGCTGGCGGCGTACCCGGGCT 2460
Qy 2732 TGTACCACTGGGCGGACCTGCTCTGATGCACTTCATGGATTTCACGGTGGCGCTGC 2791
Db 2461 TGTACCACTGGGCGGACCTGCTCTGATGCACTTCATGGATTTCACGGTGGCGCTGC 2520
Qy 2792 TTCACTCTTCAAGGTCAACAAACAGCTGGGGCCCAAGATGTCATCTGAGCAAGATGA 2851
Db 2521 TTCACTCTTCAAGGTCAACAAACAGCTGGGGCCCAAGATGTCATCTGAGCAAGATGA 2580
Qy 2852 TGAAGAGTGTCTTCTCTCTCTCTCTCTCTCGGGGTGGCTGGTAACTATGACCGTGG 2911
Db 2581 TGAAGAGTGTCTTCTCTCTCTCTCTCTCTCGGGGTGGCTGGTAACTATGACCGTGG 2640
Qy 2912 CCACGAGAGGGCTCTGAGGCGACGAGGACAGTTCCTCCAAATGATCTCTGCGCGCTCT 2971
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Db 2761 TCATGAGACAGACAACTGCTGTCGAGCGCGGCTTCTGGGACACACCTCTCGGGGCGC 2820
Qy 3092 AGGCGGAGCACTGGGCTCCAGATAGCCAACTGGCTGGTGTGCTGCTCTGCTCATCT 3151
Db 2821 AGGCGGAGCACTGGGCTCCAGATAGCCAACTGGCTGGTGTGCTGCTCTGCTCATCT 2880

Db 1 CCACGGAAGGCCCATGCTGACGAGAGCTGACCTTCAACGGGGCCGACGCAAGC 60
Qy 332 ACAGAAATTTCTCCGGCTCTCTGACCGAAGGATCCAGCTGCACTTATATGTCTGCA 391
Db 61 ACAGAAATTTCTCCGGCTCTCTGACCGAAGGATCCAGCTGCACTTATATGTCTGCA 120
Qy 392 CACGCAATGGGGCTTCCGTGCCCCGAACCTGTGTGTCAGTGTGGGGGATCGGGG 451
Db 121 CACGCAATGGGGCTTCCGTGCCCCGAACCTGTGTGTCAGTGTGGGGGATCGGGG 180
Qy 452 GCCCGCTCTCCAGACTGGCTGACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
Db 181 GCCCGCTCTCCAGACTGGCTGACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
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Db 301 GTGTGCTGTACGGGACCATGATGGCCAGACTGGGGGACCAAGGTGTGCTGCTGCTGCTG 360
Qy 632 GTGTGCTGTACGGGACCATGATGGCCAGACTGGGGGACCAAGGTGTGCTGCTGCTGCTG 691
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Db 421 TCCCTGCAAGATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
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Qy 812 ACCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
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Qy 992 CTGCGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
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Db 1081 CTTCCTCATGAGAGCCCTGCTGATGAGCCGCTGAGTTCGTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
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Db 1141 ACAGGCTCAGCTGGGACCACTTCTGACCCCGATGAGCTGGGCCCACTTACAGCGGG 1200
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Db 1441 CGCTCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 1772 TGTGCTGAGACAGGAGCAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1831
Db 1501 TGTGCTGAGACAGGAGCAGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1832 CCTGAGCTCTTGGGAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1891
Db 1561 CCTGAGCTCTTGGGAGCTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Qy 1892 AGAGAGCAGCAGAGAGAAAGCTGCGCTGCAAGTTGAGAGGATGGGCTTACCTCT 1951
Db 1621 AGAGAGCAGCAGAGAGAAAGCTGCGCTGCAAGTTGAGAGGATGGGCTTACCTCT 1680
Qy 1952 TTTGGAGATGCTATTCGAGCAGTGAAGTGAAGGAGCTGCGCTGCTGCTGCTGCTGCTGCTG 2011
Db 1681 TTTGGAGATGCTATTCGAGCAGTGAAGTGAAGGAGCTGCGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 2012 CGCTCTGGGGGATGAGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2071
Db 1741 CGCTCTGGGGGATGAGCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Qy 2072 TTTGCCAGATGGGATGAGCTTCTGCTGACACAGAAATGATGGGAGATATGGCAGCA 2131
Db 1801 TTTGCCAGATGGGATGAGCTTCTGCTGACACAGAAATGATGGGAGATATGGCAGCA 1860
Qy 2132 CTACACCATCTGGGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2191
Db 1861 CTACACCATCTGGGCTTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy 2192 TCATCACTTCAAGAAATCAGAAAGAGAGCCACACGAGGAGAGCTAGATTGATG 2251
Db 1921 TCATCACTTCAAGAAATCAGAAAGAGAGCCACACGAGGAGAGCTAGATTGATG 1980
Qy 2252 ATAGTCTATTAAATGGGAGAGGCTGTGCGGACCGCGAGCCAGCCGAGAGAGCGCGC 2311
Db 1981 ATAGTCTATTAAATGGGAGAGGCTGTGCGGACCGCGAGCCAGCCGAGAGAGCGCGC 2040
Qy 2312 TGGGGGTCCCGGCGCAGTCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2371
Db 2041 TGGGGGTCCCGGCGCAGTCCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 2372 GGTGCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2431
Db 2101 GGTGCTACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2432 TGTGAGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2491
Db 2161 TGTGAGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220

QY	2492	GGGGCGCCCGCGGCTCCCTGGAGAGCTGCGCTCTATTTCGGGCTTTACAGCTGCTGCG	2551
Db	2221	CGGCGCCCGCGCTCCCTGGAGCTGCTGCTCTATTTCGGGCTTTACAGCTGCTGTCG	2280
QY	2552	AGGAATCTCGCGCAGGGCCCTGAGCGGAGCGGGGAGCCTGCGCAGCGGGGGCCCGGAC	2611
Db	2281	AGGAATCTCGCGCAGGGCCCTGAGCGGAGCGGGGAGCCTGCGCAGCGGGGGCCCGGAC	2340
QY	2612	CTGGCGATGCTCTACTAGGCCAGCGCTGCGCTCTACTCTGGCGACAGCTGGAAACAGT	2671
Db	2341	CTGGCGATGCTCTACTAGGCCAGCGCTGCGCTCTACTCTGGCGACAGCTGGAAACAGT	2400
QY	2672	GGGACCTTAGTGAGCTCTACCTGCTCTCTGGGCGTGGGCTGCGCGGCTGACCCCGGGT	2731
Db	2401	GGGACCTTAGTGAGCTCTACCTGCTCTCTGGGCGTGGGCTGCGCGGCTGACCCCGGGT	2460
QY	2732	TGTACACCTTGAGCGCGCAGCTGCTCTGTGCATGCACTTATGATGTTTACCGGTGCGCTGC	2791
Db	2461	TGTACACCTTGAGCGCGCAGCTGCTCTGTGCATGCACTTATGATGTTTACCGGTGCGCTGC	2520
QY	2792	TTTCAATCTTACCGGTTCACAAACAGCGTGGGGCCCAATGTGTCATGTGAGCAAGATGA	2851
Db	2521	TTTCAATCTTACCGGTTCACAAACAGCGTGGGGCCCAATGTGTCATGTGAGCAAGATGA	2580
QY	2852	TGAAAGAGCTGTCTTCTTCTTCTCTTCTTCTCTGCGGCTGTGCTGTAGCCCTATGAGCTGG	2911
Db	2581	TGAAAGAGCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTGCGGCTGTGCTGTAGCCCTATGAG	2640
QY	2912	CCACGGAGGGGCTCTTAGGCGCAGGGGACATGATCTTCCCAAGTACTCTGGCGCGCTCT	2971
Db	2641	CCACGGAGGGGCTCTTAGGCGCAGGGGACATGATCTTCCCAAGTACTCTGGCGCGCTCT	2700
QY	2972	TCTACCGTCCCTACCTGACGATCTTCCGGGACAGTATCCCAAGAGACATGAGCGTGGCC	3031
Db	2701	TCTACCGTCCCTACCTGACGATCTTCCGGGACAGTATCCCAAGAGACATGAGCGTGGCC	2760
QY	3032	TCATGAGCACAGCAACTGCTCTGTCGAGCCCGCTTCTGGCACACCTCTCTGAGGCTCC	3091
Db	2761	TCATGAGCACAGCAACTGCTCTGTCGAGCCCGCTTCTGGCACACCTCTCTGAGGCTCC	2820
QY	3092	AGGGGGGACCTGGGCTCCCGAGTAGGCCACTGGCTGTGGTGCTGCTCCGCTCATCT	3151
Db	2821	AGGGGGGACCTGGGCTCCCGAGTAGGCCACTGGCTGTGGTGCTGCTCCGCTCATCT	2880
QY	3152	TCCTGCTCGTGCGCAACATCTCTGTGTCAACTTGCTCATTTGCCATGTTCACTACAT	3211
Db	2881	TCCTGCTCGTGCGCAACATCTCTGTGTCAACTTGCTCATTTGCCATGTTCACTACAT	2940
QY	3212	TCGGGAAGTACAGGGCAACAGCGATCTCTACTGGAAGCGCAGCGTTAACCGGCTCATCC	3271
Db	2941	TCGGGAAGTACAGGGCAACAGCGATCTCTACTGGAAGCGCAGCGTTAACCGGCTCATCC	3000
QY	3272	GGGAATTCACACTCTGGGCGCGCGCTGAGCCCGCCCTTTATGTGATCTTCCCACTTGGCC	3331
Db	3001	GGGAATTCACACTCTGGGCGCGCGCGTGGCCCGCCCTTTATGTGATCTTCCCACTTGGCC	3060
QY	3332	TCCTGCTCAGGCATTTGTGCAGGCGACCCCGGAGCCCGCAGCGCTCTCTCCCGGCTCTG	3391
Db	3061	TCCTGCTCAGGCATTTGTGCAGGCGACCCCGGAGCCCGCAGCGCTCTCTCCCGGCTCTG	3120
QY	3392	AGCATTTCCGGGTTTAACTTTCTTAGAAGCCGAGCGGAAGGTGCTTAAGTGGGAATCGG	3451
Db	3121	AGCATTTCCGGGTTTAACTTTCTTAGAAGCCGAGCGGAAGGTGCTTAAGTGGGAATCGG	3180
QY	3452	TGCATTAAGAGAACTTTCTGTCTGGCAGCGCTTAGGGACAAGCGGGAGAGCACTTCGAGC	3511
Db	3181	TGCATTAAGAGAACTTTCTGTCTGGCAGCGCTTAGGGACAAGCGGGAGAGCACTTCGAGC	3240
QY	3512	GTCGTAAAGCAGCGTCCCAAGAGGTGACTTGGCACTAAACAGCTGGGACACATTCGCG	3571
Db	3241	GTCGTAAAGCAGCGTCCCAAGAGGTGACTTGGCACTAAACAGCTGGGACACATTCGCG	3300

OY	3572	AGTACGAA	CACGGCTGAAATGCTGGAGCGGGAGGATCACAGATGTAGCGCGTCTGG	3633
Db	3301	AGTACGAA	CACGGCTGAAATGCTGGAGCGGGAGGATCACAGATGTAGCGCGTCTGG	3366
OY	3632	GGTGGGTGGCGGAGGCGCTGAGCGGCTTGTGCTTGCTGCCCCAGGTGGGCGGCCACCC	3691	
Db	3351	GGTGGGTGGCGGAGGCGCTTGTGAGTAAAGGCTATGTGGGCGTGGGCGCCCGACCTGGGAGCT	3542	
OY	3692	CTGACCTGCTGGGGTCCAAAGACTGAGCCTTGCTGGCGGACTTCAAGGAGAAAGCCCCAC	3751	
Db	3421	TTGACCTGCAATGGGTCGAAAGAGTGAAGCCATGCTGGCGGATTTTAAAGAGAAAGCCCCAC	3486	
OY	3752	AGGGGATTTTGCTCCTTAAGTAAAGGCTATCTGGGCGTGGGCGCCCGACCTGGGAGCT	3811	
Db	3481	AGGGGATTTTGCTCTTAAAGTAAAGGCTATGTGGGCGTGGGCGCCCGACCTGGTGGGCT	3542	
OY	3812	TGTCCTTAGGTGAGGCCCATGTCCATCTGGGCACTGTTCAGGACCAACCTTTGGAGTGT	3872	
Db	3541	TGTCCTTAGGTGAGGCCCATGTCCATCTGGGCACTGTTCAGGACCAACCTTTGGAGTGT	3602	
OY	3872	CATCCTTAACAACCAACAGACTGCGCGCTCTCCAGAACCAAGTCCACAGCCTGGAGGAT	3933	
Db	3601	CATCCTTAACAACCAACAGACTGCGCGCTCTCCAGAACCAAGTCCACAGCCTGGAGGAT	3662	
OY	3932	CAAGGCTCGATCCCGGGCGCTTATCCATCTGGAGGCTGCAAGGCTCTTGGGGTAAACAG	3992	
Db	3661	CAAGGCTCGATCCCGGGCGCTTATCCATCTGGAGGCTGCAAGGCTCTTGGGGTAAACAG	3722	
OY	3992	GACCAACAGACCCCTCACCACCTCACAAGATTCTCTCACACTGGGGAAATAAGCCATTTCAG	4051	
Db	3721	GACCAACAGACCCCTCACCACCTCACAAGATTCTCTCACACTGGGGAAATAAGCCATTTCAG	3782	
OY	4052	GGAAAAAAA	4061	
Db	3781	GGAAAAAAA	3790	
RESULT 11				
ADSI2778				
ID	ADSI2778	standard; cDNA; 3810 BP.		
XX	ADSI2778;			
AC				
XX	16-DEC-2004	(first entry)		
DT				
XX				
DE				
XX				
KW	transient receptor potential cation channel, subfamily M; member 4;			
KM	TRPM4; phospholipase A1-A; PLAA; butyryl coenzyme A synthetase 1; BUCS1;			
XX	prostate cancer; TRPM4a; gene; ss; splicing variant.			
OS	Homo sapiens.			
XX				
PH	Key	Location/Qualifiers		
FT	CDS	324..3574		
XX		/*tag= a		
PN	JP2004267118-A.	/product= "Human TRPM4a splicing variant protein"		
XX				
PD	30-SEP-2004.			
XX				
PF	10-MAR-2003; 2003JP-00063578.			
XX				
PR	10-MAR-2003; 2003JP-00063578.			
XX				
PA	(SANY) SANKYO CO LTD.			
XX				
DR	WPI; 2004-693915/68.			
XX				
DR	P-PesDB; ADSI2779.			
PT	Detecting prostatic cancer, comprises extracting RNA fractions from test substance of subject and normal human, measuring and analyzing the			

PT difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT expression levels.

PS Claim 1; SEQ ID NO 5; 126bp; Japanese.

XX The invention comprises a method for detecting prostatic cancer in a
CC subject. The method involves measuring the expression levels of specific
CC genes: transient receptor potential cation channel, subfamily M, member 4
CC (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
CC (BUCS1). The method of the invention is useful for the detection and
CC treatment of prostate cancer. The present cDNA sequence encodes the human
CC TRPM4 splicing variant protein of the invention.

XX Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 92.6%; Score 3759.6; DB 13; Length 3810;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3771; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Oy 272 CCACGAGAAAGCCACCGATGCTTACGAGAGCTGGAATTCACGCGGGGCGCGCGCAAGC 331
Db 1 CCACGAGAAAGCCACCGATGCTTACGAGAGCTGGAATTCACGCGGGGCGCGCGCAAGC 60
Oy 332 ACAGCAATTTCTCCGCGCTCTGACCGAACCGATCCAGCTGCAATTAATGCTGCTCA 391
Db 61 ACAGCAATTTCTCCGCGCTCTGACCGAACCGATCCAGCTGCAATTAATGCTGCTCA 120
Oy 392 CACGCAATGAGGCTTCCGCTGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 451
Db 121 CACGCAATGAGGCTTCCGCTGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Oy 452 GCCCGCTCTCCAGACTGCTGCAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 511
Db 181 GCCCGCTCTCCAGACTGCTGCAAGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Oy 512 AGAGCAGAGAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 571
Db 241 AGAGCAGAGAGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Oy 572 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 631
Db 301 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Oy 632 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 691
Db 361 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Oy 692 TCCCTGCGAGTACCGGCTGCGGCTGACCCGAGAGACGCGGCTCCAGTTTCCCTGAGCT 751
Db 421 TCCCTGCGAGTACCGGCTGCGGCTGACCCGAGAGACGCGGCTCCAGTTTCCCTGAGCT 480
Oy 752 ACAACTACTCGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
Db 481 ACAACTACTCGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Oy 812 ACCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 871
Db 541 ACCGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Oy 872 CTGGAATGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 931
Db 601 CTGGAATGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Oy 932 GAATGAGAGCGCACCCAGAGCTCAGCTTCCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTG 991
Db 661 GAATGAGAGCGCACCCAGAGCTCAGCTTCCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTG 720
Oy 992 CTGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
Db 721 CTGCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Oy 1052 GGCAGAGCGAAGCCGAGATCGAATCAGGCGTTTCTTTCCAAAGGGGACTTGAAGTCC 1111
Db 1111
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Db 781 GGCAGAGCGAAGCCGAGATCGAATCAGGCGTTTCTTTCCAAAGGGGACTTGAAGTCC 840
Oy 1112 TGCAGGCCAGGTGAGAGATTATGACCCGGAAGAGACTCCTGACATGATTTCTG 1171
Db 841 TGCAGGCCAGGTGAGAGATTATGACCCGGAAGAGACTCCTGACATGATTTCTG 900
Oy 1172 AGGATGGCTGAGAAATTCGAGACCATAGTTTGAAGGCGCTTGTGAAGGCTGTGGA 1231
Db 901 AGGATGGCTGAGAAATTCGAGACCATAGTTTGAAGGCGCTTGTGAAGGCTGTGGA 960
Oy 1232 GCTCGAGGCTCAGCTTACCTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
Db 961 GCTCGAGGCTCAGCTTACCTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020
Oy 1292 ACATTGCCAGAGTAATCTTTTGGGGGGGACATCCAAATGCGGCTTCCATTCGAA 1351
Db 1021 ACATTGCCAGAGTAATCTTTTGGGGGGGACATCCAAATGCGGCTTCCATTCGAA 1080
Oy 1352 CTTCCTCATGAGACGCTGCTGATGACCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1411
Db 1081 CTTCCTCATGAGACGCTGCTGATGACCGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
Oy 1412 ACAGCTCAGCTGAGGCTTCTGACCCCGATGCGCTGAGCCCACTTACAGCGCG 1471
Db 1141 ACAGCTCAGCTGAGGCTTCTGACCCCGATGCGCTGAGCCCACTTACAGCGCG 1200
Oy 1472 CGCCTTCAATCTGCTATCCGCAACTTTTGGACCAAGGCGTCCACAGCCGAGCACCA 1531
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Oy 1532 AAGCCCAAGCCCTTAAAGGGGAGCTGAGAGCTCGGCGCCCTGACGCTGAGGACATGTC 1591
Db 1261 AAGCCCAAGCCCTTAAAGGGGAGCTGAGAGCTCGGCGCCCTGACGCTGAGGACATGTC 1320
Oy 1592 TGAAGATCTCTGAGGAAATGTCGCGCCGAGGTACCTCTCGGAGGCGCTTGGAGAC 1651
Db 1321 TGAAGATCTCTGAGGAAATGTCGCGCCGAGGTACCTCTCGGAGGCGCTTGGAGAC 1380
Oy 1652 CTCACCCAGGCTCAGGAGCTTGGGAGAGACATGATCTGCTGCGACAAAGGCTACCTGCG 1711
Db 1381 CTCACCCAGGCTCAGGAGCTTGGGAGAGACATGATCTGCTGCGACAAAGGCTACCTGCG 1440
Oy 1712 CGCTCTGCTGAGTCTGAGCTCGGAGGAGGCGCCCTGAGAGGACCTGCTTCTTGGGAC 1771
Db 1441 CGCTCTGCTGAGTCTGAGCTCGGAGGAGGCGCCCTGAGAGGACCTGCTTCTTGGGAC 1500
Oy 1772 TGTGCTGAACAGGCAAGATGAGCATGATCTTCTGGAATGAGGTTCCATGACATTT 1831
Db 1501 TGTGCTGAACAGGCAAGATGAGCATGATCTTCTGGAATGAGGTTCCATGACATTT 1560
Oy 1832 CCTCAGCTCTGGGAGCTGTTTGTCTGCTCGGAGTATGACAGCTTGAAGCTTACGCTG 1891
Db 1561 CCTCAGCTCTGGGAGCTGTTTGTCTGCTCGGAGTATGACAGCTTGAAGCTTACGCTG 1620
Oy 1892 AGGAGGCGACCGAGAGAAACCTGAGGCTTCAAGTTTGAAGGAGATGAGGCGTTGACTCT 1951
Db 1621 AGGAGGCGACCGAGAGAAACCTGAGGCTTCAAGTTTGAAGGAGATGAGGCGTTGACTCT 1680
Oy 1952 TTAGGAGTGTATCGACAGTGAAGTGAAGGCTCGCGGCTCCTCTCTCGTCTGCTGCTG 2011
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Oy 2012 CGCTCTGGGAGATGCCCTTGTCTCAGCTGAGGCTGAGCAAGCTGAGCGCTGCTGCTTCT 2071
Db 1741 CGCTCTGGGAGATGCCCTTGTCTCAGCTGAGGCTGAGCAAGCTGAGCGCTGCTGCTTCT 1800
Oy 2072 TTAGCCAGAGTGGGATCAGTCTGCTGACACAGAAATGAGGAGAGATATGAGCAGACA 2131
Db 1801 TTAGCCAGAGTGGGATCAGTCTGCTGACACAGAAATGAGGAGATATGAGCAGACA 1860
Oy 2132 CTACACCATCTGAGGCTGAGTCTGCTGCTTCTTGTGCTTCACTCATCCCGCGC 2191
Db 1861 CTACACCATCTGAGGCTGAGTCTGCTGCTTCTTGTGCTTCACTCATCCCGCGC 1920
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2192 TCATCACTTCAGAAATCAGAGAGAGCCACACGGAGAGCTAGATTGACATGG 2251
2191 TCATCACTTCAGAAATCAGAGAGAGCCACACGGAGAGCTAGATTGACATGG 1980
2252 ATAGTGTCTTAAATGGGGAAGGGCTGTGCGAGCGGCGGACCCAGCCGAGAACGCCCG 2311
1981 ATAGTGTCTTAAATGGGGAAGGGCTGTGCGAGCGGCGGACCCAGCCGAGAACGCCCG 2040
2312 TGGGGGTCCCGCGCCAGTGGGGCGGTCCGGGTGCTGCGGGGGCCCTGCGGGGGCGCC 2371
2041 TGGGGGTCCCGCGCCAGTGGGGCGGTCCGGGTGCTGCGGGGGCCCTGCGGGGGCGCC 2100
2372 GGTGCTACGCGCGCTGATTCATCTTGGGGCGCGCGGATGACATCTTCAATGGCAAG 2431
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2432 TGGTCAAGTACCTGCTGCTCTGCTGCTTCTCGCGGGTGTGCTGCTGCTGCTGCTGCT 2491
2161 TGGTCAAGTACCTGCTGCTCTGCTGCTTCTCGCGGGTGTGCTGCTGCTGCTGCTGCT 2220
2492 CGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2551
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2552 AGGACCTGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2611
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2672 GCGACCTAGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2731
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2732 TGTACCACTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2791
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2912 CCAAGGAGGGGCTCTGAGGCAAGGAGCAAGTACTTCCCAAGATCTCTGCGCGCTCT 2971
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3212 TCGGCAAAAGTACAGGGGCAAGGAGATCTTCTAGGAAAGGCGCAGCTTACCGCTCATCC 3271
2941 TCGGCAAAAGTACAGGGGCAAGGAGATCTTCTAGGAAAGGCGCAGCTTACCGCTCATCC 3000

3272 GGGAAATTCACCTCTGCGCCCGCGCTGCGCCCGCCCTTATCGTCACTTCCACTTGGCC 3331
3001 GGGAAATTCACCTCTGCGCCCGCGCTGCGCCCGCCCTTATCGTCACTTCCACTTGGCC 3060
3332 TCTGCTCAAGGCAATTTGTGACGGCAGCCCGGAGGCCCTCCAGCCGCTCTCTCCCGGCTTGG 3391
3061 TCTGCTCAAGGCAATTTGTGACGGCAGCCCGGAGGCCCTCCAGCCGCTCTCTCCCGGCTTGG 3120
3392 AGCATTTCCGGGTTTACCTTTCTTAAAGAAAGCCGAGGAAAGCTGTCTTAAAGTGGAAATCCG 3451
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3752 AGGGGATTTTGGCTTCAAGATTAAGGCTCATCTGAGGCTGAGGCGCGCCGCGCTGCTGCTGCT 3811
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3872 CATCTTCAAAACACAGCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3931
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3932 CAAGGCTGAGTCCCGGCGCTTATCATCTGAGGCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3991
3661 CAAGGCTGAGTCCCGGCGCTTATCATCTGAGGCTGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3720
3992 GACCAAGACCCCTCAACATGACAGATTCCTCACTGAGGAAATTAAGCCATTTGACA 4051
3721 GACCAAGACCCCTCAACATGACAGATTCCTCACTGAGGAAATTAAGCCATTTGACA 3780
4052 GGGAAAAAAA 4061
3781 GGGAAAAAAA 3790

RESULT 12
AAH76383
ID AAH76383 standard; cDNA; 3900 BP.
XX
XX AAH76383;
XX
XX 30-NOV-2001 (first entry)
XX
XX Human TLCC polypeptide encoding cDNA.
DE
XX TLCC: transient receptor potential; TRP: TRP-like calcium channel; human;
XX hepatotropic; cardiant; antiarteriosclerotic; antiinflammatory; vinicide;
KW cytostatic; analgesic; cerebroprotective; nootropic; neuroprotective;
XX gene therapy; ss.
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	CDS	138..3527
FT		/+tag= a
FT		/product= "TLCC polypeptide"
FT		/note= "coding sequence (AAH6384) specifically claimed"
PN	WO200162794-A2.	
PD	30-AUG-2001.	
PF	20-FEB-2001; 2001WO-US005529.	
PR	22-FEB-2000; 2000US-00510706.	
PR	31-MAY-2000; 2000US-00583373.	
PR	08-AUG-2000; 2000US-00634669.	
PA	(MILL-) MILLENNIUM PHARM INC.	
P1	Glucksmann MA, Curtis RAJ, Lora JM;	
DR	WPI; 2001-557700/62.	
DR	P-PSDB; AAB85974.	
XX		
PT	New isolated nucleic acid encoding a transient receptor potential-like calcium channel for identifying modulators that can be used to treat hepatic or cardiovascular disorders.	
PS	Claim 1; Fig 1A-D; 160pp; English.	
XX		
CC	The invention provides isolated nucleic acids encoding a human transient receptor potential (TRP) family member, called TRP-like calcium channel (TLCC) polypeptide. The TLCC polynucleotides can be expressed by standard recombinant methodology. The TLCC polynucleotides and polypeptide are used to identify modulators that can be used to treat a hepatic or a cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other disorders that can be treated are hepatitis, liver tumours, cirrhosis of the liver, hemochromatosis, liver parasite induced disorders, central nervous system disorders, pain disorders, or disorders of cellular growth, differentiation or migration. The TLCC polynucleotides, polypeptide, protein homologs and antibodies to the proteins can be used in predictive medicine (e.g. diagnostic assays), prognostic assays, monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies can isolate TLCC proteins, regulate the bioavailability of TLCC proteins, and modulate TLCC activity. The present sequence represents a cDNA encoding the human TLCC polypeptide	
SQ	Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;	
Query Match	91.6%; Score 3721.4; DB 5; Length 3900;	
Best Local Similarity	99.6%; Pred. No. 0;	
Matches 3731; Conservative	0; Mismatches 16; Indels 0; Gaps 0	
D5	315 GGGGCGCCGCCCAAGACACAGAATTTCTCCGGCTCTGTAGCGGAACGATTCAGCTC 374	
D5	125 GTGCCCGCTCCCATGTGTCACAGACTTCTCCGGCTCTGTAGCGGAACGATTCAGCTC 184	
D5	375 AGTTATAGTGTGTACACGACACATGGGGCTTCCGTCGCCGAACCTGGTGATCACT 434	
D5	185 AGTTATAGTGTGTGTACACGACACATGGGGCTTCCGTCGCCGAACCTGGTGATCACT 244	
D5	435 GCTGGGGGGATGGGGGGGGCCCCGTCTCCAGACCTGGCTGCAGAGACTGCTCGTGTGG 494	
D5	245 GCTGGGGGGATGGGGGGGGCCCCGTCTCCAGACCTGGCTGCAGAGACTGCTCGTGTGG 304	
D5	495 GCTGGTGCAGGCTGCACCAGACACAGAGACTGGAATTGTCACTGGGGGCTCTCACACGG 554	
D5	305 GCTGGTGCAGGCTGCACCAGACACAGAGACTGGAATTGTCACTGGGGGCTCTCACACGG 364	
D5	555 CATGGCGCGGACATGTTGGTGTGGCTGTACGGGACCATCATGATGGCCAGACATGGGGGAC 614	
D5	365 CATGGCGCGGACATGTTGGTGTGGCTGTACGGGACCATCATGATGGCCAGACATGGGGGAC 424	

QY	615	CAAGTGGTGGCCATGGGTGTGGCCCCCTGGGGGTGGTGGTCCGGAATAGAGACACCTCAT	674
Db	425	CAAGGTGGTGGCCATGGGTGTGGCCCCCTGGGGGTGTGGTCCGGAATAGAGACACCTCAT	484
QY	675	CAACCCCAAGGGCTGTCCCTCGGAGGGTACCGGGTGGCGGGTGAACCGGAGAGCGGGGT	734
Db	485	CAACCCCAAGGGCTGTGTTCCTTGCAAGGTACCGGTGGCGGGTGAACCGGAGAGCGGGGT	544
QY	735	CCAGTTTCCCTGAGCTACAACTACTCGGCTTTCTTCTGTGTGACGACCGGACACACGG	794
Db	545	CCAGTTTCCCTGAGCTACAACTACTCGGCTTTCTTCTGTGTGAGACGACGACACACGG	604
QY	795	CTGCTTGGGGGGCGGAACCGCTTCCGCTTGGCGCTTGAAGTCTTACATTCACACAGAGA	854
Db	605	CTGCTTGGGGGGCGGAACCGCTTCCGCTTGGCGCTTGAAGTCTTACATTCACAGAGAGA	664
QY	855	GACGGGCGTGGGAGGAGACTGGAAATTGATCCCTGTCCGTGCTCCCTGATTTGATGGTGA	914
Db	665	GACGGGCGTGGGAGGAGACTGGAAATTGATCCCTGTCCGTGCTCCCTGATTTGATGGTGA	724
QY	915	TGAGAGAATGTGTGACGCGCAATAGAGAACGCCAACCGAGCTCAGCTCCCATGTCTCTCGT	974
Db	725	TGAGAGAATGTGTGACGCGCAATAGAGAACGCCAACCGAGCTCAGCTCCCATGTCTCTCGT	784
QY	975	GAGTGGCTCAGGGGGAGCTGCGGACTGCTCTGTGGCGGAGACCTTGAAGACATCTTGACCC	103
Db	785	GAGTGGCTCAGGGGGAGCTGCGGACTGCTCTGTGGCGGAGACCTTGAAGACATCTTGACCC	844
QY	1035	AGGAGTGTGGGAGAGCCAGGCAAGGCGGAAGCCGANAATGGAATCAGGCGTTCTTTCGCCAA	109
Db	845	AGGAGTGTGGGAGAGCCAGGCAAGGCGGAAGCCGANAATGGAATCAGGCGTTCTTTCGCCAA	904
QY	1095	AGGGGACCTTAGAGCTCTGCAGAGCCACAGTGGAGAGATTATGACCCGGAGAGAGCTCCT	115
Db	905	AGGGGACCTTAGAGCTCTGCAGAGCCACAGTGGAGAGATTATGACCCGGAGAGAGCTCCT	964
QY	1155	GACAGTCTATTCTTCTGAGAGTGGGTCTGAGGAATTGAGACCAATAGTTTGAAGGCCCT	121
Db	965	GACAGTCTATTCTTCTGAGAGTGGGTCTGAGGAATTGAGACCAATAGTTTGAAGGCCCT	102
QY	1215	TGTGAAAGGCTGTGGGAGCTCGGAAGGCTCAGGCTTACCTGATAGAGCTGGCTTGGCTGT	127
Db	1025	TGTGAAAGGCTGTGGGAGCTCGGAAGGCTCAGGCTTACCTGATAGAGCTGGCTTGGCTGT	108
QY	1275	GAGTTTGGAAACGCGGTGAGCATTTGCCACAGTGAATCTTTTGGGGGGAGACATCCAATGGG	133
Db	1085	GAGTTTGGAAACGCGGTGAGCATTTGCCACAGTGAATCTTTTGGGGGGAGACATCCAATGGG	114
QY	1335	GTCCTTCATCTGAAAGGCTCCCTCATGGAAGCGCTGTGTAATGAACGGGCTGAGTTGGT	139
Db	1145	GTCCTTCATCTGAAAGGCTCCCTCATGGAAGCGCTGTGTAATGAACGGGCTGAGTTGGT	120
QY	1385	GCGCTTGTCTATTTTCCACGGGCTTGAAGCTTGGGCCATTTCTGACCCCGATGCGCTGGC	145
Db	1205	GCGCTTGTCTATTTTCCACGGGCTTGAAGCTTGGGCCATTTCTGACCCCGATGCGCTGGC	126
QY	1455	CCAACTTACAGCGGGGGGCGCCCTCAACCTGTATTCGCGCAACTTTTGGACAGAGCGTC	151
Db	1265	CCAACTTACAGCGGGGGGCGCCCTCAACCTGTATTCGCGCAACTTTTGGACAGAGCGTC	132
QY	1515	CCAACAAGCGACGACCAAAAGCCCAAGCCCTTAAAGAGGGAGGCTGTCGGAAGCTTCGGACCC	157
Db	1325	CCAACAAGCGACGACCAAAAGCCCAAGCCCTTAAAGAGGGAGGCTGTCGGAAGCTTCGGACCC	138
QY	1575	TGACGTGGGGCAATGTGTGTGAGAGTGTCTGTGGGGAAGATGTGTCCGGCCGAGGTATCCCTTC	163
Db	1385	TGACGTGGGGCAATGTGTGTGAGAGTGTCTGTGGGGAAGATGTGTCCGGCCGAGGTATCCCTTC	144
QY	1635	CGGGGGGCGCTTGGGAGACCTTCAACCGGCGCAAGGCTTGGGGGAGACATGTATCTGCTCTC	169
Db	1445	CGGGGGGCGCTTGGGAGACCTTCAACCGGCGCAAGGCTTGGGGGAGACATGTATCTGCTCTC	150
QY	1695	GGACAAGGCAACTTGCAGCTTCTGCTGTGATGTGTGGCTTCGGAGACGACCCCTTGAAGGA	175

1505 GGACAGGCGCACTCCGCGCTCGCTGATGCTGGCCCTCGGCGAGCCCTCGAGGACA 1564
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1565 CCGCTCTCTTTGGGCACTGTGTGTAAGAGGCGACAGATGGCCATTAATTCTGGAGAT 1624
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1685 CCGAGCCTGACGCTGAGAGGCGACAGAGAAAAGACTGGCCTTCAAGTTGAGG 1744
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1745 GATGGGCGTTGACCTCTTTGGGAGGTATGACACAGTGAAGGTGAGGGCTCCGCGCT 1804
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2115 GGGAGATGAGGCGAGACTACACCATGAGGCCCTGGTTCTGACCTTTGGCCCTCC 2174
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2655 CAGACGTGAGCAAGAGGCACTAAGTGTCTCACTGTTTCTCTGGGCGTGGCG 2714
2465 CAGACGTGAGCAAGAGGCACTAAGTGTCTCACTGTTTCTCTGGGCGTGGCG 2524
2715 CCGGCTGACCCCGGGTTTGTACCACTGGGCGGCACTGTCTCTGACATCACTTCAATGT 2774
2525 CCGGCTGACCCCGGGTTTGTACCACTGGGCGGCACTGTCTCTGACATCACTTCAATGT 2584
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2585 TTTCAAGTGGGCTGCTTCACTTCACTGATCAACAAACAGCTGGGGCCCAAGTCT 2644
2835 CATCGGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2894
2645 CATCGGAGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2704
2895 GGTAGCTATGAGCGTGGCCACGAGGGGCTCTGAGGCCACGGAAGTGAATTCCCAAG 2954
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3315 CATTCGCCACTTGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3374
3125 CATTCGCCACTTGGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3184
3375 GTCCTCCCGGCGCTGAGCAATTCGCGGTTTACTTTTGAAGAAAGCGAGAGAGCT 3434
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3615 GTGTAGCGCGCTCTGGGGTGGGTGGCGAGGCCCTGAGCGCTGCTTGTGCTGCCCC 3674
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3675 AGGTGGGCGGCAACCCCTGAGCTGCTGGGTTCAGAGCTGAGCGCTGCGGAGCTT 3734
3485 AGGTGGGCGGCAACCCCTGAGCTGCTGGGTTCAGAGCTGAGCGCTGCGGAGCTT 3544
3735 CAAGAGAGAGCCCGCAAGGGGATTTTGTCTTGAAGTGAAGCTCATCTGGGCTTGGGC 3794
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3795 CCGGACCTGTGAGCTTGTCTTGAAGTGAAGCTCATCTGGGCTTGGGCCTGTGAG 3854
3605 CCGGACCTGTGAGCTTGTCTTGAAGTGAAGCTCATCTGGGCTTGGGCCTGTGAG 3664
3855 ACCACTTTTGGAGTGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3914
3665 ACCACTTTTGGAGTGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3724

QY 3915 TCCAGCCCTGGAGGATCAAGGCTGATCCCGGCGCTTATCATCTGAGGCTGCAGG 3974
DB 3725 TCCAGCGCTGGAGGATCAAGGCTGATCCCGGCGCTTATCATCTGAGGCTGCAGG 3784
QY 3975 GTCTTGGGGTAAACAGGACCAAGCCCTCAACCACTACAGATTCTCTACACTGGGGA 4034
DB 3785 GTCTTGGGGTAAACAGGACCAAGCCCTCAACCACTACAGATTCTCTACACTGGGGA 3844
QY 4035 AATAAGCATTTCAGAGGAAAAAAA 4061
DB 3845 AATAAGCATTTCAGAGGAAAAAAA 3871

RESULT 13
ABSS8041
ID ABSS8041 standard; cDNA; 3900 BP.
XX
AC ABSS8041;
XX
DT 14-FEB-2003 (first entry)
XX
DE Human transient receptor potential (TRP)-like calcium channel (TLCC).
KW Human; gene; ss; transient receptor potential-like calcium channel; TRP;
KW TLCC; 18607; calcium signalling; growth; differentiation;
KW capacitative calcium channel; store-operated calcium channel; SOC;
KW plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
KW action potential; excitation; neurite outgrowth; synaptogenesis;
KW signal transduction; angiogenesis; cell proliferation; vascular tone;
KW gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
KW restenosis; endothelial cell disorder; tumour metastasis; psoriasis;
KW rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
KW central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; cancer;
KW cellular proliferation disorder; migration disorder; therapeutic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..137
FT CDS /*tag= a
FT 138..3390 /*tag= b
FT /product= "TLCC"
FT /note= "This CDS is specifically claimed in claim 1"
FT 3'UTR 3391..3900 /*tag= c
XX
PN US2002142377-A1.
XX
PD 03-OCT-2002.
XX
PE 20-FEB-2001; 2001US-00789481.
XX
PR 22-FEB-2000; 2000US-00510706.
PR 31-MAY-2000; 2000US-00583373.
PR 08-AUG-2000; 2000US-00634669.
XX
PA (GLUC/) GLUCKSMANN M A.
PA (CURT) CURTIS R A J.
PA (LORA/) LORA J M.
PI Glucksmann MA, Curtis RAJ, Lora JM;
XX
DR WPI; 2003-102516/09.
DR P-PSDB; ABG72088.
XX
PT Isolated transient receptor potential-like calcium channel polypeptide,
PT useful for treating cardiovascular, hepatic, central nervous system
PT disorders, pain, cellular proliferation, or migration disorder.
XX
PS Claim 1; Fig 1; 80pp; English.

XX
CC The invention discloses an isolated transient receptor potential (TRP)-
CC like calcium channel (TLCC) polypeptide (18607). Calcium signalling has
CC been implicated in the regulation of a variety of cellular responses,
CC such as growth and differentiation. TLCC is a member of the capacitative
CC calcium channel group or store-operated calcium channel (SOC) which is
CC activated in the plasma membrane to import calcium ions from the
CC extracellular environment to the cytosol. The nucleic acids, polypeptides
CC and antibodies of TLCC are useful for detecting its presence in a sample,
CC for identifying a compound which binds to it and identifying a compound
CC which modulates its activity. Modulators of TLCC can be used to modulate
CC membrane excitability, wave forms and frequencies of action potentials,
CC thresholds of excitation, neurite outgrowth and synaptogenesis, signal
CC transduction, angiogenesis, endothelial cell proliferation and vascular
CC tone. The nucleic acid and polypeptide are also useful (using gene
CC therapy) for diagnosing and treating cardiovascular disorders, such as
CC atherosclerosis and restenosis, rheumatoid arthritis and diabetes, hepatic
CC tumour metastasis and psoriasis, central nervous system disorders,
CC disorders such as hepatitis and cirrhosis, multiple sclerosis and
CC such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and
CC epilepsy, cellular proliferation disorders, such as cancer, and growth.
CC differentiation or migration disorders. TLCC can also be used in
CC predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomics) and in methods of
CC treatment (e.g. therapeutic and prophylactic). The sequence presented is
CC the human TLCC, 18607, cDNA
SQ Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

Query Match 91.6%; Score 3721.4; DB 8; Length 3900;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3731; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 315 GGGGCGGCGGCAAGACAGCAATTTCTTCGCTCTTGAACGAGATCCAGCTGC 374
DB 125 GTGCCCGCTCCATGTGTCCAGATTCTTCGCGCTCTGAACGAGATCCAGCTGC 184
QY 375 AGTTATATGTGTGTACACAGACATGGGGCTTCGTCGCCGAACTGGTGTCTAGT 434
DB 185 AGTTATATGTGTGTACACAGACATGGGGCTTCGTCGCCGAACTGGTGTCTAGT 244
QY 435 GCTGGGGGATCGGGGGGCGCCGCTCTCAGACCTGCTGAGGACCTGCGTCTGG 494
DB 245 GCTGGGGGATCGGGGGGCGCCGCTCTCAGACCTGCTGAGGACCTGCGTCTGG 304
QY 495 GCTGTGCGGCTGCCAGACAGAGAGCTGTGATCTGAGGGGTCTGCACACGGG 554
DB 305 GCTGTGCGGCTGCCAGACAGAGAGCTGTGATCTGAGGGGTCTGCACACGGG 364
QY 555 CATGCGCCGCGATGT 614
DB 365 CATGCGCCGCGATGT 424
QY 615 CAAGTGTGTGCAATGGGTGTGCGCCCTCTGGGGTGTGTGTGTGTGTGTGTGTGTGT 674
DB 425 CAAGTGTGTGCAATGGGTGTGCGCCCTCTGGGGTGTGTGTGTGTGTGTGTGTGTGT 484
QY 675 CAACCCCAAGGCTGT 734
DB 485 CAACCCCAAGGCTGT 544
QY 735 CCAATTTTCCCTGTGACATCACTACTGCGCTTCTTCTGTGTGTGTGTGTGTGTGTGT 794
DB 545 CCAATTTTCCCTGTGACATCACTACTGCGCTTCTTCTGTGTGTGTGTGTGTGTGTGT 604
QY 795 CTGCTGTGGGGGCGAGAACGCTTCGCTGCGCTGCGCTGAGTCTTACATCTGCAGCGAA 854
DB 605 CTGCTGTGGGGGCGAGAACGCTTCGCTGCGCTGCGCTGAGTCTTACATCTGCAGCGAA 664
QY 855 GACGGGCGTGGAGGAGACTGGAATTGACATCTCTGTCTGTCTCTGATTTGATGTGA 914
DB 665 GACGGGCGTGGAGGAGACTGGAATTGACATCTCTGTCTGTCTCTGATTTGATGTGA 724

QY	915	TGAGAAAGATTGTTAAGCGCAATTAAGAAAGCCACCAAGGCTACGCTCCATATCTCTCCGT	974
Db	725	TGAGAAAGATTGTTAAGCGCAATTAAGAAAGCCACCAAGGCTACGCTCCATATCTCTCCGT	784
QY	975	GGCTGGCTCAGGGGGAGCGCTGGCGAATCTGCTTGGCGGAGACCTCTGAAAGACACTTGGGCCCC	1034
Db	785	GGCTGGCTCAGGGGGAGCGCTGGCGAATCTGCTTGGCGGAGACCTCTGAAAGACACTTGGGCCCC	844
QY	1035	AGGAGTGGGGGAGCCAGGCAAGCGGAAGCCCGAATCGAATCAGGCGTTTCTTTCCAA	1094
Db	845	AGGAGTGGGGGAGCCAGGCAAGCGGAAGCCCGAATCGAATCAGGCGTTTCTTTCCAA	904
QY	1095	AGGGGACCTTGAAGTCTCTGAGAGCCCAAGTGAAGAGATTATGACCCGGGAAGAGCTCCT	1154
Db	905	AGGGGACCTTGAAGTCTCTGAGAGCCCAAGTGAAGAGATTATGACCCGGGAAGAGCTCCT	964
QY	1155	GACAGTCAATTCTTCTGAAGATGGGTCTGAAGAAATTCAGACCAATAGTTTGAAGGCCCT	1214
Db	965	GACAGTCAATTCTTCTGAAGATGGGTCTGAAGAAATTCAGACCAATAGTTTGAAGGCCCT	1024
QY	1215	TGTGAAGGCGTGTGGAGCTCGGAGGCGCTCAGCGCTCAGCTGATGAGTGCCTTGGCTGT	1274
Db	1025	TGTGAAGGCGTGTGGAGCTCGGAGGCGCTCAGCGCTCAGCTGATGAGTGCCTTGGCTGT	1084
QY	1275	GGCTTGGAAACCGCGTGGAGCATTTGCCCAAGTGAATCTTTTGGGGGGGACATTCAAATGGCG	1334
Db	1085	GGCTTGGAAACCGCGTGGAGCATTTGGCAAGATGAATCTTTTGGGGGGGACATTCAAATGGCG	1144
QY	1335	GTCTTCCATCTCGAAGGCTCCCTCATGAGAAGCCCTGTGTAATGACCGGGCGTAGTTCGT	1394
Db	1145	GTCTTCCATCTCGAAGGCTCCCTCATGAGAAGCCCTGTGTAATGACCGGGCGTAGTTCGT	1204
QY	1395	GGCTTGTCTATTTTCCAGGCGCTCAGCGCTGAGGCCATTCCTGACCCCGATGCGCTGCG	1454
Db	1205	GGCTTGTCTATTTTCCAGGCGCTCAGCGCTGAGGCCATTCCTGACCCCGATGCGCTGCG	1264
QY	1455	CCAATCTTACAGCGCGCGGCGCTCCCACTCGCTATCTCGCAACTTTTGGACCAAGGCGTC	1514
Db	1265	CCAATCTTACAGCGCGCGGCGCTCCCACTCGCTATCTCGCAACTTTTGGACCAAGGCGTC	1324
QY	1515	CCAGAGCCGAGGCAACAAAGGCCCGCCTAAAGGGGGAGCTGGAGGCTCCGGGCCCCC	1574
Db	1385	CCAGAGCCGAGGCAACAAAGGCCCGCCTAAAGGGGGAGCTGGAGGCTCCGGGCCCCC	1384
QY	1575	TGACCTGGGGGCATGTGCTGAGAGTCTGCTGGGGAAAGTGTGTGGCGCCGAGGTACCCCTC	1634
Db	1385	TGACCTGGGGGCATGTGCTGAGAGTCTGCTGGGGAAAGTGTGTGGCGCCGAGGTACCCCTC	1444
QY	1635	CGGGGGCGCTTGGGACCTCTCACAGGCCAAGGGCTTGGGGGAGAGCATGTATCTGCTCTC	1694
Db	1445	CGGGGGCGCTTGGGACCTCTCACAGGCCAAGGGCTTGGGGGAGAGCATGTATCTGCTCTC	1504
QY	1695	GGACAAGGCACTGCGCGCTGTGCTGATGTGGCTCTGGGCAAGGCCCCCTGGAAGGA	1754
Db	1505	GGACAAGGCACTGCGCGCTGTGCTGATGTGGCTCTGGGCAAGGCCCCCTGGAAGGA	1564
QY	1755	CTGTCTTCTTTGGGCACTGTGCTGAACAGGGCAAGATGGCAATGTACTTCTGGGAGAT	1814
Db	1565	CTGTCTTCTTTGGGCACTGTGCTGAACAGGGCAAGATGGCAATGTACTTCTGGGAGAT	1624
QY	1815	GGGTTTCCAATGACGATTTCTCACTCTTGGGGCGTGTGCTGCTCGGGGTGATGGACG	1874
Db	1625	GGGTTTCCAATGACGATTTCTCACTCTTGGGGCGTGTGCTGCTCGGGGTGATGGACG	1684
QY	1875	CCTTGAAGCCTGACCGCTGAAGAGGCAAGCAAGAGAAACCTTGGGGTTCAACTTTGAAGG	1934
Db	1685	CCTTGAAGCCTGACCGCTGAAGAGGCAAGCAAGAGAAACCTTGGGGTTCAACTTTGAAGG	1744
QY	1935	GATGGGCGTTGACCTCTTTTGGGAGAGTCTATGACAGCATGATGAGGTGAAGGCGCCGCT	1994
Db	1745	GATGGGCGTTGACCTCTTTTGGGAGAGTCTATGACAGCATGATGAGGTGAAGGCGCCGCT	1804
QY	1995	CTCTCTCCGTCCGTCGCGCTTGGGGGGATGCCACTTGTCTCAGCTGGCCATGCAAGC	2054

Db	1805	CCTCTCCCTGCGCTGCGCGCTCTGCGGGGAGATGCCACTTGGCTCCAGCTGGCCATGCAAGC	1864
Qy	2055	TGAAGCCCGTGCCTTCTTTTGCCAGAGTGGAGTACAGTCTCTGCTGACACAGAAATGTGT	2114
Db	1865	TGAGCCCGCTGCTTCTTTTGCCAGAGTGGAGTACAGTCTCTGCTGACACAGAAATGTGT	1924
Qy	2115	GGAGAGATATGGCCAGCACTACACCACTATGGGCGCTGTCTCGGCTCTTTTTCGCTCC	2174
Db	1925	GGGAGATATGGCCAGCACTACACCACTATGGGCGCTGTCTCGGCTCTTTTTCGCTCC	1984
Qy	2175	ACTCATCTACACCGGCGCTCATCACTTCAGAAATTCAGAAAGGAGGCCACACGGAGAGA	2234
Db	1985	ACTCATCTACACCGGCGCTCATCACTTCAGAAATTCAGAAAGGAGGCCACACGGAGAGA	2044
Qy	2235	GCTAGAGTTTGACATGATAGTGTCAATTAATGGGAAAGGAGCTGTGCGGACCGCGAGACC	2294
Db	2045	GCTAGAGTTTGACATGATAGTGTCAATTAATGGGAAAGGAGCTGTGTGCGGACCGCGAGACC	2104
Qy	2295	AGCCGAGAGACGCGCGCTGGGGGATCCCGCGCACTGGGCGCTCCGGGTTGTCTGGGGGG	2354
Db	2105	AGCCGAGAGACGCGCGCTGGGGGATCCCGCGCACTGGGCGCTCCGGGTTGTCTGGGGGG	2164
Qy	2355	CCGCTGCGGGGGGGGCGCGGTGCTTAAGCGCGCTGTTTCACTTCTGCGGGCGCGCGGTAGAC	2414
Db	2165	CCGCTGCGGGGGGGGCGCGGTGCTTAAGCGCGCTGTTTCACTTCTGCGGGCGCGCGGTAGAC	2224
Qy	2415	CATCTTCAATGGGCAACGCTGTCAGCTTACCTGTCTCTGCTGTTTCTTCGCGGGTGT	2474
Db	2225	CATCTTCAATGGGCAACGCTGTCAGCTTACCTGTCTCTGCTGTTTCTTCGCGGGTGT	2284
Qy	2475	GCTGTGTGATTTTCAAGCGCGCGCGCGCTCCCTGTAGAGTGTGCTCTATTTTCTTGGGC	2534
Db	2285	GCTGTGTGATTTTCAAGCGCGCGCGCGCTCCCTGTAGAGTGTGCTCTATTTTCTTGGGC	2344
Qy	2535	TTTCAACGCTGTGTGTGCGAGGAACTGGGCGCAAGGGCTGAGGCGAGGCGAGGGGAGGCTTCGC	2594
Db	2345	TTTCAACGCTGTGTGTGCGAGGAACTGGGCGCAAGGGCTGAGGCGAGGCGAGGGGAGGCTTCGC	2404
Qy	2595	CAGCGGGGGGCGCGGGCGCTGTGCATATGCTCTCACTAGGCGAGCGGCTTCGCTTACCTTCGC	2654
Db	2405	CAGCGGGGGGCGCGGGCGCTGTGCATATGCTCTCACTAGGCGAGCGGCTTCGCTTACCTTCGC	2464
Qy	2655	GCAACGCTGAGCAACAGTGCAGCTTAATGAGTCTTCACTGCTTCTCTGGGCGTGGGCTG	2714
Db	2465	GCAACGCTGAGCAACAGTGCAGCTTAATGAGTCTTCACTGCTTCTCTGGGCGTGGGCTG	2524
Qy	2715	CCGGGTGACCCCGGGTTTGTACCACTGGGCGGACGTCTCTGTGCATTCGACTTAATGAGT	2774
Db	2525	CCGGGTGACCCCGGGTTTGTACCACTGGGCGGACGTCTCTGTGCATTCGACTTAATGAGT	2584
Qy	2775	TTTTCAGGTGTGGGCTGCTTCACTATCTTCAACGCTCAACAAACAGCTGGGGGCGCAAGATCGT	2834
Db	2585	TTTTCAGGTGTGGGCTGCTTCACTATCTTCAACGCTCAACAAACAGCTGGGGGCGCAAGATCGT	2644
Qy	2835	CATGCTGAGCAAGATGATGAAAGAGCGTGTCTTCTTCTTCTTCTTCTGGCGTGTGACT	2894
Db	2645	CATGCTGAGCAAGATGATGAAAGAGCGTGTCTTCTTCTTCTTCTTCTTCTGGCGTGTGACT	2704
Qy	2895	GGTACGCTATATGGCGTGGCCACGAGAGGGGCTCTTAAGGCGCAAGGACAGTATCTTCCCAAG	2954
Db	2705	GGTACGCTATATGGCGTGGCCACGAGAGGGGCTCTTAAGGCGCAAGGACAGTATCTTCCCAAG	2764
Qy	2955	TATCCGTGGCGCGGCTTCTTACGCGGCTTACCTTGACAGATTTTTCGGGAGAGATTCCCAAGAG	3014
Db	2765	TATCCGTGGCGCGGCTTCTTACGCGGCTTCTTACGCGGCTTCTTTCGGGAGAGATTCCTCCAGAG	2824
Qy	3015	GGACATGAGACGTGGCGCTCATGAGACACAGCACTGCTGTGAGAGCGCGGCTTCTTGGGC	3074
Db	2825	GGACATGAGACGTGGCGCTCATGAGACACAGCACTGCTGTGAGAGCGCGGCTTCTTGGGC	2884
Qy	3075	ACAACCTTCTGGGGCCCAAGCGGGGACCTGTGCTCCCAAGTATGCCAATGTGCTGTGTGT	3134

Db	2885	AACCCCTCCTGGGGGCCAGGGGGGACCTGGCTCTCCAGATATGCCAATGGCTGGTGGT	2944
OY	3135	GCTGCTCTCGTCATCTTCTCTGCTCGTGGGCAACATCTGCTGTCAACTTGTCTATTGC	3194
Db	2945	GCTGCTCTCGTCATCTTCTGCTCGTGGCAACATCTGCTGTCAACTTGTCTATTGC	3004
OY	3195	CATGTTCAGTTTACAATTCGGCAAGTACAGGGCAACAGCCATCTCTACTGGAAGCGCA	3255
Db	3005	CATGTTCAGTTTACAATTCGGCAAGTACAGGGCAACAGCCATCTCTACTGGAAGCGCA	3066
OY	3255	GCGTTACCGGCTCATCCGGGAATTGCATCTCGCCCGCGCTGGGCCCGCCCTTATAGT	3314
Db	3065	GCGTTACCGGCTCATCCGGGAATTGCATCTCGGCCGCGCTGGGCCCGCCCTTATAGT	3125
OY	3315	CATCTCCCACTTGGCGCTCTGCTCAGGCAATTGTGAGCGCACCCCGAGACCCCAAGC	3374
Db	3125	CATCTCCCACTTGGCGCTCTGCTCAGGCAATTGTGAGCGCACCCCGAGACCCCAAGC	3186
OY	3375	GTCCTCCCCGGCCCTCGAGCAATTCGCGGTTTACCTTCTAAGAAAGCCGAGCCGAACCT	3434
Db	3185	GTCCTCCCCGGCCCTCGAGCAATTCGCGGTTTACCTTCTAAGAAAGCCGAGCCGAACCT	3244
OY	3435	GCTAACGTGGGATCGTGTGCATTAAGAGAACTTTCTGTGCGCACGCGCTAAGGACAAAGC	3494
Db	3245	GCTAACGTGGGATCGTGTGCATTAAGAGAACTTTCTGTGCGCACGCGCTAAGGACAAAGC	3306
OY	3495	GGAGAGCACTTCCGAGCGTCTGAACGCAACGTCCTCCAGAAAGTGAATTGGACACTGAACA	3554
Db	3305	GGAGAGCACTTCCGAGCGTCTGAACGCAACGTCCTCCAGAAAGTGAATTGGACACTGAACA	3366
OY	3555	GCTGGGACACATCCGCGGATACGAAACAGCGCTGAATGTCTGGAGCGGGAGGTCCAGCA	3614
Db	3365	GCTGGGACACATCCGCGGATACGAAACAGCGCTGAATGTCTGGAGCGGGAGGTCCAGCA	3426
OY	3615	GTTGAGCCGCGTCTGTGGGTGGGTGGCCGAGGCGCTGACCGCTTGTGCTGCGCCCC	3674
Db	3425	GTTGAGCCGCGTCTGTGGGTGGGTGGCCGAGGCGCTTGTGCTGCGCCCC	3486
OY	3675	AGGTGGCCGCGCACCCCTTGACTGCTGCGGTCCAAAGACTGAGCCCTGTGGCGGACTT	3734
Db	3485	AGGTGGCCGCGCACCCCTTGACTGCTGCGGTCCAAAGACTGAGCCCTGTGGCGGACTT	3546
OY	3735	CAAGGAGAGCCCCACAGGGGATTTTCTCTAAGTAAGGCTCATCTGGGCGTGGGCC	3794
Db	3545	CAAGGAGAGCCCCACAGGGGATTTTCTCTAAGTAAGGCTCATCTGGGCGTGGGCC	3606
OY	3795	CCCGGACCTGTGTGGCTTGTCTTGTAGGTGAGCCCATGTGCATCTGGGCACTGTACAG	3854
Db	3605	CCCGGACCTGTGTGGCTTGTCTTGTAGGTGAGCCCATGTGCATCTGGGCACTGTACAG	3666
OY	3855	ACCACCTTTGGGAGTGTATCTCTTAACAACAACAAGCATGCCCCGCTCTCCCAAGACAG	3914
Db	3665	ACCACCTTTGGGAGTGTATCTCTTAACAACAACAAGCATGCCCCGCTCTCCCAAGACAG	3726
OY	3915	TCCCAAGCTGGGAGGATCAAGGCGCTGGATCCCGGCGCTTATCCATCTGAGGCTGACAG	3974
Db	3725	TCCCAAGCTGGGAGGATCAAGGCGCTGGATCCCGGCGCTTATCCATCTGAGGCTGACAG	3786
OY	3975	GTCCTTGGGGTAAACAGGACACAAGACCCCTCACACTCACAGATTCTCTACACTGGGGA	4034
Db	3785	GTCCTTGGGGTAAACAGGACACAAGACCCCTCACACTCACAGATTCTCTACACTGGGGA	3846
OY	4035	AATAAGCCATTTTCAGAGAAAAAAA 4061	
Db	3845	AATAAGCCATTTTCAGAGAAAAAAA 3871	

RESULT 14
ADH51622
ID ADH51622 standard; cDNA; 3900 BP.
XX
AC ADH51622;
XX

DT	25-MAR-2004	(first entry)
DE	Human 18607 protein cDNA sequence.	
KX	cytostatic; vasotropic; haemostatic; nephrotropic; gastrointestinal-gen;	
KM	respiratory-gen; muscular-gen; osteopathic; antiinflammatory;	
KM	immunosuppressive; cardiovascular-gen; hepatocytotoxic; virucide; analgesic;	
KM	antianemic; endocrine-gen; neuroprotective; nootropic; cardiant;	
KM	gene therapy; cellular proliferative; differentiative disorder; brain;	
KM	blood vessel; platelet; breast; colon; kidney; lung; ovarian; prostate;	
KM	pancreatic; skeletal muscle; testicular; hormonal; bone metabolism;	
KM	immune disorder; inflammatory disorder; cardiovascular disorder;	
KM	endothelial cell; liver; viral; pain; metabolic; anaemia; angiogenesis;	
KM	neoplastic; endocrine disorder; neurological; heart; tissue typing;	
KM	chromosomal mapping; predictive medicine; pharmacogenomic; human; gene;	
KW	ss; 18607.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003219806-A1.	
XX		
PD	27-NOV-2003.	
XX		
PF	18-MAR-2003; 2003US-00391399.	
XX		
PR	22-FEB-2000; 2000US-00510706.	
PR	07-APR-2000; 2000US-0195734P.	
PR	31-MAY-2000; 2000US-00583373.	
PR	26-JUN-2000; 2000US-0214176P.	
PR	08-AUG-2000; 2000US-00634669.	
PR	31-AUG-2000; 2000US-0229036P.	
PR	19-SEP-2000; 2000US-023537P.	
PR	01-FEB-2001; 2001US-0267076P.	
PR	20-FEB-2001; 2001US-00789481.	
PR	12-MAR-2001; 2001US-0275078P.	
PR	12-MAR-2001; 2001US-0275172P.	
PR	06-APR-2001; 2001US-00828035.	
PR	26-JUN-2001; 2001US-0089176Z.	
PR	29-AUG-2001; 2001US-00942447.	
PR	17-SEP-2001; 2001US-0322983P.	
PR	19-SEP-2001; 2001US-00957683.	
PR	27-SEP-2001; 2001US-0325854P.	
PR	04-DEC-2001; 2001US-0336936P.	
PR	31-JAN-2002; 2002US-00062937.	
PR	08-MAR-2002; 2002US-00094214.	
PR	11-MAR-2002; 2002US-00095139.	
PR	17-SEP-2002; 2002US-00245121.	
PR	26-SEP-2002; 2002US-00255532.	
PR	04-DEC-2002; 2002US-00309804.	
XX		
PA	(MILL-) MILLENNIUM PHARM INC.	
PI	Gluckmann MA, Curtis RAJ, Lora JM, Galvin KM, Silos-Santiago I;	
DR	WPI; 2004-010868/O1.	
P	P-Psdbj; ADH51623.	
PT	New 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324,	
PT	55063, 52991, 59914, 59921 or 33751 nucleic acid molecule or polypeptide,	
PT	useful for diagnosing, preventing or treating e.g. proliferative or brain	
XX	disorders.	
PS	Claim 1; SEQ ID NO 1; 276pp; English.	
XX		
CC	This invention relates to novel human DNA sequences (designated 18607,	
CC	15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55063,	
CC	52991, 59914, 59921 or 33751) and the proteins encoded by them. The	
CC	invention may be useful for the development of compounds with a	
CC	cytostatic, vasotropic, haemostatic, nephrotropic, gastrointestinal-gen,	
CC	respiratory-gen, muscular-gen, osteopathic, antiinflammatory,	
CC	immunosuppressive, cardiovascular-gen, hepatocytotoxic, virucide, analgesic,	
CC	antianemic, endocrine-gen, neuroprotective, nootropic or cardiant	
CC	activity. In addition, the sequences may be useful for gene therapy. The	

invention may be useful in diagnosing, preventing or treating disorders characterized by aberrant 18607, 15603, 69318, 12303, 48000, 52920, 5433, 38554, 57301, 58324, 55053, 52991, 59914, 59921 or 33751 activity, for example cellular proliferative and/or differentiative disorder, brain disorder, blood vessel disorder, platelet disorder, breast disorder, colon disorder, kidney disorder, lung disorder, ovarian disorder, prostate disorder, pancreatic disorder, skeletal muscle disorder, testicular disorder, hormonal disorder, disorder associated with bone metabolism, immune disorder, inflammatory disorder, cardiovascular disorder, endothelial cell disorder, liver disorder, viral disease, pain, metabolic disorder, anaemia, angiogenesis disorder, neoplastic disorder, endocrine disorder, neurological disorder or heart disorder. They may also be used in screening assays, tissue typing, chromosomal mapping, predictive medicine or pharmacogenomics. The present sequence is that of the cDNA which encodes the human 18607 protein of the invention.

Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

Query Match 91.6%; Score 3721.4; DB 12; Length 3900;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 3731; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY	315	GGGGGGCGGGCGGACACAGCAATTCCTCGGCTCTGTGACCGAAGGATCAGCTGC	374
DB	125	GTGCCCGGCTCCATGTGTCCACAGTTCTCCGGCTCTGACCGAAGGATCAGCTGC	184
QY	375	AGTTATAGTCTGTGTACACAGCAATGGGCTTCCTGCCCCGACCTGTGTGTCAAT	434
DB	185	AGTTATAGTCTGTGTACACAGCAATGGGCTTCCTGCCCCGACCTGTGTGTCAAT	244
QY	435	GCTGGGGGAGTCGGGGGGGCGCCCTCTCCAGACCTGAGCTGACAGACTGTGCTGTG	494
DB	245	GCTGGGGGAGTCGGGGGGGCGCCCTCTCCAGACCTGAGCTGACAGACTGTGCTGTG	304
QY	495	GCTGTGTGCGGGCTGCCAGAGACAGAGAGCTGATTTGTCACTGGGGGTCTGCACGG	554
DB	305	GCTGTGTGCGGGCTGCCAGAGACAGAGAGCTGATTTGTCACTGGGGGTCTGCACGG	364
QY	555	CATGCGCGGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	614
DB	365	CATGCGCGGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	424
QY	615	CAAGTGTGTGACCATGATGTGTGCGCCCTGGGGGTGTGTGTGTGTGTGTGTGTGT	674
DB	425	CAAGTGTGTGACCATGATGTGTGCGCCCTGGGGGTGTGTGTGTGTGTGTGTGTGT	484
QY	675	CAACCCCAAGAGGCTGCTTCCCTGTGAGTACCGGTGTGCGGTGTGACCCGGAGG	734
DB	485	CAACCCCAAGAGGCTGCTTCCCTGTGAGTACCGGTGTGCGGTGTGACCCGGAGG	544
QY	735	CCAGTTTCCCTGTGACCTAATCTAGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGT	794
DB	545	CCAGTTTCCCTGTGACCTAATCTAGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGT	604
QY	795	CTGCTGGGGGGGAGAACCGCTTCCGCTTGCGCTGTGAGTCCATCATCTCACAGAA	854
DB	605	CTGCTGGGGGGGAGAACCGCTTCCGCTTGCGCTGTGAGTCCATCATCTCACAGAA	664
QY	855	GACGGGCTGTGAGGAGACTGGAATTGACATCCCTGTCTCTCTCTGTGTGTGTGT	914
DB	665	GACGGGCTGTGAGGAGACTGGAATTGACATCCCTGTCTCTCTCTGTGTGTGTGT	724
QY	915	TGAGAAATTTTGAACCGGAATTAAGAAAGCCACCCAGGCTCAGCTCCATGTCTCT	974
DB	725	TGAGAAATTTTGAACCGGAATTAAGAAAGCCACCCAGGCTCAGCTCCATGTCTCT	784
QY	975	GCGGTGCTCAAGGGGGAGCTGCGAGCTGCGGGGAGAACCTGGAAGACACTGGGCC	1034
DB	785	GCGGTGCTCAAGGGGGAGCTGCGAGCTGCGGGGAGAACCTGGAAGACACTGGGCC	844
QY	1035	AGGAGATGTGGGAGACAGGCAAGGCGAAGCCGAGATCGATCAGGCTTCTTCCAA	1094
DB	845	AGGAGATGTGGGAGACAGGCAAGGCGAAGCCGAGATCGATCAGGCTTCTTCCAA	904

QY	1095	AGGAGACTTGAGGTCTTGCAGAGCCAGGTGAGAGATTATGACCCGAGAGACTCT	1154
DB	905	AGGAGACTTGAGGTCTTGCAGAGCCAGGTGAGAGATTATGACCCGAGAGACTCT	964
QY	1155	GACAGCTATTCTTCTGAGAGATGGGTCTGAGAAATTCGAGACATTAATTTTGAAG	1214
DB	965	GACAGCTATTCTTCTGAGAGATGGGTCTGAGAAATTCGAGACATTAATTTTGAAG	1024
QY	1215	TTTGAAGGCTGTGGAGAGCTGGAGGCGCTACGCTTACGATGAGTGTGCTGTGT	1274
DB	1025	TTTGAAGGCTGTGGAGAGCTGGAGGCGCTACGCTTACGATGAGTGTGCTGTGT	1084
QY	1275	GCGTTGAAACCCGCTGACATTTGCCAGAGTGAATCTTTCCGGGGGACATCAATG	1334
DB	1085	GCGTTGAAACCCGCTGACATTTGCCAGAGTGAATCTTTCCGGGGGACATCAATG	1144
QY	1335	GTCTTCCATTCGAAAGCTTCCCTCATGAGAGCCCTCTGTAATGACCGGCTGAT	1394
DB	1145	GTCTTCCATTCGAAAGCTTCCCTCATGAGAGCCCTCTGTAATGACCGGCTGAT	1204
QY	1395	GCGCTTGTCAATTTCCACAGGCTGAGCTGGGCACTTCCGAGCCGAGTGGCTG	1454
DB	1205	GCGCTTGTCAATTTCCACAGGCTGAGCTGGGCACTTCCGAGCCGAGTGGCTG	1264
QY	1455	CCAACTCTACAGCGGCGGCGCTCCCAACTGCTCATCCGCAACTTTTGAACAGG	1514
DB	1265	CCAACTCTACAGCGGCGGCGCTCCCAACTGCTCATCCGCAACTTTTGAACAGG	1324
QY	1515	CCAACTCTACAGCGGCGGCGCTCCCAACTGCTCATCCGCAACTTTTGAACAGG	1574
DB	1325	CCAACTCTACAGCGGCGGCGCTCCCAACTGCTCATCCGCAACTTTTGAACAGG	1384
QY	1575	TGACGTGGGGCAATGTGTGAGATGCTGTGGGGAAGATGTCGCGGAGGTAAC	1634
DB	1385	TGACGTGGGGCAATGTGTGAGATGCTGTGGGGAAGATGTCGCGGAGGTAAC	1444
QY	1635	CGGGGGGCGCTGGGAGCCCTCACCAAGGCGAGGCTTCCGGGAGAGATATCTG	1694
DB	1445	CGGGGGGCGCTGGGAGCCCTCACCAAGGCGAGGCTTCCGGGAGAGATATCTG	1504
QY	1695	GGAACAAGGCACCTGCGGCTCTGCTGATGCTGTGGGAGAGGCGCCCTGAGCG	1754
DB	1505	GGAACAAGGCACCTGCGGCTCTGCTGATGCTGTGGGAGAGGCGCCCTGAGCG	1564
QY	1755	CTGCTTCTTTGGGACCTGTGTGTGAACAGGCAAGATGAGCATTTCTGGAGAT	1814
DB	1565	CTGCTTCTTTGGGACCTGTGTGTGAACAGGCAAGATGAGCATTTCTGGAGAT	1624
QY	1815	GGGTTCATATGAGTTTCTCAGCTTGTGGGCGTGTGTGTGTGTGTGTGTGTGT	1874
DB	1625	GGGTTCATATGAGTTTCTCAGCTTGTGGGCGTGTGTGTGTGTGTGTGTGTGT	1684
QY	1875	CCTGAGCTGAGCGCTGAGAGGAGCAGCAGAGAAAGACTGTGCTTCAAGTTGAG	1934
DB	1685	CCTGAGCTGAGCGCTGAGAGGAGCAGCAGAGAAAGACTGTGCTTCAAGTTGAG	1744
QY	1935	GATGGGCTTGAACCTTTTGGAGTGTCTATGTGACAGTGAAGTGAAGGCTGCG	1994
DB	1745	GATGGGCTTGAACCTTTTGGAGTGTCTATGTGACAGTGAAGTGAAGGCTGCG	1804
QY	1995	CCCTCCGCTGCGCTGCGGCTGCGGGGAGTGCATTTGCTCAGCTGAGCCATG	2054
DB	1805	CCCTCCGCTGCGCTGCGGCTGCGGGGAGTGCATTTGCTCAGCTGAGCCATG	1864
QY	2055	TGACGCCGCTGCTTTTGGCCAGAGATGGGTATAGTCTGTCTGACAAGAGTGT	2114
DB	1865	TGACGCCGCTGCTTTTGGCCAGAGATGGGTATAGTCTGTCTGACAAGAGTGT	1924
QY	2115	GGAAGATATGCGCAGCACTAACCATCTGGGCTTGTGCTTCTTTTGGCTTCC	2174
DB	1925	GGAAGATATGCGCAGCACTAACCATCTGGGCTTGTGCTTCTTTTGGCTTCC	1984

2175 ACTCATACACCCGCTCATCAGCTTACAGAAATCAGAGAGAGCCCAACGGAGAGA 2234
1985 ACTCATACACCCGCTCATCAGCTTACAGAAATCAGAGAGAGCCCAACGGAGAGA 2044
2235 GCTAAGTTTGAATGATAGTGTCTTAATAGGGAGAGGGCTGTGCGGACGACGAGACC 2294
2045 GCTAAGTTTGAATGATAGTGTCTTAATAGGGAGAGGGCTGTGCGGACGACGAGACC 2104
2295 AGCCGAGAGAGAGCGCGCTGGGGGGTCCCGGCGCAGTCGGGGCGTCCGGGTTTGTGCGGGG 2354
2105 AGCCGAGAGAGAGCGCGCTGGGGGGTCCCGGCGCAGTCGGGGCGTCCGGGTTTGTGCGGGG 2164
2355 CGCTGCGGGGGCGCGCGCTGTGCTCAACCGCTGTCTCACTTCTGGGGCGCGCGGTGAC 2414
2165 CGCTGCGGGGGCGCGCGCTGTGCTCAACCGCTGTCTCACTTCTGGGGCGCGCGGTGAC 2224
2415 CATCTTCAATGGGCAACGTGTGAGCTACCTGTGTCTGTCTGTCTTTCTCGCGGGTGT 2474
2225 CATCTTCAATGGGCAACGTGTGAGCTACCTGTGTCTGTCTGTCTTTCTCGCGGGTGT 2284
2475 GCTGTGATTTTCCAGCGCGCGCGCGCGCTCCCTGAGAGCTGTCTTATTTCTGGGC 2534
2285 GCTGTGATTTTCCAGCGCGCGCGCGCGCTCCCTGAGAGCTGTCTTATTTCTGGGC 2344
2535 TTTCAACGCTGTGTGAGAGAACTGCGCAGAGGCTTGAAGCGAGGCGGGGCGAGCTGCG 2594
2345 TTTCAACGCTGTGTGAGAGAACTGCGCAGAGGCTTGAAGCGAGGCGGGGCGAGCTGCG 2404
2595 CAGCGGGGGCGCGCGCGCTGTGCTCACTGAGCCAGCGCTGTGCGCTTCACTGTGCG 2654
2405 CAGCGGGGGCGCGCGCGCTGTGCTCACTGAGCCAGCGCTGTGCGCTTCACTGTGCG 2464
2655 CGAAGCTGTGAACCAAGTGTGAGCTGTGCTCACTGTGCTTCTTCTGGGGGTGGGCTG 2714
2465 CGAAGCTGTGAACCAAGTGTGAGCTGTGCTCACTGTGCTTCTTCTGGGGGTGGGCTG 2524
2715 CGGCTGTGACCCCGGGTTTGTATCACCTGGGCGGCACTGTCTCTGTGATGATTTATGAT 2774
2525 CGGCTGTGACCCCGGGTTTGTATCACCTGGGCGGCACTGTCTCTGTGATGATTTATGAT 2584
2775 TTTCAACGCTGTGTGAGAGAACTGCGCAGAGGCTTCACTGAGCCAGCGCTTCACTGTGCG 2834
2585 TTTCAACGCTGTGTGAGAGAACTGCGCAGAGGCTTCACTGAGCCAGCGCTTCACTGTGCG 2644
2835 CATGTGTGAGCAAGATGATGAGAGAGCTGTCTTCTTCTTCTTCTTCTGGGGTGTGCT 2894
2645 CATGTGTGAGCAAGATGATGAGAGAGCTGTCTTCTTCTTCTTCTTCTTCTGGGGTGTGCT 2704
2895 GGTAGCTTATGAGCTGTGAGCAAGAGAGGCTCTGAGGCGCAGAGCAATGATTTTCCCAAG 2954
2705 GGTAGCTTATGAGCTGTGAGCAAGAGAGGCTCTGAGGCGCAGAGCAATGATTTTCCCAAG 2764
2955 TATCTGTGCGCGCTGTCTTCACTGAGCTTCACTGTGAGATTTCTGGGAGATTTCCCAAG 3014
2765 TATCTGTGCGCGCTGTCTTCACTGAGCTTCACTGTGAGATTTCTGGGAGATTTCCCAAG 2824
3015 GGAATGTGAGCTGTGAGCTTCACTGAGAGCAAGCACTGTGTGTGAGAGCCCGCTTCTGGGC 3074
2825 GGAATGTGAGCTGTGAGCTTCACTGAGAGCAAGCAAGCACTGTGTGTGAGAGCCCGCTTCTGGGC 2884
3075 AACACCTCTGTGGGGCGCAGGGGGGCAACGCGGTCTCCAGATATGCAATGCGCTGTGAGT 3134
2885 AACACCTCTGTGGGGCGCAGGGGGGCAACGCGGTCTCCAGATATGCAATGCGCTGTGAGT 2944
3135 GCTGTCTCTGTGATCTTCTGTGCTGTGAGCAACCTGTGTGTGCAATTTGCTGATTTG 3194
2945 GCTGTCTCTGTGATCTTCTGTGCTGTGAGCAACCTGTGTGTGCAATTTGCTGATTTG 3004
3195 CATGTGTGATTTCAATTTCTGTGAGAGTACAGGGGCAACAGCGATCTTCTATGAGAGCGCA 3254
3005 CATGTGTGATTTCAATTTCTGTGAGAGTACAGGGGCAACAGCGATCTTCTATGAGAGCGCA 3064
3255 GCGTTACGCGCTCATCCGGGAATTCACATCTGTGCGCGCGGCTGTGCGCGCTTTATGCT 3314

3065 GCGTTACCGGCTCATCCGGGAATTCACATCTGTGCGCGCGGCTGTGCGCGCTTTATGCT 3124
3315 CATCTTCCACCTTGGCGCTCTGTGCTGAGCAATTTGTGAGGCGACCCCGAGCCCAAGCC 3374
3125 CATCTTCCACCTTGGCGCTCTGTGCTGAGCAATTTGTGAGGCGACCCCGAGCCCAAGCC 3184
3375 GTCCTTCCCGGCGCTGTGAGCAATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGGAGCT 3434
3185 GTCCTTCCCGGCGCTGTGAGCAATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGGAGCT 3244
3435 GCTAAGTGTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3494
3245 GCTAAGTGTGAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3304
3495 GGAAGAGCACTTCCAGAGCTTGAACCGCACTGCCAGAAAGTGAATTTGCACTGAACA 3554
3305 GGAAGAGCACTTCCAGAGCTTGAACCGCACTGCCAGAAAGTGAATTTGCACTGAACA 3364
3555 GCTGTGAGACATCCCGGAGTACGAACAGCGCTGAAAGTGTGAGAGCGGAGAGTCCAGCA 3614
3365 GCTGTGAGACATCCCGGAGTACGAACAGCGCTGAAAGTGTGAGAGCGGAGAGTCCAGCA 3424
3615 GTGTAGCCGCGCTCTGTGAGTGTGAGGCGAGGCGCTGAGCGCTGTGCTGTGCTGCTGCTGCTG 3674
3425 GTGTAGCCGCGCTCTGTGAGTGTGAGGCGAGGCGCTGAGCGCTGTGCTGTGCTGCTGCTGCTG 3484
3675 AGTGTGAGCGCGCAACCCCTGACCTGTGAGTGTGAGGCGTCAAGAGCTGAGCGCGAGCTT 3734
3485 AGTGTGAGCGCGCAACCCCTGACCTGTGAGTGTGAGGCGTCAAGAGCTGAGCGCGAGCTT 3544
3735 CAAGGAGAGAGCGCGCGCAAGGGGATTTTGTCTTCAAGTGAAGCTGATCTGTGCGGCTCGGCG 3794
3545 CAAGGAGAGAGCGCGCGCAAGGGGATTTTGTCTTCAAGTGAAGCTGATCTGTGCGGCTCGGCG 3604
3795 CCCGACCTGTGAGCTTGTCTTGAAGTGAAGCCCATGTGCTGATGAGGCGCACTGTGAGG 3854
3605 CCCGACCTGTGAGCTTGTCTTGAAGTGAAGCCCATGTGCTGATGAGGCGCACTGTGAGG 3664
3855 ACCACCTTGTGAGAGTGTATCTTCAACCAACAGCATGAGCCCGGCTCTTCCAGAAACCG 3914
3665 ACCACCTTGTGAGAGTGTATCTTCAACCAACAGCATGAGCCCGGCTCTTCCAGAAACCG 3724
3915 TCCAGAGCTGTGAGAGATCAAGGCTGTGATCCCGGGCGTATCTTCACTGTGAGGCTGTGAGG 3974
3725 TCCAGAGCTGTGAGAGATCAAGGCTGTGATCCCGGGCGTATCTTCACTGTGAGGCTGTGAGG 3784
3975 GTCCTGTGAGGATTAAGAGGAGCAACAGACCCCTCAACCATCAAGATTTCTCACTGTGAGG 4034
3785 GTCCTGTGAGGATTAAGAGGAGCAACAGACCCCTCAACCATCAAGATTTCTCACTGTGAGG 3844
4035 AATAAGGCAATTTAGAGAGAAAAAAA 4061
3845 AATAAGGCAATTTAGAGAGAAAAAAA 3871

RESULT 15
ABK28677
ID ABK28677 standard, cDNA, 3599 BP.
XX
XX ABK28677;
DT 09-APR-2002 (first entry)
XX
XX
DE Human cDNA encoding secreted protein SECP44.
XX
XX Human, ss; gene, SECP; antiinflammatory; cytosolic; cardiant;
XX immunosuppressive; antiviral; anti-HIV; antithrombotic; antineumatic;
XX muscular active general; anticonvulsant; nootropic; neuroprotective;
XX antiallergic; hypotensive; cardiovascular disorder; atherosclerosis;
XX hypertension; myocardial infarction; autoimmune disorder;
XX inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy;
XX rheumatoid arthritis; cell proliferative disorder; cancer;

KM developmental disorder; Duchenne muscular dystrophy;
 KW neurological disorder; epilepsy; Alzheimer's disease.
 XX Homo sapiens.
 OS WO200198353-A2.
 XX
 XX 27-DEC-2001.
 PD
 XX 20-JUN-2001; 2001MO-US019862.
 PF
 XX 20-JUN-2000; 2000US-0212890P.
 PR 23-JUN-2000; 2000US-0213466P.
 PR 27-JUN-2000; 2000US-0214601P.
 PR 31-JUL-2000; 2000US-0223722P.
 PR 08-SEP-2000; 2000US-0231435P.
 PR 15-SEP-2000; 2000US-0232889P.
 XX
 XX (INCYTE GENOMICS INC.
 PI Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley CM, Lee EA;
 PI Rankumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Baughn MR;
 PI Azimtai Y, Batra S, Buford N, Yao MG, Nguyen DB, Lu DM, Walla NK;
 PI Gandhi AR, Au-Young J, Patterson C;
 XX
 DR WPI; 2002-090431/12.
 DR P-PSDB; AUB02018.
 XX
 XX Forly four human secreted proteins (referred to as SECP-1 to SECP-44),
 PT useful in the diagnosis, treatment and prevention of cardiovascular (e.g.
 PT atherosclerosis), autoimmune/inflammatory (e.g. allergies) and cell
 PT proliferative disorders.
 PS
 PS Claim 5; Page 195; 195pp; English.
 XX
 CC The invention relates to forty four human secreted proteins (referred to
 CC as SECP-1 to SECP-44) and the nucleic acids encoding them. Also included
 CC are a host cell transformed with the nucleic acid, a transgenic animal
 CC comprising the nucleic acid, an anti-SECP antibody, use of the SECP
 CC proteins in isolating agonists and antagonists of SECP activity and a
 CC method of isolating compounds which alter the expression of the SECP
 CC nucleic acid. The SECP polynucleotides and polypeptides are useful in the
 CC diagnosis, treatment and prevention of cardiovascular (e.g.
 CC atherosclerosis, hypertension, myocardial infarction),
 CC autoimmune/inflammatory (e.g. acquired immunodeficiency syndrome (AIDS),
 CC allergies, rheumatoid arthritis), cell proliferative (e.g. cancer),
 CC neurological (e.g. Duchenne and Becker muscular dystrophy), and
 CC other examples of each disorder are given in the specification. Numerous
 CC present sequence is a cDNA encoding a SECP protein
 CC
 CC
 SO Sequence 3599 BP; 602 A; 1137 C; 1139 G; 721 T; 0 U; 0 Other;
 Query Match 88.2%; Score 3579.8; DB 6; Length 3599;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 3592; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 688 TCGTTCCTCGAGGATACCGGTGGCGGAGACCCGAGGACCGAGTTCCCTTG 747
 DB 241 TCGTTCCTCGAGGATACCGGTGGCGGAGACCCGAGGACCGAGTTCCCTTG 300
 QY 748 GACTACAACTACTCGGACCTTTCTTCTGTGTGACGACGACACACGCGCTGCGGGGGC 807
 DB 301 GACTACAACTACTCGGACCTTTCTTCTGTGTGACGACGACACACGCGCTGCGGGGGC 360
 QY 808 GAGAACCGCTTCGCTTGGCGCTGAGTCTCTCATCTCACAGACAGAGGCGCTGGGA 867
 DB 361 GAGAACCGCTTCGCTTGGCGCTGAGTCTCTCATCTCACAGACAGAGGCGCTGGGA 420
 QY 868 GGAAGTGAATTAACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 927
 DB 421 GGAAGTGAATTAACATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
 QY 928 AGCGCAATGAGAACGCGCACCCAGGCTCAGCTCCCATGTCTCTCTCTCTCTCTCTCTCT 987
 DB 481 AGCGCAATGAGAACGCGCACCCAGGCTCAGCTCCCATGTCTCTCTCTCTCTCTCTCTCT 540
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 DB 781 GGGAGCTCGGAGGCTCAGCTCAGCTCAGTGAAGCTGCTGTGTGCTTGAAGCCG 840
 QY 1288 GTGACATTTGCCAGAGTGAATCTTTTGGGGGGAATTCATATGGGGGCTTCCATTC 1347
 DB 841 GTGACATTTGCCAGAGTGAATCTTTTGGGGGGAATTCATATGGGGGCTTCCATTC 900
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Job time : 1366.41 secs

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Db	CCAGCAATATCCATG--CTTATGGGTGTGTGTCTCAACAACACTGCACAGTATACCGAGGA	3393
OY	TTACAAACCAAGCATGCGCGGCTCTCCCAAGACCAATGCCAGCTTGGAGGATCAAGG	3936
Db	CTCCTCCCAAGCAGCCTCAACTTGGGTGATCAAGCTCTGAGCTGCAAGTTGGCCT	3453
OY	CTGTGATCCCGGGCGCTTATCATCTGGAGGTGAGGGTCTTGGGGTAAACGAGACCA	3996
Db	CTTTGTGGGCCCGAGCACAACAGCAGAGAAAGCAGAGAGGTCT--GGGGTCAAGAACCA	3511
OY	CAGACCCCTCAACACTCAAGATTCTCAACTGGGGAAATTAAGCCATTTC	4049
Db	CAGACC-----CTACACACAGCTTCCCAACATGGGGAATTAACAATTGGA	3559

[illegible]

REFERENCE	1 (bases 1 to 912)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strusberg, Ph.D.

Tissue Procurement: Kristi A. Eglund, Ira Pastan
CNA Library Preparation: Invitrogen Corp
CNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LRAM14278 Row: 1 Column: 23
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/clone_1fb="MMPCL"
/notes="vector: pCMV-SPORT6; site 1: EcoRV; site 2: Not I;
subtracted with brain, liver, lung, kidney and muscle.
directionally cloned. Priming method: oligo-dT. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bangook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
manuscript submitted."

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ORIGIN

Query Match	19.0%	Score 773.6;	DB 6;	Length 912;
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Matches 812;	Conservative 0;	Mismatches 47;	Indels 2;	Gaps 1;
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[illegible]

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DEFINITION	UI-CF-FN0-afl-C-16-0-UI 3', mRNA sequence.				
ACCESSION	CA312705				
VERSION	CA312705.1	GI:24530803			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 734)				

AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704447
8889548
McCray Lab
Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
source

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/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human Lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@iowa.edu
TAG_TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG_LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 17.8%; Score 724; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 1.2e-145;
Matches 724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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734 TCAGGCATTGTGCGAGGAGCCCGGAGCCCGGAGCCGCTCCCGGCGCTCCAGCATTT 675
3398 TCCGGGTTTACCTTCTAAGGAGCGGAGCGGAACTCTAACTGAGGAATCGGTGATA 3457
674 TCCGGGTTTACCTTCTAAGGAGCGGAGCGGAACTCTAACTGAGGAATCGGTGATA 615
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DB 194 TACAACACACAGCATGCGCGGCTCTCCAGAACAGTCCAGCGTGGAGAGATCAAGGC 135
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DB 134 CTGATCCCGGCGCGTTATTCATCTGAGGCTGAGGCTCTTGGGTTAAGAGGAGCAC 75
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DB 14 AAAA 11

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ACCESSION B0687299
VERSION B0687299.1 GI:23543033
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704447
8889548
McCray Lab
Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES
source

Location/Qualifiers
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/clone_11b="UI-CF-EC1"
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 TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383
 TAG_LIB=UI-CF-EC1
 TAG_SEQ=AGGCTTAC"

ORIGIN

Query Match 17.8%; Score 721.4; DB 5; Length 733;
 Best Local Similarity 99.9%; Pred. No. 4.5e-145;
 Matches 722; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 4059 AAA 4061
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 DB 13 AAA 11

RESULT 5
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ACCESSION BUB58032
 VERSION BUB58032.1 GI:24043024
 KEYWORDS EST.

SOURCE
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REFERENCE
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE NIH-MGC http://mgi.nci.nih.gov/.

JOURNAL
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
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 http://image.llnl.gov
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 High quality sequence start: 11
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FEATURES

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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6647959"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_11b="NIH_MGC_107"
 /note="Organ: breast; Vector: pOT87; Site 1: EcoRI;
 Site 2: XhoI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN

Query Match 17.7%; Score 719; DB 5; Length 879;
 Best Local Similarity 96.6%; Pred. No. 1.5e-144;
 Matches 799; Conservative 0; Mismatches 20; Indels 8; Gaps 6;

2412 GACCATCTTCAATGGCAACGTGTAGCTACTGCTGCTGCTGCTTCTTCTGCGGGCT 2471
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 1 GACCATCTTCAATGGCTACTGTGTACGTACTGCTGCTGCTGCTTCTTCTGCGGGCT 60
 |||
 2472 GCTGCTGTTGATTTCCAGCGGCGCGCGCGGCTCCCTGGAGCTGCTGCTATTTCTG 2531
 |||
 61 GCTGCTGTTGATTTCCAGCGGCGCGCGCGGCTCCCTGGAGCTGCTGCTATTTCTG 120
 |||
 2532 GCTTTCACGCTGTGTGCGAGAACTGCGCAGGCGCTGAGCGAGCGGCGGAGCGCT 2591
 |||
 121 GCTTTCACGCTGTGTGCGAGAACTGCGCAGGCGCTGAGCGAGCGGCGGAGCGCT 180
 |||
 2592 CGCCAGCGGCGGCGCGCGGCGCTGCGCATGCTCACTAGCGCAGGCGCTGCTTACT 2651
 |||
 181 CGCCAGCGGCGGCGCGCGGCGCTGCGCATGCTCACTAGCGCAGGCGCTGCTTACT 240
 |||

[illegible]

RESULT 6	774 bp	mRNA	linear	EST_15-MAY-2001
BG759687				
LOCUS				
DEFINITION	602713380.1	NIH_MGC_48	Homo sapiens CDNA clone IMAGE:4853634 5',	
ACCESSION	774 bp			
VERSION	BG759687			
KEYWORDS	BG759687.1	GI:14070340		
SOURCE	EST.			
ORGANISM	Homo sapiens (human)			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (bases 1 to 774)			
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-r@mail.nih.gov Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LTCM1699 row: p column: 19 High quality sequence stop: 771. location/Qualifiers			
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/clone="IMAGE:4853634"
/tissue_type="primary B-cells from consls (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/notes="Organ: B-cells; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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Query Match	Similarity	99.6%	Pred.	4.4e-143	DB 4	Length	774
Best Local	Similarity	99.6%	Pred.	4.4e-143	DB 4	Length	774
Matches	714	Conservative	0	Mismatches	3	Indels	0
Gaps	0						
QY	3320	CCCACTTGGCGCTCTCTGCTCAGGCAATTGTGCAAGCCGACCCCGAGCCCGGACGCTGCT	3379				
Db	2	CCCACTTGGCGCTCTCTGCTCAGGCAATTGTGCAAGCCGACCCCGAGCCCGGACGCTGCT	61				
QY	3380	CCCCGCGCTCTGACCATTTTCCGGTTTAACTTTTCTTAAGAAAGCCGACCCGAAAGCTGTCTAA	3439				
Db	62	CCCCGCGCTCTGACCATTTTCCGGTTTAACTTTTCTTAAGAAAGCCGACCCGAAAGCTGTCTAA	121				
QY	3440	CGTGGGAATCGGTGCATTAAGAGAACTTTCTGCTGGCACGCGCTAGGGACAAAGCGGGAGA	3499				
Db	122	CGTGGGAATCGGTGCATTAAGAGAACTTTCTGCTGGCACGCGCTAGGGACAAAGCGGGAGA	181				
QY	3500	GCGACTCCGACGCTCTGAGGCGCACGTTCCGAAAGTGGACTTGGCACTGAACACGCTGG	3555				
Db	182	GCGACTCCGACGCTCTGAGGCGCACGTTCCGAAAGTGGACTTGGCACTGAACACGCTGG	241				
QY	3580	GACACATTCGCGGAGTAACGAACAGGCGCTGAAAGTGTGTGAGACGGGAGGTCACAGATCTA	3619				
Db	242	GACACATTCGCGGAGTAACGAACAGGCGCTGAAAGTGTGTGAGACGGGAGGTCACAGATCTA	301				
QY	3620	GCAGGCTCTGGGGTGGGGTGGCCGAGGCGCTGACGCGCTGACCTTGCGTGGCCCCAGGTG	3679				
Db	302	GCAGGCTCTGGGGTGGGGTGGCCGAGGCGCTGACGCGCTGACCTTGCGTGGCCCCAGGTG	361				
QY	3680	GGCGCCGACCCCTCTGACCTGCTGGGTCTCAAGACTGAGCCCTGCGCGGACTTCAAG	3739				
Db	362	GGCGCCGACCCCTCTGACCTGCTGGGTCTCAAGACTGAGCCCTGCGCGGACTTCAAG	421				
QY	3740	AGAGCCCGCCACAGGGGATTTTGCTCTTCTAGATAGGCTCATCTGGGCTTGGCCCCCGC	3799				
Db	422	AGAGCCCGCCACAGGGGATTTTGCTCTTCTAGATAGGCTCATCTGGGCTTGGCCCCCGC	481				
QY	3800	ACCTGGTGGGCTTGTCTCTGAGTGAAGGCCCATCTCATCTGGGCGACCTGCAAGACAC	3859				
Db	482	ACCTGGTGGGCTTGTCTCTGAGTGAAGGCCCATCTCATCTGGGCGACCTGCAAGACAC	541				
QY	3860	CTTTGGGAGTGTCACTCTTCAAAACCAACAGCATCCCGGCTCTCTCCAGAACCACTGCCA	3919				
Db	542	CTTTGGGAGTGTCACTCTTCAAAACCAACAGCATCCCGGCTCTCTCCAGAACCACTGCCA	601				
QY	3920	GCTTGGGAGATCAAGGCTTGAGATCCGGGCGCTTATTCATCTGAGGCTGCGAGGCTCT	3979				
Db	602	GCTTGGGAGATCAAGGCTTGAGATCCGGGCGCTTATTCATCTGAGGCTGCGAGGCTCT	661				
QY	3980	TGGGGTAAACAGGGGACCAAGACCCCTCAACCACTACAGATTCCTCACACTGGGGAAA	4036				
Db	662	TGGGGTAAACAGGGGACCAAGACCCCTCAACCACTACAGATTCCTCACACTGGGGAAA	718				

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VERSION      CN402549.1  GI:47390143
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE    1 (bases 1 to 700)
              Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
              Li, Y., Xu, C., Pang, R., Guejler, K., Rao, M. S., Mandalam, R.,
              Lebowicki, J. and Stanton, L. W.
              Transcriptional characterization elucidates signaling networks that
              control human ES cell growth and differentiation
              Nat. Biotechnol. 22 (6), 707-716 (2004)
TITLE        JOURNAL
              Contact: Brandenberger R
              Regenerative Medicine
              Geron Corporation
              230 Constitution Drive, Menlo Park, CA 94025, USA
              Tel: 650 473 8658
              Fax: 650 473 7760
              Email: rbrandenberger@geron.com
              Insert Length: 700  Std Error: 0.00.
FEATURES     Location/Qualifiers
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              /db_xref="taxon:9606"
              /tissue_type="embryonic stem cells, cell lines H1, H7, and
              H9"
              /clone_lib="GRN ES"
              /note="oligo dt primed, full-length enriched cDNA library
              from undifferentiated hES cell lines H1 (p32), H7 (p29),
              and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match      17.2%; Score 697.4; DB 7; Length 700;
Best Local Similarity 99.9%; Pred. No. 6,9e-140;
Matches 698; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 370 GCTGCAAGTTATAGTCTGTGTCACACGACATGGGGCTTCGTCGCCGAACCTGGTGGTG 429
DB 2 GCTGCAGTTATATAGTCTGTGTCACACGACATGGGGCTTCGTCGCCGAACCTGGTGGTG 61
QY 430 TCAGTGTGGGGGAGATCGGGGGGCCCCGCTCTCCACAGCTGGCTGACAGACCTGTGCGCT 489
DB 62 TCAGTGTGGGGGAGATCGGGGGGCCCCGCTCTCCACAGCTGGCTGACAGACCTGTGCGCT 121
QY 490 CTTGGGCTGTGTCGGGGCTGCCAGACAGACAGAGAGCTGATGTCATCGGGGGTCTGCAC 549
DB 122 CTTGGGCTGTGTCGGGGCTGCCAGACAGACAGAGAGCTGATGTCATCGGGGGTCTGCAC 181
QY 550 ACGGCGATGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 609
DB 182 ACGGCGATGGCGCGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241
QY 610 GGCACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 669
DB 242 GGCACCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301
QY 670 CTCATCAACCCCAAGGGCTGTTTCCCTGTGGAGTACCGGTGGCGGGGTACCCGGAGAC 729
DB 302 CTCATCAACCCCAAGGGCTGTTTCCCTGTGGAGTACCGGTGGCGGGGTACCCGGAGAC 361
QY 730 GGGGTCACAGTTCCCTGTGATCACTACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 789
DB 362 GGGGTCACAGTTCCCTGTGATCACTACACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 421
QY 790 CACGGCTGCTGGGGGCGAGAACCGCTTCGCTTGCGCTGAGCTCACTACACTTCACAG 849
DB 422 CACGGCTGCTGGGGGCGAGAACCGCTTCGCTTGCGCTGAGCTCACTACACTTCACAG 481
QY 850 CAGAAGACGGGCGTGGGAGGAGACTGGAAATTGACATCCCTGCTCTCTCTGATTGAT 909
DB 482 CAGAAGACGGGCGTGGGAGGAGACTGGAAATTGACATCCCTGCTCTCTCTGATTGAT 541
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QY 910 GGTGATGGAAGATGTTGACCGCAATAGAGAACCGCACCGCTCAGCTCCATGTC 969
DB 542 GGTGATGGAAGATGTTGACCGCAATAGAGAACCGCACCGCTCAGCTCCATGTC 601
QY 970 CTCGTGGCTGCTCAGGGGGAGCTGCGGAGCTGCTGGGGGAGACCTTGGAGACACTCTG 1029
DB 602 CTCGTGGCTGCTCAGGGGGAGCTGCGGAGCTGCTGGGGGAGACCTTGGAGACACTCTG 661
QY 1030 GCCCAGGAGTGGGGGAGCGCAGCGAAGGCCGAGCCGA 1068
DB 662 GCCCAGGAGTGGGGGAGCGCAGCGAAGGCCGAGCCGA 700

RESULT 8
LOCUS    B0942718
DEFINITION B0942718 933 bp mRNA linear EST 21-AUG-2002
          AGENCOURT 8842138 lupski_sciatic_nerve Homo sapiens cDNA clone
          IMAGE:6204319 5', mRNA sequence.
ACCESSION B0942718
VERSION   B0942718.1  GI:22358196
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 933)
          NIH-MGC http://mgc.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: csagbs-remail.nih.gov
          Tissue Procurement: Dr. James R. Lupski
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Agencourt Bioscience Corporation (LNLN)
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLN at:
          http://image.llnl.gov
          Plate: LNLN13625 row: 9 column: 08
          High quality sequence stop: 501.
FEATURES     Location/Qualifiers
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              /note="Vector: pCMV-Sport6 (Life Technologies); Site_1:
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              Directionally cloned using the following adaptors:
              5'-TCGACCCAGGCGTCCG-3' and
              5'-GACGTGTCATGATCGAGCGCGCGCCCT(15)-3'. Size selected >
              1 kb for average insert length 1.87 kb. This is a primary
              library, non-amplified. Library constructed by Life
              Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
              College of Medicine) and is available through Life
              Technologies."
ORIGIN
Query Match      17.0%; Score 690; DB 5; Length 933;
Best Local Similarity 92.3%; Pred. No. 2.9e-138;
Matches 783; Conservative 0; Mismatches 55; Indels 10; Gaps 5;

QY 1489 ATCCGCAACCTTTTGGACAGGCGCTCCACAGCGGACCAAGGCCCGACCTTA 1548
DB 4 ATCCGCAACCTTTTGGACAGGCGCTCCACAGCGGACCAAGGCCCGACCTTA 63
QY 1549 GGGGAGCTGGGAGACTCCGCCCTTGACGTGGGGCATGTGCTGAGATGCTGCTGGG 1608
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[illegible]

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>

Plate: L1AM14281 row: i column: 10
High quality sequence stop: 571.
Location/Qualifiers

FEATURES

source

1. 864
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/lab_host="EMD10B"
/clone_id="MAPCL"
/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subcloned with brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."

ORIGIN

Query Match 15.9%; Score 646.8; DB 6; Length 864;

Best Local Similarity 94.4%; Pred. No. 6.3e-128; Indels 1; Gaps 1;

Matches 668; Conservative 0; Mismatches 39; Indels 1; Gaps 1;

2966 GCGCTTTTACCGTCCCTACCTGAGATCTTGGGAGATTCCCGAGAGACATGACG 3025
1 GCGCTTTTACCGTCCCTACCTGAGATCTTGGGAGATTCCCGAGAGACATGACG 60
3026 TGGCCCTATGAGACAGCACTGCTGTGGAGCCCGCTTCTGGGACACCTCTCTG 3085
61 TGGCCCTATGAGACAGCACTGCTGTGGAGCCCGCTTCTGGGACACCTCTCTG 120
3086 GGGCCGAGGGGGGACCTGGCGTCCAGTATGCCAATGCTGTGGTGTGCTGCTCCG 3145
121 GGGCCGAGGGGGGACCTGGCGTCCAGTATGCCAATGCTGTGGTGTGCTGCTCCG 180
3146 TCATCTTCTGCTGCTGGGCAACATCTGTGTCACTTGTCTTCCATGTTCACTT 3205
181 TCATCTTCTGCTGCTGGGCAACATCTGTGTCACTTGTCTTCCATGTTCACTT 240
3206 ACACATTTGGCAAGATGACAGGCAACAGCATCTCTACTGAAAGCGGAGCTTAC 3265
241 ACACATTTGGCAAGATGACAGGCAACAGCATCTCTACTGAAAGCGGAGCTTAC 300
3266 TCATCTTCTGCTGCTGGGCAACATCTGTGTCACTTGTCTTCCATGTTCACTT 3325
301 TCATCTTCTGCTGCTGGGCAACATCTGTGTCACTTGTCTTCCATGTTCACTT 360
3326 TGGCCCTCTGCTGAGCAATTTGTCAGAGCCCGGAGCCCGGAGCCCGGAGCCCG 3385
361 TGGCCCTCTGCTGAGCAATTTGTCAGAGCCCGGAGCCCGGAGCCCGGAGCCCG 420
3386 CCTCTGAGCATTTCCGGGTTTACCTTTCTAAGAAAGCCGAGGGAAGCTGTAACT 3445
421 CCTCTGAGCATTTCCGGGTTTACCTTTCTAAGAAAGCCGAGGGAAGCTGTAACT 480
3446 AATGGTTCATTAAGAGAACTTTTCTGTGGGACCGGCTAAGGAGGAGAGGAGT 3505
481 AATGGTTCATTAAGAGAACTTTTCTGTGGGACCGGCTAAGGAGGAGAGGAGT 540
3506 CCGAGCGTCTAAGAGGAGGCTCCGAGAGGTGGAATTGGAACAGCTGGAGGACCA 3565
541 CCGAGCGTCTAAGAGGAGGCTCCGAGAGGTGGAATTGGAACAGCTGGAGGACCA 600
3566 TCCGGAAGTACGAACAGGCGCTGAAAGTCT-GGAGCGGAGGTCACAGGTAGCCG 3624
601 TCCGGAAGTACGAACAGGCGCTGAAAGTCTGAGGAGGCGGAGGTCTACAGGTAG 660

Qy 3625 GTCCGTGGGTGAGTGAGCGAGCCCTGAGCCGCTGCTGCTGCTCC 3672
DB 661 TCCCGTGGGTGAGTGAGCGAGCCCTGAGCCGCTGCTGCTGCTCC 708

RESULT 12
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DEFINITION UI-CF-EN1-act-i-04-0-UI-61 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-act-i-04-0-UI 3', mRNA sequence.
ACCESSION BM982099
VERSION BM982099.1 GI:19605256
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.
1 (bases 1 to 655)
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PubMed 8889548
COMMENT Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
PolyA=yes.

FEATURES

source

Location/Qualifiers
1. 655
/organism="Homo sapiens"
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Cells"
/dev_str="Adult"
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/clone_id="UI-CF-EN1"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT73-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell lanes untreated LPS
6hr to LPS 24h
TAG_Lib=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 15.8%; Score 642.4; DB 5; Length 655;
Best Local Similarity 99.8%; Pred. No. 5.4e-128;

Matches 643; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 654 GAAGCCGAGCGAAGCTGCTAAAGTGGAAATCGATGATAGAGAACTTTCTGTGGCA 595

QY 3478 CCGCGTAGGGAACAGCGGAGAGCACTCCGAGCGCTTGAACGCACTGCTCCAGAAAGTG 3537

DB 554 CCGCGTAGGGAACAGCGGAGAGCACTCCGAGCGCTTGAACGCACTGCTCCAGAAAGTG 535

QY 3538 GACTTGGCACTGAAACAGCTGGGAGCAATCCGAGATAGAAACAGCGCTGAAAGTGCTG 3597

DB 534 GACTTGGCACTGAAACAGCTGGGAGCAATCCGAGATAGAAACAGCGCTGAAAGTGCTG 475

QY 3598 GAGCGGAGAGTCCAGAGATGTAGCGCGCTCTCTGGGGTGGTGGCCGAGCGCTGAGCCGC 3657

DB 474 GAGCGGAGAGTCCAGAGATGTAGCGCGCTCTCTGGGGTGGTGGCCGAGCGCTGAGCCGC 415

QY 3658 TTTGCTTGTCTGCTCCCGAGGTGGCGCCGCAACCCCTGACCTGCTGGGTCTCAAGACTGA 3717

DB 414 TTTGCTTGTCTGCTCCCGAGGTGGCGCCGCAACCCCTGACCTGCTGGGTCTCAAGACTGA 355

QY 3718 GCGCTGTGGGAGACTTCAAGAGAGAGCCCGCAAGGGGATTTGCTCTAGTAAGGCA 3777

DB 354 GCGCTGTGGGAGACTTCAAGAGAGAGCCCGCAAGGGGATTTGCTCTAGTAAGGCA 295

QY 3778 TCATCTGGGCTCTGCGCCCGGCACTGTGAGCTTGTCTCTTGAAGTGAAGCCCATGTCCA 3837

DB 294 TCATCTGGGCTCTGCGCCCGGCACTGTGAGCTTGTCTCTTGAAGTGAAGCCCATGTCCA 235

QY 3838 TCTGGGAGCACTGTCAAGAGCAACCTTTGGGAGTGTATCTTCAAAACAGAGCATATGCCG 3897

DB 234 TCTGGGAGCACTGTCAAGAGCAACCTTTGGGAGTGTATCTTCAAAACAGAGCATATGCCG 175

QY 3898 GTCTCTCCAGAGCAAGTCCAGCTGGGAGAGATCAAGGCTGAGATCCCGGGCCGCTATTC 3957

DB 174 GTCTCTCCAGAGCAAGTCCAGCTGGGAGAGATCAAGGCTGAGATCCCGGGCCGCTATTC 115

QY 3958 CATCTGAGAGCTGTGAGGCTCTTGGGGTAAACAGAGCAACAGCCCTGACCATGACAG 4017

DB 114 CATCTGAGAGCTGTGAGGCTCTTGGGGTAAACAGAGCAACAGCCCTGACCATGACAG 55

QY 4018 ATTCTCTACACTGGGGAATTAAGCCATTTCAGAGAGAAAAA 4061

DB 54 ATTCTCTACACTGGGGAATTAAGCCATTTCAGAGAGAAAAA 11

RESULT 13

BF311909 1090 bp mRNA linear EST 21-NOV-2000

LOCUS 601897749P1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126764 5',

DEFINITION mRNA sequence.

ACCESSION BF311909

VERSION BF311909.1 GI:11259680

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1090)

AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L10C1017 row: b column: 13
High quality sequence stop: 633.

FEATURES

source

Location/Qualifiers

1..1090

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/mol_type="mRNA"

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/issue_type="neuroblastoma"

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/clone_1ib="NIH MGC_19"

/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.7%; Score 637.4; DB 2; Length 1090;

Best Local Similarity 89.6%; Pred. No. 7e-127;

Matches 757; Conservative 0; Mismatches 71; Indels 17; Gaps 6;

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DB 2 GGGGAAGATGTGCGCGGAGGTACCTCCGGGGGCGCTGGAGACCTTCAACCGAGCA 61

QY 1665 GGGCTTCGGGAGAGCATGTATCTGCTCGAGACAAGGCAACCTGCGCTCGCTGGA 1724

DB 62 GGGCTTCGGGAGAGCATGTATCTGCTCGAGACAAGGCAACCTGCGCTCGCTGGA 121

QY 1725 TGCTGAGCTCGGAGAGGCGCCCTGAGAGCACTGCTTTTGGGACATGTTGCTGAACAG 1784

DB 122 TGCTGAGCTCGGAGAGGCGCCCTGAGAGCACTGCTTTTGGGACATGTTGCTGAACAG 181

QY 1785 GGCACAGATGTGCGCATGTACTTCTGGAGATGGTTCCATGCAATTTCTCACTCTTGG 1844

DB 182 GGCACAGATGTGCGCATGTACTTCTGGAGATGGTTCCATGCAATTTCTCACTCTTGG 241

QY 1845 GGCCTGTTGCTGCTCCGGGAGTATGAGAGCGCTGAGAGCTGAGAGAGAGAGAGAG 1904

DB 242 GGCCTGTTGCTGCTCCGGGAGTATGAGAGCGCTGAGAGCTGAGAGAGAGAGAGAG 301

QY 1905 GAGGAAGACCTGGGAGTCAAGTTTGAAGGAGATGAGGCTTGAACCTTTTGGGAGTCTA 1964

DB 302 GAGGAAGACCTGGGAGTCAAGTTTGAAGGAGATGAGGCTTGAACCTTTTGGGAGTCTA 361

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DB 362 TCGCAGCATGTAGTGAAGGCTGCGCGCTCTCTCTCGCTGCTGCTGCTGCGGAGGA 421

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RESULT 14

LOCUS BG341728 699 bp mRNA linear EST 27-FEB-2001

DEFINITION 602463453F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576237 5', mRNA sequence.

ACCESSION BG341728

VERSION BG341728.1 GI:13148166

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 699)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Plate: LNCM1288 row: j column: 14
High quality sequence stop: 696.

FEATURES

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location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

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/clone="IMAGE:4576237"

/tissue_type="Primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/clone_id="NIH_MGC_48"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 15.6%; Score 635.2; DB 4; Length 699;

Best Local Similarity 98.9%; Pred. No. 2e-126;

Matches 692; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

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QY 3380 CCCCGGCGCTCGAGCATTTCCGGGTTACCTTTTAAGGAAGCGAGCGGAAGTGCATA 3439

Db 62 CCGCGGCGCTCGAGCATTTCCGGGTTACCTTTTAAGGAAGCGAGCGGAAGTGCATA 121

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Db 122 CGTGGGAATCGGTGCATTAAGGAGAACTTTCTGTCTGACGCGGCTTAAGGACAAAGCGGAGA 181

QY 3500 GCGACTCCGAGCGTCTGAAGCGCAGCTCCAGAAAGTGAATTGGCACTGAACAGCTGG 3559

Db 182 GCGACTCCGAGCGTCTGAAGCGCAGCTCCAGAAAGTGAATTGGCACTGAACAGCTGG 241

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Db 362 GCGCG-CACCCCTGACCTGCTGGGTCCAAAGCTGAGCCCTGCTGGCGGACTTCAAG 420

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Db 421 AGAAGCCCCCAGAGGGATTTTGCTCTTAAGTAAGGTCAATGAGGCTCGGCCCGCC 480

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RESULT 15

LOCUS B1759746 672 bp mRNA linear EST 25-SEP-2001

DEFINITION 603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5', mRNA sequence.

ACCESSION B1759746

VERSION B1759746.1 GI:15751324

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 672)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.lnl.gov>
Plate: LLM11464 row: g column: 06
High quality sequence stop: 668.

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location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5185949"

/lab_host="DH10B"

/clone_id="NIH_MGC_116"

/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

ORIGIN

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Query Match      15.6%; Score 634.4; DB 4; Length 672;
Best Local Similarity 99.4%; Pred. No. 2.9e-126;
Matches 668; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

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QY      2469 GGTGCTGCTCGTGAATTTCCAGCCGCGCGCGCTCCCTGAGAGTGTCTCTATT 2528
DB      61 GGTGCTGCTCGTGAATTTCCAGCCGCGCGCGCTCCCTGAGAGTGTCTCTATT 120
QY      2529 CTGGGCTTTCAAGCTGTGTGAGGAATGAGCCAGAGGCTGAGGAGGCGGGGCGAG 2588
DB      121 CTGGGCTTTCAAGCTGTGTGAGGAATGAGCCA-GGCTGAGGAGGAGGCGGGGCGAG 179
QY      2589 CCTGCGCAAGCGGGGCGCCC-GGGCGCTGAGCATGCTCACTGAGCCAGCGCTGCGCTCT 2647
DB      180 CCTGCGCAAGCGGGGCGCCCTGAGGCTGAGCATGCTCACTGAGCCAGCGCTGCGCTCT 239
QY      2648 ACTTGCGGACAGCTGGAACCAAGTGAGACTTGTGCTCTCACTGCTTCTCTCGGGG 2707
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QY      2708 TGGGCTGCGGCGGCTGACCCCGGGTTTGTACCTGGGGCGGCACTGCTCTGATCGACT 2767
DB      300 TGGGCTGCGGCGGCTGACCCCGGGTTTGTACCTGGGGCGGCACTGCTCTGATCGACT 359
QY      2768 TCATGGTTTTCAGGTGCGGCTGCTTCACATCTTCAAGGTCAAAACAGCTGGGGCCA 2827
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Search completed: June 13, 2005, 08:20:49
Job time : 8527.65 secs

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 QY 2797 ATCTTACGGTCAACAAACAGCTGGGGCCCAAGATGTCATCTGTAGCAAGATGATGAAG 2856
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 DB 1390 CTTGATCCCGGCGCTTATCCATCTGAGGCTGCAAGGCTCTTGGGGTAAACAGGACCA 1449
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RESULT 2
 US-09-030-607-109
 ; Sequence 109, Application US/09030607
 ; Patent No. 6262245
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
 ; NUMBER OF SEQUENCES: 224
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SEED and BERRY LLP
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/030,607
 ; FILING DATE: 25-FEB-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Makl, David J.
 ; REGISTRATION NUMBER: 31,392
 ; REFERENCE/DOCKET NUMBER: 210121.427C3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 622-4900
 ; TELEFAX: (206) 682-6031
 ; INFORMATION FOR SEQ ID NO: 109:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1524 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; US-09-030-607-109
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1510 AAAA 1514

RESULT 3
US-09-439-313-109
; Sequence 109, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yugu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-439-313-109

Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CTGCCCCAGGGGCTTGAAGCGGAGCGGGGAGACCTTGGCCAGCGGGGGCCCCGGGCTTGGC 2616

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DB 250 ATCTTACGGGTCAACAAACAGCTGGGGCCCAAGATGTCACTGTGACAAAGATGATGAAG 309
QY 2857 GACGTGTTCTTCTTCTCTCTCTCTCTCGGGGCTGGGTAGCTCATGGGCGTGGCAGG 2916
DB 310 GACGTGTTCTTCTTCTCTCTCTCTCGGGGCTGGGTAGCTCATGGGCGTGGCAGG 369
QY 2917 GAGGGGCTCTGAGGGCCAGGAGAGTGACTTCCCAAGTATCTTGGCGCGCTCTTCTAC 2976
DB 370 GAGGGGCTCTTGGGCGCAGGAGAGTGACTTCCCAAGTATCTTGGCGCGCTCTTCTAC 429
QY 2977 CGTCCCTACCTGCAATCTTCCGGGCAAGATCCCGAGGAGAGCATGGAAGTGGCTTCAG 3036
DB 430 CGTCCCTACCTGCAATCTTCCGGGCAAGATCCCGAGGAGAGCATGGAAGTGGCTTCAG 489
QY 3037 GAGCAAGAGCAATGCTGCTGCGGAGCCCGGCTTGGGCGACACCTCTGCGGGCCAGGGG 3096
DB 490 GAGCAAGAGCAATGCTGCTGCGGAGCCCGGCTTGGGCGACACCTCTGCGGGCCAGGGG 549
QY 3097 GGCACCTGCGTCTCCAGATATGCAACTGGCTGGTGGTGTGCTCTCTGTCATCTTCTG 3156
DB 550 GGCACCTGCGTCTCCAGATATGCAACTGGCTGGTGGTGTGCTCTCTGTCATCTTCTG 609
QY 3157 CTGCTGGCCAAATCTGCTGTGTCACCTGCTCATTTGCCATGTTACAGATTGCGG 3216
DB 610 CTGCTGGCCAAATCTGCTGTGTCACCTGCTCATTTGCCATGTTACAGATTGCGG 669
QY 3217 AAGGTACAGGGGCAACAGCGATCTCTAGGAAGGCGAGGTTACGCGCTCATCGGGAA 3276
DB 670 AAGGTACAGGGGCAACAGCGATCTCTAGGAAGGCGAGGTTACGCGCTCATCGGGAA 729
QY 3277 TTCACCTCTGCGCGCGCTGCGCGCCCTTTATGTCATCTTCCGACTTGGCGCTCTG 3336
DB 730 TTCACCTCTGCGCGCGCTGCGCGCCCTTTATGTCATCTTCCGACTTGGCGCTCTG 789
QY 3337 CTGAGGCAATTGTGCAAGGCGACCCCGAGGCTCCGAGCGCTCTGCGCGCTGAGCAT 3396
DB 790 CTGAGGCAATTGTGCAAGGCGACCCCGAGGCTCCGAGCGCTCTGCGCGCTGAGCAT 849
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DB 850 TTCGCGGTTTACCTTTCTAAGGAAGCGAGCGGAGCTGTACTAGTGGGAATGGTGCAT 909
QY 3457 AAGGAACAATTCTGTGTCGACGCGCTAGGAGCAAGCGGAGAGCACTTCCGACGCTT 3516
DB 910 AAGGAACAATTCTGTGTCGACGCGCTAGGAGCAAGCGGAGAGCACTTCCGACGCTT 969
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DB 970 AAGCGCACTGTCAGGAAGGTGGAATTGGAACAAGCTGGGACACATCGCGAGTAC 1029
QY 3577 GAAACAAGCTGGAAGGTGGAAGCGGAGAGTCCAGAGTGTAGCCCGCGCTGCGGGTGG 3636
DB 1030 GAAACAAGCTGGAAGGTGGAAGCGGAGAGTCCAGAGTGTAGCCCGCGCTGCGGGTGG 1089
QY 3637 GTGGCGAGGCGCTGAGAGCGCTCTGCTTGTGCTGCGCCAGAGTGGGCGGACCCCTGAC 3696
DB 1090 GTGGCGAGGCGCTGAGAGCGCTCTGCTTGTGCTGCGCCAGAGTGGGCGGACCCCTGAC 1149
QY 3697 CTGCTGGGTCAAAAGACTGAGCCCTGCTGGCGGACTTCAAGGAAGGCCCAAGGGG 3756
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DB 1210 ATTTGCTCTTGAAGTAAGGCTCATCTGGGCTCGGCGCCCGCACCTGGTGGCTTGTCC 1269
QY 3817 TTGAGTGAAGCCCATGTCATCTGGGCACTGTACAGACCACTTTGGGAGTGTATCC 3876
DB 1270 TTGAGTGAAGCCCATGTCATCTGGGCACTGTACAGACCACTTTGGGAGTGTATCC 1329
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DB 1390 CTTGATCCCGGGCGGTTATCCATCTGAGGCTGAGGGTCTTGGGGTAAAGGAGCA 1449
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DB 1450 CAGACCCCTCACCACTCAGAGATTCCTCAACTGGGAAATAAAGCATTTACAGAGAA 1509
QY 4057 AAAAA 4061
DB 1510 AAAAA 1514

RESULT 4
US-09-352-616A-109
; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-109

Query Match 37.1%; Score 1505; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10 CTGCGCAGGGGCTGAGCGGAGCGGGGCAAGCTTCCAGCGGGGGCCCGGGCTTGGC 69
QY 2617 CATGCTCACTAGCCAGGCGCTGCGGCTCTACTCTGCGGACAGCTGGAACCAAGTCCGAC 2676
DB 70 CATGCTCACTAGCCAGGCGCTGCGGCTCTACTCTGCGGACAGCTGGAACCAAGTCCGAC 129
QY 2677 CTAGTGGCTCTACCTGCTTCCCTCGGGGCTGGGCTGCGGCTGACCCCGGGTTTGTAC 2736
DB 130 CTAGTGGCTCTACCTGCTTCCCTCGGGGCTGGGCTGCGGCTGACCCCGGGTTTGTAC 189
QY 2737 CACTGGGGCGGCACTGCTCTGTCATGCACTTCATGATGTTTCAAGGCTGGCGCTTCTAC 2796
DB 190 CACTGGGGCGGCACTGCTCTGTCATGCACTTCATGATGTTTCAAGGCTGGCGCTTCTAC 249
QY 2797 ATCTTACGGGTCAACAAACAGCTGGGGCCCAAGATGTCACTGTGACAAAGATGATGAAG 2856
DB 250 ATCTTACGGGTCAACAAACAGCTGGGGCCCAAGATGTCACTGTGACAAAGATGATGAAG 309
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QY	3097	36CACCTGGCGCTCCCACTATGCAACCTGCGGGGGGCTGCTCTCGTATCTTCCTG	3156
Db	550	GGACCTCGCGTCTCCCACTATGCAACCTGCGGGGGGCTGCTCTCGTATCTTCCTG	609
QY	3157	CTCGTGGCCAACTCTGCTGCTGATCACTTGCTCATTTGCCATGTTCAATTACATTGCGC	3216
Db	610	CTCGTGGCCAACTCTGCTGCTGATCACTTGCTCATTTGCCATGTTCAATTGCGC	669
QY	3217	AAAGTACAGGGGCACAGGATCTCTACTGGAAGGCGAGCGTTACCCGCTTATCCGGGAA	3276
Db	670	AAAGTACAGGGGCACAGGATCTCTACTGGAAGGCGAGCGTTACCCGCTTATCCGGGAA	729
QY	3277	TTCCACTCTCGAGCCCGCGCTGAGCCCGGCTTTTATCGTCATCTCCCACTTGCGCTCCG	3336
Db	730	TTCCACTCTCGAGCCCGCGCTGAGCCCGGCTTTTATCGTCATCTCCCACTTGCGCTCCG	789
QY	3337	CTCAGGCAATTGTGTGACGGCAACCCCGAGCCCGCAAGCCGCTCTCCCGGACCTCGAGCAT	3396
Db	790	CTCAGGCAATTGTGTGACGGCAACCCCGAGCCCGCAAGCCGCTCTCCCGGACCTCGAGCAT	849
QY	3397	TTCCGGGGTTTACCTTTCTTAAGAAAGCCAGGGGAAGCTGTCTAAGTGGAAATCCGTGAT	3456
Db	850	TTCCGGGGTTTACCTTTCTTAAGAAAGCCAGGGGAAGCTGTCTAAGTGGAAATCCGTGAT	909
QY	3457	AAGGAGAACTTTCTGCTGGCAGCGCTTACGAGACAAGCGGAGAGCGATCTCCGAGCGTCTG	3516
Db	910	AAGGAGAACTTTCTGCTGGCAGCGCTTACGAGACAAGCGGAGAGCGATCTCCGAGCGTCTG	969
QY	3517	AAGGCAAGTCCAGAGAGTGTGACTTTGGCACTGAACAGCTGGGACAATCCGGAGTAC	3576
Db	970	AAGGCAAGTCCAGAGAGTGTGACTTTGGCACTGAACAGCTGGGACAATCCGGAGTAC	1029
QY	3577	GAAACAGGCGCTGAAAAGTCTGGAAGGAGGAGGTCACAGTGAAGCGCGCTCTGGAGTGG	3636
Db	1030	GAAACAGGCGCTGAAAAGTCTGGAAGGAGGAGGTCACAGTGAAGCGCGCTCTGGAGTGG	1089
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QY	3757	ATTTTGTCTCTAGAGTAAAGGCTCATCTGAGGCGCTGGAGCCCGGCACTGTGTGACCTTGCTC	3816
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QY	3817	TTGAGGTGAGCCCACTGTCATCTTGAGGCACTGTGAGGACAACCTTTGGAGGTGCATCC	3876
Db	1270	TTGAGGTGAGCCCACTGTCATCTTGAGGCACTGTGAGGACAACCTTTGGAGGTGCATCC	1329
QY	3877	TTTACAAACCAAGCATGCCCCGCGCTCTCTCCCAAGACCATGCTCCAGCTTGGAGGATCAAGG	3936
Db	1330	TTTACAAACCAAGCATGCCCCGCGCTCTCTCCCAAGACCATGCTCCAGCTTGGAGGATCAAGG	1389
QY	3937	CCTGATCCCGGAGCGGTTATCATCTGAGAGGCTGAGAGGCTCTTGAGGGTAAACAGGACCA	3996
Db	1390	CCTGATCCCGGAGCGGTTATCATCTGAGAGGCTGAGAGGCTCTTGAGGGTAAACAGGACCA	1449
QY	3997	CAGACCCCTCAACACTCAACAATTCTCACACTGGGGAATTAAGCCATTTCAAGAGAAA	4056
Db	1450	CAGACCCCTCAACACTCAACAATTCTCTCACACTGGGGAATTAAGCCATTTCAAGAGAAA	1509
QY	4057	AAAAA 4061	
Db	1510	AAAAA 1514	

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; Patent No.6613872
; GENERAL INFORMATION:
;
; APPLICANT: Xu, Jiangchun
;
; APPLICANT: Dillon, Davin C.
;
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
;
; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
;
; FILE REFERENCE: 210121.428C5
;
; CURRENT APPLICATION NUMBER: US/09/159,812A
;
; CURRENT FILING DATE: 1998-09-23
;
; NUMBER OF SEQ ID NOS: 306
;
; SOFTWARE: FastSeq for Windows Version 3.0
;
; SEQ ID NO 109
;
; LENGTH: 1524
;
; TYPE: DNA
;
; ORGANISM: Homo sapien
;
; US-09-159-812-109

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Query Match		37.1%; Score 1505; DB 4; Length 1524;			
Best Local Similarity		100.0%; Pred. No. 0;			
Matches 1505; Conservative		0; Mismatches		0; Indels	
		0; Gaps		0;	
QY	2557	CTGCGCCACAGGCGCTGAGCGGAGCGGGGACAGCTCCGACAGCGGGGGCCCCGGGCGTGGC	2616		
Db	10	CTGGCGCAGGGCCCTGAGCGGAGCGGGGGGCGAGCTCCGACGCGGGGGCCCCGGGCGTGGC	69		
QY	2617	CATGCGTCACTGAGCCAGCGCGCTGCGGCTCACTCCGCGCAGCAGCTGGAAACAGTGGCGAC	2676		
Db	70	CATGCGTCACTGAGCCAGCGCGCTGCGGCTCACTCCGCGCAGCAGCTGGAAACAGTGGCGAC	129		
QY	2677	CTAGTGGCTCAACCTGCTTCCCTCGGCGGTGGGCTGCCGGCTGACCCCGGGTTTGTAC	2736		
Db	130	CTAGTGGCTCAACCTGCTTCCCTCGGCGGTGGGCTGCCGGCTGACCCCGGGTTTGTAC	189		
QY	2737	CACCTGGGCGGCACTGTCTCTTGATGACTTACGTGTTTACGCGTGGCGCTGCTTAC	2796		
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QY	2797	ATCTTCAAGGTCACAAAACAGCTGGGGCCCAAGTCGATCGTGAGCAAGATGATGAAG	2856		
Db	250	ATCTTCAAGGTCACAAAACAGCTGGGGCCCAAGTCGATCGTGAGCAAGATGATGAAG	309		
QY	2857	GACGTTGTTCTTCTTCTTCTTCTCGGCGGTGTGGCTGTAGGCTTATGGCGTGGCAAG	2916		
Db	310	GACGTTGTTCTTCTTCTTCTTCTCGGCGGTGTGGCTGTAGGCTTATGGCGTGGCAAG	369		
QY	2917	GAGGGGCTCTGAGGGCCACGGGACAGATGACTTCCCAAGTATCCGCGCCGGCTTCTTAC	2976		
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QY	2977	CGTCCCTAATCTGACAGATCTTGGGCAAGTTCGCCAGAGACATGACGTGGCCCTCATG	3036		
Db	430	CGTCCCTAATCTGACAGATCTTGGGCAAGTTCGCCAGAGACATGAGAGTGGCCCTCATG	489		
QY	3037	GAGCAGACGAATGCTGCTGTCGAGACCCGGGCTTCTGGGCAACCCCTCTGGGGCCCAAGCG	3096		
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QY	3097	GGCACTGGCGCTCCCAATATGCCAACCTGGGTTGGTGGTGGCGTCCCTGATCTTCTCG	3156		
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QY	3157	CTCGTGGCAACATCTGCTGGTCAAACTTGCTCATTTGGCAAGTTCAAGTTACACATTTGGC	3216		
Db	610	CTCGTGGCAACATCTGCTGGTCAAACTTGCTCATTTGGCAAGTTCAAGTTACACATTTGGC	669		
QY	3217	AAAGTACAGGGCAACAGGATCTTATCTGGAAGCGCAGCGTTAACCGCTCATCCGGAA	3276		
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QY	3277	TTCCACTCTCGGGCCCGCGGTGGCCCGGCTTTATCGATCGTCCACTTGGGCTCTCG	3336		
Db	730	TTCCACTCTCGGGCCCGCGGTGGCCCGGCTTTATCGATCGTCCACTTGGGCTCTCG	789		

Db 790 CTCAGCAATTGTGACAGGAGCCCGGAGCCCGTCCCTCCCGGCTCTGAGCAT 849
QY 3397 TTCCGGGTTTACCTTTCTAAGAAAGCGGAGCTGCTAAGTGGAAATCGGTCAT 3456
Db 850 TTCCGGGTTTACCTTTCTAAGAAAGCGGAGCTGCTAAGTGGAAATCGGTCAT 909
QY 3457 AAGGAAATTTCTGCTGACGCGCTAGGAGCAAGCGGAGAGCGACTCCGAGCTCTG 3516
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QY 3517 AAGCGCACTCCCAAGAGTGAAGCTTGGCACTGAAAAGCTGGGAGCAATCCGAGTAC 3576
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QY 3577 GAACAGCGCTGAAAGTGTGAGCGGAGGTCACAGTATCCGCTCTGGGGTGG 3636
Db 1030 GAACAGCGCTGAAAGTGTGAGCGGAGGTCACAGTATCCGCTCTGGGGTGG 1089
QY 3637 GTGGCGAGGCGCTGAGCGGCTCTGCTTGGCTGCCCCAGTGGGCGCCACCCCTGAC 3696
Db 1090 GTGGCGAGGCGCTGAGCGGCTCTGCTTGGCTGCCCCAGTGGGCGCCACCCCTGAC 1149
QY 3697 GTGGCGAGGCTCAAGAGCTGAGCGCTGCTGGCGGACTTCAAGGAGAACCCCAAGGG 3756
Db 1150 GTGGCGAGGCTCAAGAGCTGAGCGCTGCTGGCGGACTTCAAGGAGAACCCCAAGGG 1209
QY 3757 ATTGCTCTTAAAGTAAAGTCTGATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTG 3816
Db 1210 ATTGCTCTTAAAGTAAAGTCTGATCTGGGCTCTGGGCTCTGGGCTCTGGGCTCTG 1269
QY 3817 TTGAGTGAAGCCCATGTCATCTGAGGCACTGTCAGAGCACTTTGGAGTGTATCC 3876
Db 1270 TTGAGTGAAGCCCATGTCATCTGAGGCACTGTCAGAGCACTTTGGAGTGTATCC 1329
QY 3877 TTAACAACAACAGATGCGCGCTCTCCCAAGCAATGCCCTGGAGGATCAAG 3936
Db 1330 TTAACAACAACAAGATGCGCGCTCTCCCAAGCAATGCCCTGGAGGATCAAG 1389
QY 3937 CCGTGAATCCCGGCGCTTATCCATCTGAGGCTGAGGCTCTGGGGTAAAGGAGCA 3996
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QY 4057 AAAAA 4061
Db 1510 AAAAA 1514

RESULT 8
US-09-685-166A-109
; Sequence 109, Application US/09685166A
; Patent No. 6630305

GENERAL INFORMATION:

APPLICANT: Xu, Jianshun
APPLICANT: Dillon, David C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C21
; CURRENT APPLICATION NUMBER: US/09/685,166A
; NUMBER OF SEQ ID NOS: 898
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-685-166A-109

Query Match 37.1%; Score 1505; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2677 CTAGTGGCTCTCACTGCTTCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 2736
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QY	2557	CTGGGCGACGGGCTGAGGCGAGGCGGGGGGAGGCTCCGACGGGGGGCCCCGGGCGCTGGC	2616
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QY	2617	CATGCGTCACTGAGGCAAGCGCGCTGCGGCTTACTACCTCGCCGACAGCTGGAAACAGTGGCAG	2676
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Db	130	CTAGTGGCTCTACCTGCTTCTCTCTGCGCGTGGGCTGCGCGGCTGACCCCGGGATTGTAC	189
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QY	2857	GACGTGTCTTCTTCTTCTTCTTCTGCGGCGTGGCGTGTAGCTTATGCGTGGCCACG	2916
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QY	2917	GAGGGGCTCTTGAGGCCACGGGACAGTGACTTCCCAAGTACTCTGCGCGCGCTTCTTAC	2976
Db	370	GAGGGGCTCTTGAGGCCACGGGACAGTGACTTCCCAAGTACTCTGCGCGCGCTTCTTAC	429
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Db	430	CGTCCCTAACCTGGAGATCTTCCGGGCAATTTCCGAGAGGACATGAGACGTGGCCCTATG	489
QY	3037	GAGCACAAGCACTCTCGTGGAGCCCGGGCTTCTGGGCACACCTCTCGTGGGGCCAGAGCG	3096
Db	490	GAGCACAAGCACTCTCGTGGAGCCCGGGCTTCTGGGCACACCTCTCGTGGGGCCAGAGCG	549
QY	3097	GGCACCCTGGCTCTCCAGATATGCCACTGCTGGTGGTGTCTCTCTGTACTTCTCTG	3156
Db	550	GGCACCCTGGCTCTCCAGATATGCCACTGCTGGTGGTGTCTCTCTGTACTTCTCTG	609
QY	3157	CTCGTGGCCAACTCCGCTGGTGTCACTTGTCTATTCGCAATTTTCACTTACATTTGGC	3216
Db	610	CTCGTGGCCAACTCCGCTGGTGTCACTTGTCTATTCGCAATTTTCACTTACATTTGGC	669
QY	3217	AAAGTACAGGGCAACAGGATCTCTACTGGAAGCGAGGCTTACCCGCTCATTCGGGAAA	3276
Db	670	AAAGTACAGGGCAACAGGATCTCTACTGGAAGCGAGGCTTACCCGCTCATTCGGGAAA	729
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Db	730	TTTCGACTCTCGGCGCGGCTGGGCCCGGCCCTTTATCTGTCACTTCCACTTGGCGCTCTG	789
QY	3337	CTCAGGCAATTGTGACAGCGACCCCGGAGCCCGACCGCTCTCTCCGGGCTTGTAGCAT	3396
Db	790	CTCAGGCAATTGTGACAGCGACCCCGGAGCCCGACCGCTCTCTCCGGGCTTGTAGCAT	849
QY	3397	TTTCGGGGTTTACCTTTCTAAGGAAGCGAGCGGAAGCTGTCAACGTGGGAATCGGTGCAT	3456
Db	850	TTTCGGGGTTTACCTTTCTAAGGAAGCGAGCGGAAGCTGTCAACGTGGGAATCGGTGCAT	909
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Db	910	AAGGAGAATTCTCTGTGACGCGGCTTAGGACAAGCGGGAGAGCGACTCCGACGCTCG	969
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Db	970	AAGCGCACGTCCGAAAGGTGACTTTGGCACTGAAACAGCTGGGACACATCCCGGATAC	1029
QY	3577	GAAACAGGCGCTGAAAGGTGAGCGGAGCGGAGATCAGACAGTGTAGCGCGCTGTGGGTTGG	3636
Db	1030	GAAACAGGCGCTGAAAGGTGAGCGGAGCGGAGATCAGACAGTGTAGCGCGCTGTGGGTTGG	1089
QY	3637	GTGCGCCAGGCGCTGAGCGGCTCTGCGCTTCTGCGCCCAAGTGGGCGGCCACCCCTCTGAC	3696

Db	1090	GTGGCCGAGGCCCTGAGCCGCTCTGCTTGCCGCCCGAGGTGGGCGGCACCCCTGAC	1149
OY	3697	CTGCTTGAGGTCAAAAGACTGAGCCCTGCTGGAGACTTCAAGAGAAAGCCCCACAGGG	3756
Db	1150	CTGCTGGGTCCAAAGACTGAGCCCTGCTGGCGGACTTCAAGAGAAAGCCCCACAGGG	1209
OY	3757	ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCTCTGGGCCCCCGCACCTGGTGGCTTTC	3816
Db	1210	ATTTTGCTCCTAGAGTAAGGCTCATCTGGGCTCTGGGCCCCCGCACCTGGTGGCTTTC	1269
OY	3817	TTGAGGTGAGGCCCATGTCCATCTGGGCACTGTCAAGACCACTTTGGAGTTCATCC	3876
Db	1270	TTGAGGTGAGGCCCATGTCCATCTGGGCACTGTCAAGACCACTTTGGAGTTCATCC	1329
OY	3877	TTACAAACCAAGCATGCCGGGCTCCCTCCAGAACAGTCCAGCTGGGAGATCAAG	3936
Db	1330	TTACAAACCAAGCATGCCGGGCTCCCTCCAGAACAGTCCAGCTGGGAGATCAAG	1389
OY	3937	CCTGATCCCGGGCGTATCATCTGGAGCTCAGGGTCTTGGGTTAACAGGACA	3996
Db	1390	CCTGATCCCGGGCGTATCATCTGGAGCTCAGGGTCTTGGGTTAACAGGACA	1449
OY	3997	CAGACCCCTCAACACTCAAGATTCCTACACTGGGAAATPAAAGCATTTCAAGGAAA	4056
Db	1450	CAGACCCCTCAACACTCAAGATTCCTACACTGGGAAATPAAAGCATTTCAAGGAAA	1509
OY	4057	AAAAA 4061	
Db	1510	AAAAA 1514	

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RESULT 10
US-09-688-489-109
; Sequence 109, Application US/09688489
; Patent No. 6664377
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427D2
; CURRENT APPLICATION NUMBER: US/09/688,489
; CURRENT FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-688-489-109

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Query Match	37.1%	Score 1505;	DB 4;	Length 1524;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 1505; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	2557	TTGGCCGACGGGCGCTTAGCGGAGAGCGCGGGGAGACCTTCGCGACCGGGGGCCCCGGGCGCTGGC	2616
Db	10	CTGGCCGACGGGCGCTTAGCGGAGAGCGCGGGGAGACCTTCGCGACCGGGGGCCCCGGGCGCTGGC	69
QY	2617	CATGGCTCACTAGAGCAGACGCGCTGGGCGCTTAACCTCGCGGACAGCTGGGAACAGTGGAC	2676
Db	70	CATGGCTCACTAGAGCAGACGCGCTGGGCGCTTAACCTCGCGGACAGCTGGGAACAGTGGAC	129
QY	2677	CTAGTGGCTTCACCTGGCTTCCTCTCTGGGCGTGGGCTGCGGAGTGAACCCCGGGTTTGGAC	2736
Db	130	CTAGTGGCTTCACCTGGCTTCCTCTCTGGGCGTGGGCTGCGGAGTGAACCCCGGGTTTGGAC	189
QY	2737	CACCTGGGCGGACGTGTCTCTGCATGACATTATGATGTTTTCACGGGTGGGCTGCTTCAC	2796
Db	190	CACCTGGGCGGACGTGTCTCTGCATGACATTATGATGTTTTCACGGGTGGGCTGCTTCAC	249

OY	2797	TTCTTCAACGGTCAACAACAAGCTGGGGGCCAAGAATGTCATTCGTGACCAAGATGATGAAG	2856
Db	250	ATCTTCAACGGTCAACAACAAGCTGGGGGCCAAGAATGTCATTCGTGACCAAGATGATGAAG	309
OY	2857	GACGTGATCTCTCTCTCTCTCTCTCTCTGGGGGTGGCTGGTAGCTTATGGCGTGGCAGC	2916
Db	310	GACGTGATCTCTCTCTCTCTCTCTCTGGGGGTGGCTGGTAGCTTATGGCGTGGCAGC	369
OY	2917	GAGGGGCTCTGAGGGCCAGGGAGACGTACTTCCCAAGTATCTGGCGCGGTCTTTTAC	2976
Db	370	GAGGGGCTCTGAGGGCCAGGGAGACGTACTTCCCAAGTATCTGGCGCGGTCTTTTAC	429
OY	2977	CGTCCCTAACCTGGACGATCTTCGGGCAGATTCCCAAGAGAGACATGAGACGTGGCCCTATG	3036
Db	430	CGTCCCTAACCTGGACGATCTTCGGGCAGATTCCCAAGAGAGACATGAGACGTGGCCCTATG	489
OY	3037	GAGCAGACAGCACTGCTGCTGGAGCCCGGGCTCTTGGGCACACCCTCTGGGGGCCAGAGC	3096
Db	490	GAGCAGACAGCACTGCTGCTGGAGCCCGGGCTCTTGGGCACACCCTCTGGGGGCCAGAGC	549
OY	3097	GGCACCCTGCGTCTCCAGTATGCCAACCTGGCTGGGTGGCTGCTCTGTATCTTCTCTG	3156
Db	550	GGCACCCTGCGTCTCCAGTATGCCAACCTGGCTGGGTGGCTGCTCTGTATCTTCTCTG	609
OY	3157	CTCGTGGCCCAACATCCCTGCTGGTCTACCTTGTCTATTCGCATGTTCACTTACATTTGGC	3216
Db	610	CTCGTGGCCCAACATCCCTGCTGGTCTACCTTGTCTATTCGCATGTTCACTTACATTTGGC	669
OY	3217	AAAGTACAGGGCCACAGGATCTCTACTGGAAGGCGAGCGCTTACCCCTCATCTCGGGAA	3276
Db	670	AAAGTACAGGGCCACAGGATCTCTACTGGAAGGCGAGCGCTTACCCCTCATCTCGGGAA	729
OY	3277	TTCCACTCTCGGCCCGCGCTGGCCCGGCCCTTATATGTCATCTTCCACTTGGCGCTCTCG	3336
Db	730	TTCCACTCTCGGCCCGCGCTGGCCCGGCCCTTATATGTCATCTTCCACTTGGCGCTCTCG	789
OY	3337	CTCAGGCAATTGTGACAGGCCACCCCGGAGCCCCAGCGCTCTCCCGGCGCTTGAGCAT	3396
Db	790	CTCAGGCAATTGTGACAGGCCACCCCGGAGCCCCAGCGCTCTCCCGGCGCTTGAGCAT	849
OY	3397	TTCCGGGGTTTACCTTTCTAAGGAAGCGAGCGGAAGCTGTAACTGTGGAAATCGTGTCAT	3456
Db	850	TTCCGGGGTTTACCTTTCTAAGGAAGCGAGCGGAAGCTGTAACTGTGGAAATCGTGTCAT	909
OY	3457	AAGAGAACTTTCGTGTGGCAGCGGCTTATAGGACAAGCGGAGAGACGACTCCGACGCTCTG	3516
Db	910	AAGAGAACTTTCGTGTGGCAGCGGCTTATAGGACAAGCGGAGAGACGACTCCGACGCTCTG	969
OY	3517	AAGGCGACGTCCCGAAGAGTGGACTTGGCACTGTAAACAAGCTGGGACATTCGCGGAAATAC	3576
Db	970	AAGGCGACGTCCCGAAGAGTGGACTTGGCACTGTAAACAAGCTGGGACATTCGCGGAAATAC	1029
OY	3577	GACACAGCGCTCGAAGAGTGTGGAGCGGAGGTTCCAGCAGTGTACCGCGGTCTTGGGGTGG	3636
Db	1030	GACACAGCGCTCGAAGAGTGTGGAGCGGAGGTTCCAGCAGTGTACCGCGGTCTTGGGGTGG	1089
OY	3637	GTGGCCGAGGCGCTGAGCGGCTCTTGCCTTTCGCCCCCAGGTGGGCGCCACCCCTGAC	3696
Db	1090	GTGGCCGAGGCGCTGAGCGGCTCTTGCCTTTCGCCCCCAGGTGGGCGCCACCCCTGAC	1149
OY	3697	CTGCGTGGGTTCCAAAGACTGAGCCCTGTGTGGCGGACTTCAAAGAGAAACCCCCACAGGGG	3756
Db	1150	CTGCGTGGGTTCCAAAGACTGAGCCCTGTGTGGCGGACTTCAAAGAGAAACCCCCACAGGGG	1209
OY	3757	ATTTTTGCTCCCAAGAGTAAAGGCTCATTCGGGCTCTGGGCCCGCGACCTGGTGGCTTGTCC	3816
Db	1210	ATTTTTGCTCCCAAGAGTAAAGGCTCATTCGGGCTCTGGGCCCGCGACCTGGTGGCTTGTCC	1269
OY	3817	TTGAGGTGAGCCCAATGTCATCTTGGGCACTGTACAGGACCACTTTTGGAGTGTCAATCC	3876
Db	1270	TTGAGGTGAGCCCAATGTCATCTTGGGCACTGTACAGGACCACTTTTGGAGTGTCAATCC	1329
OY	3877	TTTAAACAACACAGATGCCGGGCTCTTCCAGAAACAGTCCACGCTTGGAGGATCAAGG	3936

Db 1330 TTACAAACACAGATGCGCGCTCTCCAGAAACAGTCCAGCGCTGGAGATCAAG 1389
QY 3937 CCTGATCCCGGCGCGTTATCATCTGAGAGGTCTTGGGGTAACAGGACCA 3996
Db 1390 CCTGATCCCGGCGCGTTATCATCTGAGAGGTCTTGGGGTAACAGGACCA 1449
QY 3997 CAGACCCCTCAACATCAAGATTCTCACTGGGGAATTAAGCTATTTCAGAGAAA 4056
Db 1450 CAGACCCCTCAACATCAAGATTCTCACTGGGGAATTAAGCTATTTCAGAGAAA 1509
QY 4057 AAAAA 4061
Db 1510 AAAAA 1514

RESULT 11
US-09-679-426-109
; Sequence 109, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-109

Query Match 37.1%; Score 1505; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CTGCGCCAGGGCTTGAAGCGAGGCGGGGCGAGCTTCGCCAGCGGGGCGCGGCTTGGC 2616
Db 10 CTGCGCCAGGGCTTGAAGCGAGGCGGGGCGAGCTTCGCCAGCGGGGCGCGGCTTGGC 69
QY 2617 CATGCTCACTGAGCAGGCGCTGAGCTTACCTCGCGACAGCTGGAAACAGTGGCAG 2676
Db 70 CATGCTCACTGAGCAGGCGCTGAGCTTACCTCGCGACAGCTGGAAACAGTGGCAG 129
QY 2677 CTAGTGGCTTCACTGCTTCTCTGAGCGTGGGCTGCGAGCTGACCCCGGGTTTGTAC 2736
Db 130 CTAGTGGCTTCACTGCTTCTCTGAGCGTGGGCTGCGAGCTGACCCCGGGTTTGTAC 189
QY 2737 CACCTGGGCGGACCTGTCTCTGATCGACTTCATGATTTTTCAGGTGGGCTGCTTAC 2796
Db 190 CACCTGGGCGGACCTGTCTCTGATCGACTTCATGATTTTTCAGGTGGGCTGCTTAC 249
QY 2797 ATCTTCAGGTCGAACAAACAGCTGGGCGCAAGATCTCATGTAGAGCAAGTATGAAG 2856

Db 250 ATCTTCAGGTCGAACAAACAGCTGGGCGCAAGATCTCATGTAGAGCAAGTATGAAG 309
QY 2857 GACGATTCCTTCTTCTTCTTCTGCGGCTGAGGCTGATGAGCTATGAGGCTGAGCA 2916
Db 310 GACGATTCCTTCTTCTTCTTCTGCGGCTGAGGCTGATGAGGCTGAGGCTGAGCA 369
QY 2917 GAGGCGCTCTGAGGCGCAGGAGAGTGAATTTCCAAATATCTTGGCGCGGCTTCTAC 2976
Db 370 GAGGCGCTCTGAGGCGCAGGAGAGTGAATTTCCAAATATCTTGGCGCGGCTTCTAC 429
QY 2977 GGTCTTCACTGAGATTTTGGGAGATTTCCCAAGAGAGCAATGAGAGTGGCTTAC 3036
Db 430 GGTCTTCACTGAGATTTTGGGAGATTTCCCAAGAGAGCAATGAGAGTGGCTTAC 489
QY 3037 GAGCAGCAATCTGCTGAGAGCGGCTTGGGAGCAACCTCTGGGGGCGGAGGCG 3096
Db 490 GAGCAGCAATCTGCTGAGAGCGGCTTGGGAGCAACCTCTGGGGGCGGAGGCG 549
QY 3097 GGCACCTGCTCTCCAGTATGCAACTGAGTGGTGTGCTCTCTGATCTTCTG 3156
Db 550 GGCACCTGCTCTCCAGTATGCAACTGAGTGGTGTGCTCTCTGATCTTCTG 609
QY 3157 CTGCTGCGCAATCTGCTGCTGCACTTGTCTCATTTGATGTTCAATTCATTCG 3216
Db 610 CTGCTGCGCAATCTGCTGCTGCACTTGTCTCATTTGATGTTCAATTCATTCG 669
QY 3217 AAAGTACAGGCGCAACAGGATCTCTAGTGAAGGCGGAGCTTACCGGCTTACCGG 3276
Db 670 AAAGTACAGGCGCAACAGGATCTCTAGTGAAGGCGGAGCTTACCGGCTTACCGG 729
QY 3277 TTCCACTGCGGCGGCTGAGCGGCGGCTTATTCGATCTCCCACTTGGCGCTCTG 3336
Db 730 TTCCACTGCGGCGGCTGAGCGGCGGCTTATTCGATCTCCCACTTGGCGCTCTG 789
QY 3337 CTACAGCAATTTGTAGAGCGACCCCGAGCCCGAGCGGCTCTCCGAGCAT 3396
Db 790 CTACAGCAATTTGTAGAGCGACCCCGAGCCCGAGCGGCTCTCCGAGCAT 849
QY 3397 TTCCGGGTTTACCTTTCTAAGAAAGCGAGGAGCTCTAAGTGGAAATCGGTGAT 3456
Db 850 TTCCGGGTTTACCTTTCTAAGAAAGCGAGGAGCTCTAAGTGGAAATCGGTGAT 909
QY 3457 AAGGAGACTTTGCTGAGCGGCTGAGCAAGGAGGAGAGGAGCTCCGAGGCTG 3516
Db 910 AAGGAGACTTTGCTGAGCGGCTGAGCAAGGAGGAGAGGAGCTCCGAGGCTG 969
QY 3517 AAGGAGACTTTGCTGAGCGGCTGAGCAAGGAGGAGAGGAGCTCCGAGGCTG 3576
Db 970 AAGGAGACTTTGCTGAGCGGCTGAGCAAGGAGGAGAGGAGCTCCGAGGCTG 1029
QY 3577 GAACAGCGCTGAAAGTCTGAGCGGAGGCTCCAGAGTGTAGCGGCTTGGGGTGG 3636
Db 1030 GAACAGCGCTGAAAGTCTGAGCGGAGGCTCCAGAGTGTAGCGGCTTGGGGTGG 1089
QY 3637 GTGGCGGAGCGCTGAGCGGCTGAGCGGCTTGGCGGAGGAGGAGGAGGAGGAGG 3696
Db 1090 GTGGCGGAGCGCTGAGCGGCTGAGCGGCTTGGCGGAGGAGGAGGAGGAGGAGG 1149
QY 3697 CTGCTGAGGCTCAAAAGACTGAGCGGCTGAGCGGCTTCAAGAGAGAGGAGGAGG 3756
Db 1150 CTGCTGAGGCTCAAAAGACTGAGCGGCTGAGCGGCTTCAAGAGAGAGGAGGAGG 1209
QY 3757 ATTTTGTCTTGAAGTAAGGCTCATTTGAGGCTTGGGCGGCGGAGCTTGGCTT 3816
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QY 3817 TTGAGTGAAGCGGAGTGCATTTGAGGAGCTTGGGAGAGAGAGAGAGAGAGAG 3876
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QY 3877 TTACAAACACAGAGATGCGGCTCTCCAGAAACAGATCCCAAGTGGAGAGATCAAG 3936
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QY 3937 CCTGATCCCGGGCGTTATCCATCTGAGGCTGAGGGGCTTGGGGTAAACAGGGAGCA 3996
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Db 1390 CCTGATCCCGGGCGTTATCCATCTGAGGCTGAGGGGCTTGGGGTAAACAGGGAGCA 1449
QY 3997 CAGACCCCTCACCCTCAGAGATTCCTCAGCTGAGGGAATAAGCCATTTCAGAGGAA 4056
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Db 1450 CAGACCCCTCACCCTCAGAGATTCCTCAGCTGAGGGAATAAGCCATTTCAGAGGAA 1509
QY 4057 AAAAA 4061
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Db 1510 AAAAA 1514

RESULT 12
US-09-759-143-109
; Sequence 109, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqun
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Ranger, Gary R.
; APPLICANT: Reiter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-759-143-109

Query Match 37.1%; Score 1505; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 1505; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2557 CTGCGCAGAGGCTGAGCGGAGGCGGGGAGGCTGCGCAGCGGGGCCCCGGGCTTGGC 2616
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Db 10 CTGCGCAGAGGCTGAGCGGAGGCGGGGAGGCTGCGCAGCGGGGCCCCGGGCTTGGC 69
QY 2617 CATGCTCACTAGGCGAGGCGCTGCGCTTACTCTGCGGACAGCTGGAACAGTGGAC 2676
| | | | |
Db 70 CATGCTCACTAGGCGAGGCGCTGCGCTTACTCTGCGGACAGCTGGAACAGTGGAC 129
QY 2677 CTAGTGGCTCTCACTGCTTCTCTGCGGAGTGGGCTGCGGCTGACCCCGGTTTGTAC 2736
| | | | |
Db 130 CTAGTGGCTCTCACTGCTTCTCTGCGGAGTGGGCTGCGGCTGACCCCGGTTTGTAC 189
QY 2737 CACCTGGGCGGCACTGCTCTGTCATGACTTCATGATTTTCACTGAGTGGGCTTGCAC 2796
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Db 190 CACCTGGGCGGCACTGCTCTGTCATGACTTCATGATTTTCACTGAGTGGGCTTGCAC 249
QY 2797 ATCTTCAAGGTCAACAAACAGCTGGGGCCCAAGATGTCACTGTGACAAATGATGAAG 2856
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Db 250 ATCTTCAAGGTCAACAAACAGCTGGGGCCCAAGATGTCACTGTGACAAATGATGAAG 309
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QY 2857 GACGATTTCTTCTCTCTCTTCTCTCGGCGGTGAGTGGTATGACCTATGACGTGGACAG 2916
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QY 2917 GAGGGGCTCTGAGGCGACAGGAGACAGTGAATTCCCAAGTATCTGCGCGGCTTTTAC 2976
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Db 370 GAGGGGCTCTGAGGCGACAGGAGACAGTGAATTCCCAAGTATCTGCGCGGCTTTTAC 429
QY 2977 CGTCCCTACCTGCAATCTTGGGGGAGTATCCCGAGGAGAGATGAGCGTGGCCCTCATG 3036
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Db 430 CGTCCCTACCTGCAATCTTGGGGGAGTATCCCGAGGAGAGATGAGCGTGGCCCTCATG 489
QY 3037 GAGCAACAGCACTGCTCGTCCGAGGCGGCTTCTGAGGACACCCCTTGGGGCCAGAGCG 3096
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Db 490 GAGCAACAGCACTGCTCGTCCGAGGCGGCTTCTGAGGACACCCCTTGGGGCCAGAGCG 549
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Db 550 GGCACCTGCTCTCCAGATATGCCAATGAGTGGTGTGCTGCTCTGTCATTTCTTG 609
QY 3157 CTGTTGGCCCAATCTGCTGCTCACTTGCATTTGCCATGTTGATGATTCATTCGCGC 3216
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QY 3217 AAAGTACAGGGGCAACAGCATCTCTAAGAGGCGACAGCTTACCGCTTCCGAGAA 3276
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QY 3277 TTCACTCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 3336
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Db 730 TTCACTCTGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 789
QY 3337 CTCAGGCAATTTGAGAGGAGACCCCGGAGCCCGGAGCGCTCTCCCGCGCGCGCGAGAT 3396
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Db 790 CTCAGGCAATTTGAGAGGAGACCCCGGAGCCCGGAGCGCTCTCCCGCGCGCGAGAT 849
QY 3397 TTCGGGTTTACTTTCTTAAGAGACCGGAGAGCTGCTAAGTGGATTCGATGAT 3456
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Db 850 TTCGGGTTTACTTTCTTAAGAGACCGGAGAGCTGCTAAGTGGATTCGATGAT 909
QY 3457 AAGGAACTTTCTGCTGACGCGCTGAGGACAAAGCGGAGAGCGATCCGAGCGTCTG 3516
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Db 910 AAGGAACTTTCTGCTGACGCGCTGAGGACAAAGCGGAGAGCGATCCGAGCGTCTG 969
QY 3517 AAGCGCACTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGCAATGAC 3576
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Db 970 AAGCGCACTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGCAATGAC 1029
QY 3577 GAACAGCGCTGAAGTGTGAGCGGAGGCTCCAGAGTGAAGCGCTCTGAGGAGTGG 3636
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Db 1030 GAACAGCGCTGAAGTGTGAGCGGAGGCTCCAGAGTGAAGCGCTCTGAGGAGTGG 1089
QY 3637 GTGGCCGAGGCGCTGAGCGGCTTGTGCTTGTGCTGCCCCAGGTGGCCGCACTCCCTGAC 3696
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Db 1090 GTGGCCGAGGCGCTGAGCGGCTTGTGCTTGTGCTGCCCCAGGTGGCCGCACTCCCTGAC 1149
QY 3697 CTGCTGGTCCAAAGACTGAACCTGCTGGGAGACTTCAAGAGAAAGCCCAAGAGGG 3756
| | | | |
Db 1150 CTGCTGGTCCAAAGACTGAACCTGCTGGGAGACTTCAAGAGAAAGCCCAAGAGGG 1209
QY 3757 ATTTTGTCTCTAGAGTAAAGCTCATCTGAGGCTCGGCGCCGCACTGAGTGGCTTGTGC 3816
| | | | |
Db 1210 ATTTTGTCTCTAGAGTAAAGCTCATCTGAGGCTCGGCGCCGCACTGAGTGGCTTGTGC 1269
QY 3817 TTGAGTGAAGCCCATGTCATCTGAGGCACTGTGAGACCATTTTGGAGTGTATCC 3876
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Db 1270 TTGAGTGAAGCCCATGTCATCTGAGGCACTGTGAGACCATTTTGGAGTGTATCC 1329
QY 3877 TTACAAACCAACAGCATGCGCGCTCTCCCAAGAACAGTCCAGCTGGAGAGATCAAG 3936
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Db 1330 TTACAAACCAACAGCATGCGCGCTCTCCCAAGAACAGTCCAGCTGGAGAGATCAAG 1389
QY 3937 CCTGATCCCGGGCGTTATCCATCTGAGGCTGAGGGTCTTGGGGTAAACAGGAGCA 3996
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QY 3997 CAGACCCCTCAGACCTCAGAGATTCTCTCAGACTGAGGAAATTAAGCATTTCAGAGAAA 4056
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QY 4057 AAAAA 4061
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Db 1510 AAAAA 1514
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RESULT 14
US-08-727-688-9
; Sequence 9, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road D377/AP6D
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/727,688
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Porembski, Priscilla E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5967.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 937-0378
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-727-688-9
Query Match 30.3%; Score 1230.2; DB 2; Length 1297;
Best Local Similarity 98.5%; Pred. No. 8e-281;
Matches 1279; Conservative 0; Mismatches 16; Indels 4; Gaps 4;
QY 2558 TGGGCCAGGGCTGAGGGGA-GGGGGGGGAGGCTGCGCCAGGGGGGCCCCGGGCTTGGC 2616
| | | | |
Db 1 TGGCGAGGAGCTGAGGGAGGGGTGTGCGAGGCTCGCCAGCGGGGGCCCCGGGCTTGGC 60
| | | | |
QY 2617 CA-TGACCTCAGTACAGGCGAGGCGCTCTACCTTGCGAGAGCTGAAACAGTGGCA 2675
| | | | |
Db 61 CATTTGCTTACTGAGGCGAGGCTTGC-CTTCTACTTGCGAGAGCTGGAACAGATGCCA 119
| | | | |
QY 2676 CCTAGTGGCTCTGACCTGTTCTCTCTGAGGCGTGGGCTGCGAGTGAACCCGGGTTTGA 2735
| | | | |
Db 120 CTAAGTGGCTCTGACCTGTTCTCTCTGAGGCGTGGGCTGCGAGTGAACCCGGGTTTGA 179
| | | | |
QY 2736 CCACTTGGGCGGCACTCTCTCTGATGACCTTCAATGTTTTCAGAGTGGGCTGCTTCA 2795
| | | | |
Db 180 CCACTTGGGCGGCACTCTCTCTGATGACCTTCAATGTTTTCAGAGTGGGCTGCTTCA 239
| | | | |

QY 2796 CATTTTCAAGTCAACAAACAGCTGGGGCCCAAGATGTCATCTGTAGCAGATGATGA 2855
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Db 240 CATTTTCAAGTCAACAAACAGCTGGGGCCCAAGATGTCATCTGTAGCAGATGATGA 299
| | | | |
QY 2856 GGAAGTGTCTTCTTCTTCTTCTTCTTCTGCGGCTGTGGCTGTAGGCTTAAGGGTGGCCAC 2915
| | | | |
Db 300 GGAAGTGTCTTCTTCTTCTTCTTCTTCTGCGGCTGTGGCTGTAGGCTTAAGGGTGGCCAC 359
| | | | |
QY 2916 GGAAGGGGCTCTGAGGGCCAGGGGACAGTACTTCCCAAGTATCTTGCGCGGCTTCTTA 2975
| | | | |
Db 360 GGAAGGGGCTCTGAGGGCCAGGGGACAGTACTTCCCAAGTATCTTGCGCGGCTTCTTA 419
| | | | |
QY 2976 CGTCCCTTACCTGACAGATCTTGGGAGATTCCCGAGAGACATGAGCGTGGCTCAT 3035
| | | | |
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RESULT 15
US-09-949-016-1003
Sequence 1003, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1003
LENGTH: 3498
TYPE: DNA
ORGANISM: Human
US-09-949-016-1003

Query Match 20.1%; Score 815.8; DB 4; Length 3498;
Best Local Similarity 55.6%; Pred. No. 1.2e-182;
Matches 1916; Conservative 0; Mismatches 1407; Indels 126; Gaps 13;

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86 ACTTTGAGAGGTCTGTGAGAGAGCAGAGAGATTGTATCGGGTGCAGAGGTGGCCCC 145
368 CAGTGCAGATTATAGTCTGTCAACGACATGGGGCTTCCGTGCCCCGGAACCTGTG 427
146 CGTCTGTGCTCTTGAACCTGTCTGTGAGTGGACCTGCGGCCCCCAACTGTGTG 205
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206 TGTCTCTGTGTGGTGAAGAGAGAGCTTGTGCGCATGAAGTCTGTGCGGGAGTGTGTC 265
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 QY 2261 TTATAGGAGAAAGGCTGTGCGGACGAGCCAGCCAGAGAGAGAGCGCGTGGGGTCC 2320
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Search completed: June 13, 2005, 08:38:56
 Job time : 445.26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: June 12, 2005, 06:26:36 ; Search time 10260.1 Seconds

(without alignments)
17200.018 Million cell updates/sec

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Perfect score: 3642
Sequence: 1 atgctgctgcgcgagaaaga.....acctgcctgggtccaagac 3642

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing of hits 45 summaries

Database: GenBank

1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3642	100.0	3879	9	AY297045 Homo sapi
2	3642	100.0	4042	9	HSAS575813
3	3642	100.0	4061	6	BD270156 Character
4	3642	100.0	4061	9	AF497623 Homo sapi
5	3640.4	100.0	4042	6	AX443227 Sequence
6	3421.2	93.9	3810	9	AK000048 Homo sapi
7	3374.4	92.7	3900	6	AX235183 Sequence
8	3373.8	92.6	3387	6	AX235185 Sequence
9	3333	91.5	3402	6	CO715325 Sequence
10	3253.4	89.3	3599	6	AX402516 Sequence
11	3199.8	87.9	3523	9	AY297044 Homo sapi
12	3196.6	87.8	3701	9	AY046396 Homo sapi
13	2762	75.8	3444	9	AY297046 Homo sapi
14	2424	66.6	3800	10	MMU575814 Mus muscu
15	2269.4	62.3	2695	6	AX443225 Sequence
16	2196.8	60.3	2981	9	AK000235 Homo sapi
17	2089.2	57.4	3725	10	BC049165 Mus muscu
18	1935.6	53.1	2157	9	AB097553 Macaca fa
19	1911	52.5	2393	6	BD082082 Reagents

20	1892.2	52.0	2180	6	BD270154 Character
21	1660.2	45.6	2993	10	BC058632 Mus muscu
22	1471.6	40.4	2737	10	BC046472 Mus muscu
23	1161.4	31.9	1548	6	BD134997 Human nuc
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27	1158	31.8	1524	6	AR278228 Sequence
28	1158	31.8	1524	6	AR366924 Sequence
29	1158	31.8	1524	6	AR370820 Sequence
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43	884.4	24.3	1467	10	AB112658 Mus muscu
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45	815.8	22.4	3913	9	AF177473 Homo sapi

ALIGNMENTS

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LOCUS
DEFINITION
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ACCESSION
AY297045
VERSION
AY297045.1
KEYWORDS
GI:31335332
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 3879)
Hofmann, T., Chubarov, V., Gudermann, T. and Montell, C.
TRPM5 is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel
Curr. Biol. 13 (13), 1153-1158 (2003)
JOURNAL
2276792
MEDLINE
12842017
REFERENCE
Chubarov, V., Hofmann, T., Gudermann, T. and Montell, C.
Direct Submission
Submitted (12-MAY-2003) Institut fuer Pharmakologie und Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse 1, Marburg D-35033, Germany
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1. 3879
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/product="transient receptor potential cation channel subfamily M member 4 splice variant B"
/protein_id="AAP4474.1"

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 Qy 1861 GGGATGAGCTGAGCTTCTTGGCGAGTGTCTACGACAGTGAAGTGAAGGCTGCCG 1920
 Db 1913 GGGATGAGCTGAGCTTCTTGGCGAGTGTCTACGACAGTGAAGTGAAGGCTGCCG 1972
 Qy 1921 CTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980
 Db 1973 CTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2032
 Qy 1981 GCTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040
 Db 2033 GCTACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2092
 Qy 2041 TGGGAGATATGAGCTGAGCTACCACTTCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 2100
 Db 2093 TGGGAGATATGAGCTGAGCTACCACTTCTGAGGCTGCTGCTGCTGCTGCTGCTGCT 2152
 Qy 2101 CCACTCATCTACACCGGCTCATCACTTCAAGAAATCAGAAAGAGCCCAACAGGAG 2160
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 Db 2273 CCAAGCGAAGAGACCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2332
 Qy 2281 GCGCGCTGCGGAGGCGCGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAG 2340
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 melastatin subgroup member 4 protein (TRPM4 gene).
 ACCESSION AJ575813
 VERSION AJ575813.1 GI:32487283
 KEYWORDS transient receptor potential ion channel melastatin subgroup member
 4 protein; TRPM4 gene.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens (human)
 REFERENCE 1 Nilius, B., Prenen, J., Droogmans, G., Voets, T., Vennekens, R.,
 Freichel, M., Wissenbach, U., and Flockerzi, V.
 Voltage Dependence of the Ca2+-activated Cation Channel TRPM4
 J. Biol. Chem. 278 (33), 30813-30820 (2003)

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QY	1441	TCCCACAGGCGAGGCCAACCAAGCCCCAGCCCTAAAAAGGGGGAGCTGCGGAGCTCCGAGCC	1500
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QY	1551	TCGGGGGGGCGCTTGGGAGCCCTCAACCCAGGCGAGGCTTGGGGAGAGCATGTATTCTCTC	1622
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Db	Qy	Db	RESULT 4
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VERSION	AF497623.1		
KEYWORDS	GI:20269878		
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ORGANISM	Homo sapiens		
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AUTHORS	Launay, P., Fiebig, A., Perraud, A.L., Scharenberg, A.M., Penner, R. and Kinet, J.P.		
TITLE	TRPM4 is a Gq2+-activated nonselective cation channel mediating cell membrane depolarization		
JOURNAL	Cell 109 (3), 397-407 (2002)		
MEDLINE	22011788		
PUBMED	12015988		
REFERENCE	2 (bases 1 to 4061)		
AUTHORS	Perraud, A.-L. and Scharenberg, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-APR-2002) Pediatrics, Washington, 1959 NE Pacific Ave, Seattle, WA 98195-6320, USA		
FEATURES	Location/Qualifiers		
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gene

CDS

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Db	1093	AAAGGGGACCTTGAAGTCTGTGACGAGCCCAAGTGGAGAGATTATGACCCGAGAGAGCTC	1152
Qy	1081	CTGACAGTCTATTTCTTCTGAGAGATGGGTCTGAGAAATTCGAGACATATGTTTGAAGCC	1140

Db 1153 CTGACAGCTATCTTCTTGAGAGATGGGCTGTGAGAAATTCGAGACCAATGTTTGAAGGCC 1212
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Db 1213 CTGTGAGAGGCTGTGAGAGGCTCGAGAGGCTCAGGCTACCTGAGTATGAGCTGGTTGGCT 1272
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Db 1933 GGGATGGGCGTTGACCTCTTTGGCGAGTGTATGCGACAGATGAGTGAAGGCTGCGCGC 1992
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Qy 1981 GCTGACGCGCGTCTCTTTTGGCCAGAGATGGGATGACGCTCTGCTGACACAGAAATGG 2040
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Qy 3001 GCACACCTCTCTGGGCGCACAGGCGGCACTGCGCTTCCAGTATGCCAATGCTGTG 3060
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Qy 3121 GCGATGTTCACTTACATTTGGGCAAGTATAGGCGCAACGATCTTACTTGGAGGCG 3180
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Db	3373	CCGTCCTCCCGCGCCCTCGACCATTTCCGGGTTTACCTTTCTAAGGAAAGCCGACGGAG	3432
QY	3361	CTGCTAACGTTGGGAATCGGTGTCATTAAGGAACTTTCTGCTGGACGCGCTAAGGACAAG	3420
Db	3433	CTGCTAACGTTGGGAATCGGTGTCATTAAGGAACTTTCTGCTGGACAAGCGCTAAGGACAAG	3492
QY	3421	CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCTCCAGAAAGTGGACTTGGCACTGAA	3480
Db	3493	CGGGAGAGCGACTCCGAGCGTCTGAAGCGCACGTCCTCCAGAAAGTGGACTTGGCACTGAA	3552
QY	3481	CAGCTGGGACACATCCCGGAGTAGAAGAACAGCGCCTGAAAGTCTTGAGACGGGAGTCCAG	3540
Db	3553	CAGCTGGGACACATCCCGGAGTAGAAGAACAGCGCCTGAAAGTCTTGAGACGGGAGTCCAG	3612
QY	3541	CAGGTAGCCCGGCTCTGGGGGTGGTGGCCGAGGCCCTGAGCCGCTCTGACCTTGTCTGCC	3600
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Db	3673	CCAGGTGGGCGGACACCCCTGACCTGGCTGGTCCAAAGAC	3714

LOCUS	AX443227	4042 bp	DNA	linear	PAT 02-JUL-2002
DEFINITION	Sequence 5 from Patent WO0210382.				
ACCESSION	AX443227				
VERSION	AX443227.1	GI:21690622			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1. Wisenbach, U. Tirp8, tirp9 and tirp10, markers for cancer Patent: WO 0210382-A 9 07/FEB-2002.				
AUTHORS	Wisenbach, Ulrich (DE)				
TITLE	Location/Qualifiers				
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ORIGIN	Query Match	100.0%;	Score 3640.4;	DB 6;	Length 4042;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 3641;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1	ATGGTGTGGCCGGAGGAGGAGAGGAGTGGATCCCCAAGATCTTCAAGAGAGACCTGCG	60		
DB	42	ATGGTGTGTGGCCGGAGGAGGAGAGAGGCTGGATCCCCAAGATCTTCAAGAGAGAGCCTGCG	101		
QY	61	ACGAGCTTTCATAGTTGTACTCCACAGATCCGGGAGGGACCTTGTGCGCAGTGTGGCGCCCC	120		
DB	102	ACGAGCTTTCATAGTTGTACTCCACAGATCCGGGAGGGACCTTGTGCGCAGTGTGGCGCCCC	161		
QY	121	CGAGCGGCCCAACCCCGCAGTGGCCCATGAGAGATGCTTCCGGGCGACGCTGTGTGACCTGTG	180		
DB	162	CGAGCGGCCCAACCCCGCAGTGGCCCATGAGAGATGCTTCCGGGCGACGCTGTGTGACCTGTG	221		
QY	181	TGGGACAGCGCATGACACACACCGGAGAAACCCACCGATGCCCTACCGGAGAGCTGGATTC	240		
DB	222	TGGGACAGCGCATGACACACCGGAGAAACCCACCGATGCCCTACCGGAGAGCTGGATTC	281		
QY	241	ACGGGGGCGCGGCGCAGACAGACGAATTTTCTCCGAGCTCTGTACCGAAAGGATCCAGCT	300		
DB	282	ACGGGGGCGCGGCGCAGACAGACGAATTTTCTCCGAGCTCTGTACCGAAAGGATCCAGCT	341		
QY	301	GCACTTTATAGTCTGTGTCACACGACCATGGGGCTTCCGTGCCCCGAACTGTGTGTGTCA	360		
DB	342	GCACTTTATAGTCTGTGTCACACGACCATGGGGCTTCCGTGCCCCGAACTGTGTGTGTCA	401		
QY	361	GTGCTGGGGGGGATGTGGGGGGGCCCCGTCTCTCAAGACCTGGCTGCAGAACCTGTGCGCTGT	420		
DB	402	GTGCTGGGGGGGATGTGGGGGGGCCCCGTCTCTCAAGACCTGGCTGCAGAACCTGTGCGCTGT	461		
QY	421	GGGCTGTGGGGGGCTGTGCCAGAGACAGAGAGCCGTGATGTGTCCTGGGGGGCTGTGACACG	480		
DB	462	GGGCTGTGGGGGGCTGTGCCAGAGACAGAGAGCCGTGATGTGTCCTGGGGGGCTGTGACACG	521		
QY	481	GGCATTCGGCCGGGACATGTTTGTGTGTGTGCTGTACCGGAGACCATCAGATGGCCACATGGGGGC	540		
DB	522	GGCATTCGGCCGGGACATGTTTGTGTGTGTGCTGTACCGGAGACCATCAGATGGGGGC	581		
QY	541	ACCAAGGTGTGGCCATAGGTTGTGGCCCCCTGGGGGTGTGGTCCGGAAATAGAGACACCTTC	600		
DB	582	ACCAAGGTGTGGCCATAGGTTGTGGCCCCCTGGGGGTGTGGTCCGGAAATAGAGACACCTTC	641		
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DB	642	ATCAACCCCAAAGGCTGTGCCCGGAGAGATACCGGTGGGGCGGGTGAACCCGGAGGAGCGGG	701		
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DB	702	GTCCAGTTTCCCTCTGAGCTACCACTACTCTCGGCTTCTTCTCTGTGTGACGACCGGACACAC	761		
QY	721	GGCTGTCTGGGGGGCGAGAAACCGCTTCCGCTTGGCGCTTGAGTCTTACATCTCACAGCAG	780		
DB	762	GGCTGTCTGGGGGGCGAGAAACCGCTTCCGCTTGGCGCTTGAGTCTTACATCTCACAGCAG	821		
QY	781	AAGACGGGCGTGGGAGGAGACTTGAATTAAGATCCCTGTCCGCTCCCTCCGATTTGAATGTGT	840		
DB	822	AAGACGGGCGTGGGAGGAGACTTGAATTAAGATCCCTGTCCGCTCCCTCCGATTTGAATGTGT	881		
QY	841	GATAGAGAGATGTTGAGCGCGAATGTAGAAAGCCACCCAGGCTCAGCTCCCATGTCTCTC	900		
DB	882	GATAGAGAGATGTTGAGCGCGAATGTAGAAAGCCACCCAGGCTCAGCTCCCATGTCTCTC	941		
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DB	942	GTGGCTGAGCTCAGGGGAGGCTGCGGACTGCTGGCGGAGACCTTGAAAGACACTTGTGGCC	1001		
QY	961	CCAGGAGATGGGGGAGCCAGGACAGGCGGAAGCCCGAGATGGAATCAGGCGTTTCTTTCCC	1020		
DB	1002	CCAGGAGATGGGGGAGCCAGGACAGGCGGAAGCCCGAGATGGAATCAGGCGTTTCTTTCCC	1061		

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QY 1081 CTGACAGCTCTATTCTTCTGAGAGATGGGTCTGAGAGATTTGAGACCATAGTTTGAAGGCC 1140
DB 1122 CTGACAGCTCTATTCTTCTGAGAGATGGGTCTGAGAGATTTGAGACCATAGTTTGAAGGCC 1181
QY 1141 CTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 1200
DB 1182 CTGAGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 1241
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DB 1362 GTGGCTTGTCTATTTCCAGGCGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTG 1421
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QY 1741 ATGGGTTCCAAATGAGTTCCTGAGCTCTGAGGAGGCTGTTGCTGAGTATGAGCA 1800
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QY 1801 CGGCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1860
DB 1842 CGGCTGAGGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1901
QY 1861 GAGGATGAGGAGTTCCTTTGAGGAGTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
DB 1902 GAGGATGAGGAGTTCCTTTGAGGAGTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1961
QY 1921 CTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
DB 1962 CTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2021
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QY 2101 CCACTCATCTACACCGGCTTCATCATCTTACAGAAATCAGAGAGAGGCCACAGGGAG 2160
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LOCUS	AX235183					
DEFINITION	Sequence 1 from Patent WO0162794.					
ACCESSION	AX235183					
VERSION	AX235183.1	GI:15593774				
KEYWORDS						
SOURCE						
ORGANISM	Homo sapiens (human)					
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE						
AUTHORS	Glucksmann, M.A., Curtis, R.A. and Lora, J.M.					
TITLE	18607, a human calcium channel					
JOURNAL	Patent; WO 0162794-A 1 30-AUG-2001;					
	Millennium Pharmaceuticals, Inc. (US)					
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CDS						

Query Match	92.7%	Score 3374.4	DB 6	Length 3900
Best Local Similarity	99.5%	Pred. No. 0		
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QY	303	AGTTATAGTCTGATCACACGACATAGGAGCTTCGCGCCCGAAGCTGGTGTGTCAGT	362	
Db	185	AGTTATAGTCTGATCACACGACATAGGAGCTTCGCGCCCGAAGCTGGTGTGTCAGT	244	
QY	363	GCTGGGGGAGATCGGGGGGCCCCGCTCTCCAGACCTGGCTGTGAGACCTGCTGCTGTG	422	
Db	245	GCTGGGGGAGATCGGGGGGCCCCGCTCTCCAGACCTGGCTGTGAGACCTGCTGCTGTG	304	
QY	423	GCTGTGTCGGGCTGCTCCAGAGCACAGGAAGCTGTGATGTCACTGGGGGGCTGCACAAGG	482	
Db	305	GCTGTGTCGGGCTGCTCCAGAGCACAGGAAGCTGTGATGTGACTGGGGGGCTGCACAAGG	364	
QY	483	CATGCGCGCGGATGTTGATGTGCTGTACGAGGACCATACAGATGGCCAGCATGCGGGCAC	542	
Db	365	CATGCGCGCGGATGTTGATGTGCTGTACGAGGACCATACAGATGGCCAGCATGCGGGCAC	424	
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LOCUS	3387 bp	DNA	linear	PAT 11-SEP-2001
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DEFINITION	Sequence 3 from Patent WO0162794.			
ACCESSION	AX235185			
VERSION	AX235185.1			
KEYWORDS	GI:15593776			
SOURCE				
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REFERENCE				
AUTHORS	Glucksmann, M.A., Curtis, R.A. and Lora, J.M.			
TITLE	18607, a human calcium channel			
JOURNAL	Patent: WO 0162794-A 3 30-AUG-2001;			
FEATURES	Millennium Pharmaceuticals, Inc. (US)			
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ORIGIN										
Query Match	92.6%;	Score 3373.8;	DB 6;	Length 3387;						
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VERSION CQ715325.1 GI:42276182
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Homosapiens
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS 1
TITLE Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
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humanecons or transcripts, for detecting expression and other uses
thereof
Patent: WO 02068579-A 1259 06-SEP-2002;

JOURNAL
PE Corporation (NY) (US)
Location/Qualifiers
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ORIGIN

Query Match 91.5%; Score 3333; DB 6; Length 3402;
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Db 119 TSCGTGGGGGATCGGGGGGCTTCCTCAAGCCTGCTGCAAGACCTGTCCTGTG 178
QY 422 GCGTGTGGGGCTGCGGAGACACAGAGCTTGATTTCTACTGGGGGTCTGCAACG 481
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Db	2579	TGTAAGCCTAATGCGGTGGCCACGGAGGGGGCTCTGAGGCCACGGGACAGTACTTCCCA	2635
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Db	2639	GTATCTCGCGCGCGGTCTTCTTACCGGTCCCTACCTGACAGATCTTTCGGCAGATTCCCAAG	2698
Qy	2942	AGGACATBGAAGTGGCCCTCATTGGACACAGCACTGCTCGTCCGAGGCCCGGCTTTCGG	3003
Db	2699	AGGACATBGAAGTGGCCCTCATTGGACACAGCACTGCTCGTCCGAGGCCCGGCTTTCGG	2758
Qy	3002	CACACCCCTCCGTGGGGCCCGAGCGGGACATGCTGCTCCAGTATAGCCAACTGGCTGGTGG	3063
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Qy	3362	TGCTTAAGCTGGGAATCGGTGATAGAAGAACTTTGCTGGGCAACGGCTTAAGGAACAAC	3421
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			
AUTHORS	Hillman,J.L., Tang,Y.T., Yue,H., Elliott,V.S., Tribouley,C.M.,		
	Lee,E.A., Ramkumar,J., Lal,P., Xu,Y., Warren,B.A., Hafalia,A.J.,		
	Baughn,M.R., Azimzai,Y., Batra,S., Burford,N., Yao,M.G.,		
	Nguyen,D.B., Lu,D.A., Walia,N.K., Au-Young,J. and Patterson,C.		
JOURNAL	Patent: WO 0198353-A 88 27-DEC-2001;		
	Incyte Genomics, Inc. (US)		

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QY	3316	CTCGAGCAATTTCCGGGTTTACCTTTCTPAGGAAGCCGAGCGGAAGCTGTAACTGGGAA	3375
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AUTHORS	1 (bases 1 to 3523)		
TITLE	Hofmann, T., Chubdanov, V., Gudermann, T. and Montell, C.		
JOURNAL	TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent		
MEDLINE	Cur. Biol. 13 (13), 1153-1158 (2003)		
PIRBASE	22726392		
REFERENCE	12842017		
AUTHORS	2 (bases 1 to 3523)		
TITLE	Chubdanov, V., Gudermann, T., Hofmann, T. and Montell, C.		
JOURNAL	Submitted (12-MAY-2003) Institut fuer Pharmakologie und		
FEATURES	Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse		
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QY	492	GCATGTTGTGTGTGTGTATCCGGACCAATCAGATGCGACACTG	GGGGGACCAAGTGTG	551
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QY	552	GGCCATGGGTGTGGCCCCCTGGGGTGTGTCCGGAAATGAGACACCTCAT	CAATCAACCCCA	611
Db	248	GGCCATGGGTGTGGCCCCCTGGGGTGTGTCCGGAAATGAGACACCTCAT	CAATCAACCCCA	307
QY	612	GGGCTCGTTCCCTGCGAGGTACCGGTGACGCGGTACCCGAGAGACGG	GGGTTCAGTTTCC	671
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QY	732	GGGCGAGAACCGGCTTCGGCTTGGCGCTGTGAATCTACATCTCACA	CGACGAAACGGGCGT	791
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QY	1212	CCGCGTGAACATTTGCCAGAGTGAATCTTTTGGGGGGGACATCCAT	TGGCGGTCTCTTCCA	127
Db	908	CCGCGTGAACATTTGCCAGAGTGAATCTTTTGGGGGGGACATCCAT	TGGCGGTCTCTTCCA	967
QY	1272	TCTCGAAGTTCTCTCATGAGACGCTCTGTGATGACGCGCTGAGTT	CTGTGCGCTTGTCT	133
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QY	1392	CAGGCGGCGCCCTCAACTCGCTCAATCCCAACCTTTGAGCAGGCGCTCCACAAGCG	1451
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QY	1452	AGGCACCAAAAGCCCGAGCCCTTAAAGGGGAGACTGCGAGCTCGGCCCTCGACGTGG	1511
Db	1148	AGGCACCAAAAGCCCGAGCCCTTAAAGGGGAGAGCTGCGAGCTCGGCCCTCGACGTGG	1207
QY	1512	GCAATGCTGAGAGATGCTGCTGGGGAGAGATGTCGCGCCGAGAGTACCCTCGGGGGCG	1571
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QY	1692	TTGGGCACTGTTGCTGAAACAGGGACACAGATGGCCATGTACTTCTGGGAGATGGTTCCAA	1751
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QY	1812	TGACGCTGAGAGGACAGACCGAGAGAAAGACTGGCGTTCAAGTTTGAAGGGAGATGGCGT	1871
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QY	1872	TGACCTCTTTGGCGAGTGTATGCGACAGTGAAGTGAAGGCTCCCGCTCTCTCTCCG	1931
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QY	1932	TGCGTGGCCCGCTCGGGGGGGATGGCACTGGCCCTCAGCTGGCCATGCAAGCTGACGCGCG	1991
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QY	2052	GCGCAGACATAACCCATCTGGGCGCTGGTCTTGCTTCTTTTGCCCTGCACATCATTA	2111
Db	1748	GCGCAGACATAACCCATCTGGGCGCTGGTCTTGCTTCTTTTGCCCTGCACATCATTA	1807
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VERSION	complete cds.		
KEYWORDS	Ay046396		
SOURCE	Ay046396.1 GI:15617228		
ORGANISM	Homo sapiens (human)		
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	Bukavota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 3701)		
TITLE	Xu,X.-Z., Moebius,F., Gill,D.L. and Montell,C.		
	Regulation of melastatin, a TRP-related protein, through		
	interaction with a cytoplasmic isoform		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (19), 10692-10697 (2001)		
MEDLINE	21438010		
PUBMED	11535825		
REFERENCE	2 (bases 1 to 3701)		
AUTHORS	Xu,X.-Z., Moebius,F., Gill,D.L. and Montell,C.		
TITLE	Direct Submission		
JOURNAL	Submitted (17-JUL-2001) Biological Chemistry, Johns Hopkins Univ		
FEATURES	School of Medicine, 725 N. Wolfe Street, Baltimore, MD 21205, USA		
SOURCE	Location/Qualifiers		
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VERSION AY297046.1 GI:31335334
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3444)
AUTHORS Hofmann, T., Chubunov, V., Gudermann, T. and Montell, C.
TITLE TRPM5 Is a Voltage-Modulated and Ca(2+)-Activated Monovalent Selective Cation Channel
JOURNAL Curr. Biol. 13 (13), 1153-1158 (2003)
MEDLINE 22726392
PUBMED 12842017
REFERENCE 2 (bases 1 to 3444)
AUTHORS Chubunov, V., Hofmann, T., Gudermann, T. and Montell, C.
TITLE Direct Submission
JOURNAL Submitted (12-May-2003) Institut fuer Pharmakologie und Toxikologie, Philipps-Universitaet Marburg, Karl-von-Frisch-Strasse 1, Marburg D-35033, Germany
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ORIGIN
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QY	3001	GCAACCCCTCTGGGGCCCAAGCGGGACCTGCGTCTCCAGTATGCCAATGTGCTGTG	3068
Db	2618	GCAACCCCTCTGGGGCCCAAGCGGGACCTGCGTCTCCAGTATGCCAATGTGCTGTG	2677
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QY	3301	CCGTCTCTCCCGGCTCTGAGCAATTCGGGTTTACTTTCTTAAAGAACCGAGCGAAG	3360
Db	2918	CCGTCTCTCCCGGCTCTGAGCAATTCGGGTTTACTTTCTTAAAGAACCGAGCGAAG	2977
QY	3361	CTGCTTACGTGGGAATCGGTGATTAAGAGAACTTTCTGTGTGGCAGCGGCTTAAGGACAAG	3420

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Db	3038	CGGGAGACCGCACTCCGAGCGTCTTAAGGCGCACGTCCTCCAGAAAGTGTGACTTGGCACTGAAA	3097
QY	3481	CAGCTGGGACATCCGCGAGTACGAAACAGCGCCCTGAAAGTGTGGAGCGGAGAGTCCAG	3540
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QY	3541	CAGTGTAGCCGCGTCTTGAGGTGGTGGCCGAGGCGCCTTGAGCCGCTGTGCTGTGCC	3600
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ORIGIN

Query Match 66.6%; Score 2424; DB 10; Length 3800;
Best Local Similarity 79.8%; Pred. No. 0;
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QY 118 CCGCGGACCGCCGACCGCCGAGTGGCATGTGAGATGCTTGGGGGACCGGTGTGACC 177
DB 170 CCGCGGAGATGCCACCCCTTCTGTGGCTGTGGAGAGATGCTTGGGGGACCGGTGTGACC 229
QY 178 GTGTGGGACAGCGATGACACACACAGAGAAAGCCACCGATGCTTACGGAGAGCTGAC 237
DB 230 GAGTGAACAGATGATGAGACACACAGAGAAAGCCACAGATGCTTACGGAGAGCTGAC 289
QY 238 TTCAAGGGGGGCGCGCGAGAGAGAGAGATTTCTCCGGCTCTGTGACCGAGAGAGATCCA 297
DB 290 TTCAAGTACTGTGGCGGAGAGAGAGAGAGATTTCTCCGGCTCTGTGACCGAGAGATCCA 349
QY 298 GGTGAGTTTATGATCTGTGTCACAGCAGATGGGGCTTCCGTGCCCGGACCTGGGTGG 357
DB 350 GGTGAGTTTATGATCTGTGTCACAGCAGATGGGGCTTCCGTGCCCGGACCTGGGTGG 409
QY 358 TCAGTGTGTGGGGGAGATCGGGGGGCGCCGCTCTCCAGACCTGTGACAGAGCTGTGCGT 417
DB 410 TCAGTGTGTGGGGGAGATCGGGGGGCGCCGCTCTCCAGACCTGTGACAGAGCTGTGCGT 469
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 AUTHORS Wiesenbach, U.
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ORIGIN

Query Match 62.3%; Score 2269.4; DB 6; Length 2695;
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Job time : 10276.1 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2005, 16:55:33 ; Search time 7461.25 Seconds
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Gapop 10.0 ; Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1983	54.4	4293	3	AK044094 Mus muscu
2	773.6	81.2	912	6	CA488162 AGENCOURT
3	719	19.7	879	5	BU858032 AGENCOURT
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ALIGNMENTS

RESULT 1	AK044094	LOCUS	4293 bp mRNA linear HTC 03-APR-2004
DEFINITION	Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:AB30089H3 product: similar to TRP-RELATED CATION INFLUX CHANNEL (Homo sapiens), full insert sequence.	ACCESSION	AK044094
VERSION	AK044094.1 GI:26336171	KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (house mouse)	ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning	JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
REFERENCE	99279253	PUBMED	10349636
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.	TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)	PUBMED	20499374
REFERENCE	11042159	AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasahigashi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwama, Y., Ohara, E., Matsubuchi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format	JOURNAL	sequencing pipeline with 384 multiplexed sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)	PUBMED	20530913
REFERENCE	11076861	AUTHORS	THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE	Functional annotation of a full-length mouse cDNA collection	JOURNAL	Nature 409, 685-690 (2001)
REFERENCE	5	AUTHORS	THE FANTOM Consortium and the RIKEN Genome Exploration Research

TITLE Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4293)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawaji, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,
Okasaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muraematsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/.
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ORIGIN

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Best Local Similarity 77.6%; Pred. No. 0;

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3148 GTACAGGCGCAAGGCTGAGGCTGAGGCTGAGGCTTGTACATC 3207
2813 GTGACAGGCGCAAGGCTGAGGCTGAGGCTTGTACATC 2872
3308 CACTCTGCGCGCGGCTGAGGCTGAGGCTTGTACATC 3267
2873 CACTCTGCGCGCGGCTGAGGCTGAGGCTTGTACATC 2916
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2917 ----- 2916
3328 CCGGTTTACCTTCTTGAAGAGCGGAGCGGAGCTGCTAAGTGGGATGGTGCATAG 3387
2917 TGTGTCTGTCTCTTGAAGAGCGGAGCGGAGCTGCTAAGTGGGATGGTGCATAG 2976
3388 GAGAATCTTCTGCTGAGCAGGCTGAGGAGCAAGGCGGAGCGGAGCTGAGGAG 3447
2977 GAGAATCTTCTGCTGAGCAGGCTGAGGAGCAAGGCGGAGCGGAGCTGAGGAG 3036
3448 CGCAGCTTCCAGAGGCTGAGGAGCTTGAAGCAAGGCTGAGGAGCAATCTGAGGAG 3507
3037 CGCAGCTTCCAGAGGCTGAGGAGCTTGAAGCAAGGCTGAGGAGCAATCTGAGGAG 3096
3508 CAGGCGCTGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3567
3097 CAGGCGCTGAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3156
3568 GCGAGGCGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGG 3627
3157 GCTGAGGCGCTTGAAGCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3216
3628 CTTGGGCTCAAGAGC 3642
3217 ACTGTTTCAAGAGC 3231

LOCUS	CA488162	912 bp	mRNA	linear	EST 14-NOV-2002
DEFINITION	AGENCOURT 10808068 MAPCL Homo sapiens cDNA clone IMAGE:6719903 5', mRNA sequence.				
ACCESSION	CA488162				
VERSION	CA488162.1 GI:24949318				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 912)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbbs-remail.nih.gov Tissue Procurement: Kristi A. Eglund, Ira Pastan cDNA Library Preparation: Invitrogen Corp DNA Sequencing by: The I.M.A.G.E. Consortium (LNL) Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: LLM14278 row: 1 column: 23 High quality sequence start: 28 High quality sequence stop: 78.				
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	/lab_host="EMDH10B"				
	/clone_lib="MAPCL"				
	/note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I; Subcloned with Brain, liver, lung, kidney and muscle. Directionally cloned. Priming method: oligo-dT. Average insert size: 1800 bp. Library amplification: 26,000 fold. Kristi A. Eglund, James J. Vincent, Robert Strausberg, Bungkok Lee & Ira Pastan: Discovery of new breast cancer genes encoding membrane and secreted proteins. Manuscript submitted."				
ORIGIN					
Query Match	21.2%; Score 773.6; DB 6; Length 912;				
Basic Local Similarity	94.3%; Pred. No. 1.5e-155;				
Matches 812; Conservative	0; Mismatches 47; Indels 2; Gaps 1;				
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106	GGCCACGAGGGGCTCTCTGAGGCCACGGGACAGTGAATTCCCAAGTATCTTGGCCGCGT 165				
2898	CTTCTACCGTCCCTACCTGAGAGTCTTGGGCAATTTCCCAAGAGACATGACGTCG 29577				
166	CTTCTACCGTCCCTACCTGAGAGTCTTGGGCAATTTCCCAAGAGACATGACGTCG 225				
2958	CCTCATGAGACAGCAACTGCTGTCGGAACCGGCTTCTGGGACACACCTCTTGGGGC 30177				
226	CCTCATGAGACAGCAACTGCTGTCGGAACCGGCTTCTGGGACACACCTCTTGGGGC 285				
3018	CCAGGCGGACCTGCGTCTCCCAAGTATCCCAACTGCTGTGTGCTGCTCTGTCAT 30777				
286	CCAGGCGGACCTGCGTCTCCCAAGTATCCCAACTGCTGTGTGCTGCTCTGTCAT 345				
3078	CTTCTGCTGCTGGCCAACTCTGCTGTCACTGCTCATTTGCATTTCACTTAC 31377				

Dn		346	CTTCTCCTCGTAGGCAACATCCGTGGTGTAATTTCCTCATTTGCCAATGTTCAAGTTAAC	405
Oy		3138	ATTGCACAAGTACAGGGCAAACAGCATCTCTACTGGAAGGCGCAGGTTAACGGCTTCAT	3197
Dd		406	AATTGGCAAAAGTACAGGGCAAACAGCATCTCTACTGGAAGGCGCAGGTTAACGGCTTCAT	465
Oy		3198	CCGGGAAMTTCACCTCTGAGGCCGCGGCGTGGGCCGCCGCTTATATGTCANMTCACCATTGGC	3257
Dd		466	CCGGGAAMTTCACCTCTGAGGCCGCGGCGTGGGCCGCCGCTTATATGTCANMTCACCATTGGC	525
Oy		3258	CCTCCTGCTCAGAGCAATTTGTGACAGCCAGCCCGAGGCCAGCCGCTCTCCCGGCCCT	3317
Dd		526	CCTCCTGCTCAGAGCAATTTGTGACAGCCAGCCCGAGGCCAGCCGCTCTCCCGGCCCT	585
Oy		3318	CGAGCATTTCCGGGTTTTACCTTTCTAAGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC	3377
Dd		586	CGAGCATTTCCGGGTTTTACCTTTCTAAGAAGCCGAGCGGAAGCTGCTAACGTGGGAATC	645
Oy		3378	GGTGCATAAAGAGAACTTTCTGCTGAGACCGCGCTAAGGAGCAAGCGGGAGAGCGACTCGA	3437
Dd		646	GGTGCATAAAGAGAACTTTCTGCTGAGACCGCGCTAAGGAGCAAGCGGGAGAGCGACTCGA	705
Oy		3438	GCGTCTGAAGCGCACGTGCCAGAAAGTGTGACTTTGGCACTGAAAACAGCTGGGACACATCCG	3497
Dd		706	GCGTCTGAAGCGCACGTGCCAGAAAGTGTGACTTTGGCACTGAAAACAGCTGGGACACATCCG	765
Oy		3498	CGAGTACGAACACAGCGCTGAAAGTGTGAGACGGGAGGTCCAGCATGTTAGCC--GGCTC	3555
Dd		766	CGAGTACGAACACAGCGCTGAAAGTGTGAGACGGGAGGTCCAGCATGTTAGCTACGCGGGCTC	825
Oy		3556	CTGGGGTGGGTGGGCCGACGCCCTCTGAGCCGCTCTGCCCTTGGCCCCCAGAGTGGGCGCCCA	3615
Dd		826	CGGGGGGTGGTNTNFTCNCTCTCCCTCTCCCTCCCCTCTCTCTCTCTCTCTCTCTCTCTCC	885
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Dd		886	CCCCCTCCCCGCCCCCGCTCC	906

RESULT 3
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 LOCUS
 DEFINITION BUBS8032 879 bp mRNA linear EST 16-OCT-2002
 IMAGE:6647959 5', mRNA sequence.
 BUBS8032
 BUBS8032.1 GI:24043024
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 879)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
 ftp://image.lnl.gov
 Plate: LCOM2889 row: d column: 07
 High quality sequence start: 11
 High quality sequence stop: 612.
 Location/Qualifiers
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FEATURES
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/clone="IMAGE:6647959"
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/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB1; Site 1: EcorI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcorI/XhoI sites using the
following 5' adaptor: GGCAACAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match      19.7%; Score 719; DB 5; Length 879;
Best Local Similarity 96.6%; Pred. No. 8.4e-144;
Matches 799; Conservative 0; Mismatches 20; Indels 8; Gaps 6;

QY 2340 GACCATCTTCATGGGCAACGTGTCAGTACCTGCTGTTCTGCTCTTTCTCGGGGT 2399
Db 1 GACCATCTTCATGGGCTACCTGTCAGTACCTGCTGTTCTGCTCTTTCTCGGGGT 60

QY 2400 GCTGCTCTGATTTCCAGCCGCGCGCCGCGGCTCCCTGAGCTGCTCTATTGTG 2459
Db 61 GCTGCTCTGATTTCCAGCCGCGCGCCGCGGCTCCCTGAGCTGCTCTATTGTG 120

QY 2460 GGCCTTTCAAGCTGCTGTCAGGAACCTGCGCAGGGCTTGAAGCGGCGGAGAGCT 2519
Db 121 GGCCTTTCAAGCTGCTGTCAGGAACCTGCGCAGGGCTTGAAGCGGCGGAGAGCT 180

QY 2520 CGCCAGCGGGGGCCCGGGGCTGCGCATGCTCACTGAGCAGCGCTGCGCTTCACT 2579
Db 181 CGCCAGCGGGGGCCCGGGGCTGCGCATGCTCACTGAGCAGCGCTGCGCTTCACT 240

QY 2580 CGCCGACAGCTGGAACAGTGGACCTAGTGGCTTCACTGCTTCTTCTGGGGTGG 2639
Db 241 CGCCGACAGCTGGAACAGTGGACCTAGTGGCTTCACTGCTTCTTCTGGGGTGG 300

QY 2640 CTGCGCGGTGACCCCGGGTTTGTACCACTGGGCGGCACTGCTCTGATGACTTAT 2699
Db 301 CTGCGCGGTGACCCCGGGTTTGTACCACTGGGCGGCACTGCTCTGATGACTTAT 360

QY 2700 GGTTCATCGGTGGCGGTGCTTCACTTCACTGCAACAAAGCTGGGGCCCAAGAT 2759
Db 361 GGTTCATCGGTGGCGGTGCTTCACTTCACTGCAACAAAGCTGGGGCCCAAGAT 420

QY 2760 CGTCACTGTAACAAGATGATGAAGAGCTGTTCTTCTTCTTCTTCTGCGGTGTG 2819
Db 421 CGTCACTGTAACAAGATGATGAAGAGCTGTTCTTCTTCTTCTTCTGCGGTGTG 480

QY 2820 GCTGGTACCTATGAGCGTGGCCACGAGGGGCTCTTGAAGCCACGGACAGTACTTCC 2879
Db 481 GCTGGTACCTATGAGCGTGGCCACGAGGGGCTCTTGAAGCCACGGACAGTACTTCC 540

QY 2880 AAGTATCTGGGCGCGCTCTTCACTGCTCCCTACTGAGATCTTCGGGAGATTCGCCA 2939
Db 541 AAGTATCTGGGCGCGCTCTTCACTGCTCCCTACTGAGATCTTCGGGAGATTCGCCA 600

QY 2940 GAGAGACATGACGTGGCCCTCATGAGACACAGCAATGCTGTCGAGGCC-GGCTTCT 2998
Db 601 GAGAGACATGACGTGGCCCTCATGAGACACAGCAATGCTGTCGAGGCCGCGGCTTCT 660

QY 2999 GGGGCAACCTCTCTGGGG-CCGAGGCGGGCACCTGCG-TTTCACAGTATGCCACT-GGC 3055
Db 661 GGGGCAACCTCTCTGGGGCCCGAGGCGGGCACCTGCGTCCCGATATGCGCACTGCGG 720

QY 3056 TGGTGTGCTGCG-TCTGCTGATCTTCTGCTGCTGCGCAACATCTGCTGATCACTTG 3114
Db 721 TGGTGTGCTGCTTCTCCGCACTTCTTCTGCTGCGCAACATCTTCTGCTGATCACTTG 780

QY 3115 CTCATTCGCATGTTCACTTACACA---TTGGGCAAGTACAGGGGCA 3158
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RESULT 4
LOCUS CN402549 700 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000470662623 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN402549
VERSION CN402549.1 GI:47390143
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 700)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guejler, K., Rao, M.S., Mandalam, R.,
Ledkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 700 Std Error: 0.00.
Location/Qualifiers
1..700
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ORIGIN

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Query Match      19.1%; Score 697.4; DB 7; Length 700;
Best Local Similarity 99.9%; Pred. No. 3.6e-139;
Matches 698; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 298 GCTGCAGTTATTAAGTCTGTCACAGCAATGAGGCTTCGTCGCCCCGAACTGAGTGTG 357
Db 2 GCTGCAGTTATTAAGTCTGTCACAGCAATGAGGCTTCGTCGCCCCGAACTGAGTGTG 61

QY 358 TCAGTGTCTGGGGGAGATGGGGGGGCGCGTCTCTCCAGACTGGCTGACAGACTCTGCGT 417
Db 62 TCAGTGTCTGGGGGAGATGGGGGGGCGCGTCTCTCCAGACTGGCTGACAGACTCTGCGT 121

QY 418 GGTGGGCTGTGGGCGGCTGCCAGAGACAGAGACTGAGATTGTCATGCGGGGTCTGAC 477
Db 122 GGTGGGCTGTGGGCGGCTGCCAGAGACAGAGACTGAGATTGTCATGCGGGGTCTGAC 181

QY 478 ACGGGCATCGGCGGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 537
Db 182 ACGGGCATCGGCGGCAATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 241

QY 538 GGCACCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 597
Db 242 GGCACCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301

QY 598 CTCATCAACCCCAAGGGCTGTTCTCTGACAGTACCGGTCGCGGTCAGCCGGAAGAC 657
Db 302 CTCATCAACCCCAAGGGCTGTTCTCTGACAGTACCGGTCGCGGTCAGCCGGAAGAC 361

QY 658 GGGGTCAAGTTTCCCTGGACTACCACTACTGCGCTTCTTCTCTGTCGAGCAGCGGCA 717
Db 362 GGGGTCAAGTTTCCCTGGACTACCACTACTGCGCTTCTTCTCTGTCGAGCAGCGGCA 421

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QY	718	CACGGCTCCTCGGGGGGGGAGAAACGGCTTCGGCTTGAGCTGAGAGTCTTACATCTCAAG	777		
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QY	778	CAGAAAGACGGCGCTGGGAGGAGACTGGATTGACATCCCTGTCTCTCTCTGATTGAT	837		
Db	482	CAGAAAGACGGCGCTGGGAGGAGACTGGATTGACATCCCTGTCTCTCTCTGATTGAT	541		
QY	838	GGTGATGAGAAAGATGTTACCGCAATTAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC	897		
Db	542	GGTGATGAGAAAGATGTTACCGCAATTAGAGAACGCCACCCAGGCTCAGCTCCCATGTCTC	601		
QY	898	CTCGGGCTGGCTCAGGGGGGAGCTGCGGAGCTGCCCTGGGGAGACCCCTGGAAGACACTCTG	957		
Db	602	CTCGGGCTGGCTCAGGGGGGAGCTGCGGAGCTGCCCTGGGGAGACCCCTGGAAGACACTCTG	661		
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LOCUS	BQ942718				
DEFINITION	AGENCOURT 8842138 lupski_sciatic_nerve Homo sapiens CDNA clone				
IMAGE:6204319 5', mRNA sequence.					
ACCESSION	BQ942718				
VERSION	BQ942718.1	GI:22358196			
KEYWORDS	EST.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens (human)				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 933)				
TITLE	NIH-MGC http://mgs.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999)				
	Contact: Robert Strusberg, Ph.D.				
	Email: cga@bde-mail.nih.gov				
	Tissue Procurement: Dr. James R. Lupski				
	cDNA Library Preparation: Life Technologies, Inc.				
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)				
	DNA Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LNLN at:				
	http://image.lnl.gov				
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	/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:				
	NotI; Site_2: SalI; cDNA made by oligo-dt priming.				
	Directionally cloned using the following adaptors:				
	5'-TCGACCAAGCGGCTCG-3' and				
	5'-GACATGTTCTGATCGGAGCGCGCCCT(15)-3'. Size selected				
	1 kb for average insert length 1.87 kb. This is a primary				
	library, non-amplified. Library constructed by Life				
	Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor				
	College of Medicine) and is available through Life				
	Technologies."				
ORIGIN					
Query Match	18.9%;	Score 690;	DB 5;	Length 933;	
Best Local Similarity	92.3%;	Pred.No. 1.5e-137;			

	Matches	783;	Conservative	0;	Mismatches	55;	Indels	10;	Gaps	5;
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QY	1477	GGGGAGCTGCGAGCTCCGGGCCCCCTGACCTGAGGGACATGTGCTGAGGATCTGCTGGG	1538							
Db	64	GGGGAGCTGCGAGCTCCGGGCCCCCTGACCTGAGGGACATGTGCTGAGGATCTGCTGGG	123							
QY	1537	AAGATGTGCGGCGCCAGAGTACCCCTCCGGGGGCGCTGGAGCCCTCAACCCAGCCAGGC	1596							
Db	124	AAGATGTGCGGCGCCAGAGTACCCCTCCGGGGGCGCTGGAGCCCTCAACCCAGCCAGGC	183							
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Db	244	GGCCTCCGGGCGAGGCCCCCTGGAGGACCTGCTTTTGGGACATGTTGCTAAACGGGCA	303							
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QY	1897	AGCAGTAGTGAGAGGCTCGCCGCTCCTCCTCCGTGCTGACCCGCTCTGAGGGAGATGC	1956							
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QY	1957	ACTTGCTCCAGCTGGCCAGCAAGCTGACGCCCCGTGCTTTCTTGGCCAGAGATGGGTA	2018							
Db	544	ACTTGCTCCAGCTGGCCAGCAAGCTGACGCCCCGTGCTTTCTTGGCCAGAGATGGGTA	603							
QY	2017	CAGTCTCTGCTGACACAGAAATGGT--GGGAGATATGGCCAGCACTAACCATCTGGG	2075							
Db	604	CAGCTCTGCTGACACAGAAATGGTGGGGAGATGGCCAGCACTAACCATCTGGG	663							
QY	2076	CCTGATTT--GGCCTCTTTTGGCCCTCACTCATCTAACCCGCG--TCATCACCTTGAG	2133							
Db	664	CCTGATTTCCGCTCTTTTGGCCCTCACTCTTCAACCCCGCCCTTCACTTACCTTCG	723							
QY	2133	GAATTCAGAGAGAGACCCACAC--GGGAGAGCTAGAGTTTGAATGATAGTTCAT	2189							
Db	724	GAATTCAGAGAGAGAGACCCCGCCCGGAGGAGTTGATTTGAATCGGACAGTGCTT	783							
QY	2190	TAAATGGGAGAGG--CTGTGCGGACGGCGGACCCAGCCAGAAAGACGCGCTGGGGT	2244							
Db	784	TCATATGGGAGAGGGGCTGCTTGAGAGGTGGGACCGTTTCAACAGGAGACCCCGTTGGGG	843							
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Db	844	CGCTGGCC 851								

ORIGIN	Score	DB 5	Length
Query Match	18.9%	690	933
Best Local Similarity	92.3%	Pred. No. 1.5e-137	

RESULT	6
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LOCUS	B0721564
DEFINITION	B0721564 894 bp mRNA linear EST 16-JUL-2002
ACCESSION	AGNCOCRT_8234684 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6188589 5' , mRNA sequence.
VERSION	B0721564
KEYWORDS	B0721564.1 GI:21860461
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 894)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM13584 row: g column: 22
High quality sequence stop: 500.
Location/Qualifiers

FEATURES
source

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ORIGIN

Query Match 18.3%; Score 666; DB 5; Length 894;
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Matches 720; Conservative 0; Mismatches 15; Indels 5; Gaps 4;

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DB 10 GGTCTGACATCTTCTTCTGAGAGGGCTCTGAGAAATTCGAGACCATAGTTTGA 69
QY 1137 GGCCTTGTGAAGGCTGTGGAGAGCTCGAGAGGCTCAGCTTACCTGATGAGCTGCTT 1196
DB 70 GGCCTTGTGAAGGCTGTGGAGAGCTCGAGAGGCTCAGCTTACCTGATGAGCTGCTT 129
QY 1197 GGCCTTGTGAAGGCTGTGGAGAGCTCGAGAGGCTCAGCTTACCTGATGAGCTGCTT 1256
DB 130 GGCCTTGTGAAGGCTGTGGAGAGCTCGAGAGGCTCAGCTTACCTGATGAGCTGCTT 189
QY 1257 ATGCGGCTCTTCTGATCTGAGAGCTTCCCTCATGAGAGGCTCTGATGAGAGGCTCTGA 1316
DB 190 ATGCGGCTCTTCTGATCTGAGAGCTTCCCTCATGAGAGGCTCTGATGAGAGGCTCTGA 249
QY 1317 GTTGTGAGCTTGTGATCTTCCACAGGCTCAGCTGAGGCTCAGCTTCCGATCCGAGTGC 1376
DB 250 GTTGTGAGCTTGTGATCTTCCACAGGCTCAGCTGAGGCTCAGCTTCCGATCCGAGTGC 309
QY 1377 CTTGAGCCCACTCTACAGAGGCGGCGCTCTCAACTGCTCATTCGCAACTTTTGGACCA 1436
DB 310 CTTGAGCCCACTCTACAGAGGCGGCGCTCTCAACTGCTCATTCGCAACTTTTGGACCA 369
QY 1437 GCGCTTCCACAGAGGAGCAACCAAGCCCGAGCTCTAAAGGGGAGAGCTCGGAGAGCTCG 1496
DB 370 GCGCTTCCACAGAGGAGCAACCAAGCCCGAGCTCTAAAGGGGAGAGCTCGGAGAGCTCG 429
QY 1497 GCCCCTGACGTGGGAGCATGTGCTGAGAGTGTGAGGAAAGTGTGCGGCGGAGGTA 1556

DB 430 GCCCCTGACGTGGGAGCATGTGCTGAGAGTCTGCTGAGGAAAGTGTGCGGCGGAGGTA 489
QY 1557 CCCCTCGGAGGCGGCTGTGGAGAGCTCTCAACCCAGGAGGCTTTGGGAGAGCATATATCT 1616
DB 490 CCCCTCGGAGGCGGCTGTGGAGAGCTCTCAACCCAGGAGGCTTTGGGAGAGCATATATCT 549
QY 1617 GCTCTGAGCAAGGAGCACTGCGCGCTCTGCTGAGATCTGAGCTCGGAGAGG-CCGCT 1675
DB 550 GCTCTGAGCAAGGAGCACTGCGCGCTCTGCTGAGATCTGAGCTCGGAGAGGCGGCTCT 609
QY 1676 GAGAGACCTGCTCTTTGGGAGCTGTTGCTGAACAGGAGCAAGATGAGCAATGATCTCT 1735
DB 610 GAGAGACCTGCTCTTTGGGAGCTGTTGCTGAACAGGAGCAAGATGAGCAATGATCTCT 669
QY 1736 GAGAGATGGGTTCCAAAT-GCAAGTTTCTCTAG-CTCTTGGGAGCTGTTGCTG--CTCGG 1791
DB 670 GAGAGATGGGTTCCAAATGGCAGTTTCTCTAGCTTGTGGAGCGGCTGCGGCTCGG 729
QY 1792 GTGATGGAGCGCTGAGAGCC 1811
DB 730 CGAGTGGACCCCGGAGCC 749

RESULT 7
LOCUS B0723742 883 bp mRNA linear EST 16-JUN-2002
DEFINITION AGENCOURT 8241174 lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6186968 5', mRNA sequence.
ACCESSION B0723742
VERSION B0723742.1 GI:21862639
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 883)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>
Plate: LLM13580 row: d column: 09
High quality sequence stop: 557.
Location/Qualifiers

FEATURES
source

1. .883
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6186968"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="lupski_sympathetic_trunk"
/note="Vector: PCMV-SPORE (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCGGCGGCGG-3' and 5'-GACTAGTTCTAGATGCGAGGCGGCGGCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."

ORIGIN

Query Match 17.9%; Score 651.6; DB 5; Length 883;
 Best Local Similarity 94.3%; Pred. No. 2,7e-129;
 Matches 709; Conservative 0; Mismatches 39; Indels 4; Gaps 3;

QY 1953 TGGCACTTGGCTCCAGCTGGCCATGCAAGCTGACGCCGCTCTTTGTTCCCAAGATG 2012
 DB 1 TGGCACTTGGCTCCAGCTGGCCATGCAAGCTGACGCCGCTCTTTGTTCCCAAGATG 60

QY 2013 GGTACAGTCTGCTGACACAGAAAGTGGGAGATATGGCCACACCTACACCATCTG 2072
 DB 61 GGTACAGTCTGCTGACACAGAAAGTGGGAGATATGGCCACACCTACACCATCTG 120

QY 2073 GGGCCCTGGTCTGCGCTCTTTTGGCCCTCACTACTTACACCCGCTCATACCTTGAG 2132
 DB 121 GGGCCCTGGTCTGCGCTCTTTTGGCCCTCACTACTTACACCCGCTCATACCTTGAG 180

QY 2133 GAAATCAGAGAGAGACCCACACGAGAGAGCTAGAGTTTGAATGATGATGTCATTAA 2192
 DB 181 GAAATCAGAGAGAGACCCACACGAGAGAGCTAGAGTTTGAATGATGATGTCATTAA 240

QY 2193 TGGGGAAGGGCGCTGCGGAGCGGAGCCAGCCGAGAAAGCGCGCTGGGGTCCCGG 2252
 DB 241 TGGGGAAGGGCGCTGCGGAGCGGAGCCAGCCGAGAAAGCGCGCTGGGGTCCCGG 300

QY 2253 CCAGTCGGGCGCTGCGGAGCTGCGGAGCGGCGCTGCGGAGCGGCGCGCTGCTTACGCG 2312
 DB 301 CCAGTCGGGCGCTGCGGAGCTGCGGAGCGGCGCTGCGGAGCGGCGCGCTGCTTACGCG 360

QY 2313 CTGCTTCCACTTCTGGGAGCGGCGGAGTCACTTTTATGAGCAAGTGTGCTACTT 2372
 DB 361 CTGCTTCCACTTCTGGGAGCGGCGGAGTCACTTTTATGAGCAAGTGTGCTACTT 420

QY 2373 GGTGTTCCGCTGCTTCTGCGGAGCTGCTGCTGAGATTTCCAGCGGCGGCGCGCG 2432
 DB 421 GGTGTTCCGCTGCTTCTGCGGAGCTGCTGCTGAGATTTCCAGCGGCGGCGCGCG 480

QY 2433 CTCCCTGGAGCTGCTGCTTATTTCTGGGCTTTTCAAGCTGCTGAGAGAACTGCGCA 2492
 DB 481 CTCCCTGGAGCTGCTGCTTATTTCTGGGCTTTTCAAGCTGCTGAGAGAACTGCGCA 540

QY 2493 GGGCTTGAAGGAGGCGGAGGAGCTTCTGCAAGCGGAGGCGCGGCTTGGCATGCTCT 2552
 DB 541 GGGCTTGAAGGAGGCGGAGGAGCTTCTGCAAGCGGAGGCGCGGCTTGGCATGCTCT 600

QY 2553 A-CTAGAGGAGGCGGAGGAGCTTCTGCAAGCGGAGGCGCGGCTTGGCATGCTCT 2611
 DB 601 A-CTAGAGGAGGCGGAGGAGCTTCTGCAAGCGGAGGCGCGGCTTGGCATGCTCT 659

QY 2612 CTCTACCTGCTTCTCTCTGAGG--GTGGGCTGCGGAGCTGAGCCCGGAGTTTGTACCACT 2669
 DB 660 CTCTACCTGCTTCTCTCTGAGG--GTGGGCTGCGGAGCTGAGCCCGGAGTTTGTACCACT 719

QY 2670 GGGCGGCACTGTCTCTGCTGACTTCACTG 2701
 DB 720 GGGCGGCACTGTCTCTGCTGACTTCACTG 751

RESULT 8
 CA488844 864 bp mRNA linear EST 14-NOV-2002
 LOCUS CA488844
 DEFINITION AGENCOURT 10808212 MAPcl Homo sapiens cDNA clone IMAGE:6721042 5',
 mRNA sequence.
 CA488844
 ACCESSION CA488844.1 GI:24951635
 VERSION EST.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 864)
 AUTHORS NIH-MGC <http://mgi.mgi.nhl.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Kristi A. Eglund, Ira Pastan
 cDNA Library Preparation: Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.llnl.gov>
 Plate: LLM14281 row: 1 column: 10
 High quality sequence stop: 571.
 Location/Qualifiers
 1..864
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6721042"
 /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
 hTERT-HME1, LNCaP"
 /lab_host="EMD110B"
 /clone_id="MAPcl"
 /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
 Subcloned with Brain, Liver, Lung, Kidney and muscle.
 Directionally cloned. Priming method: oligo-dT. Average
 insert size: 1800 bp. Library amplification: 26,000 fold.
 Kristi A. Eglund, James J. Vincent, Robert Strausberg,
 Bunkook Lee & Ira Pastan: Discovery of new breast
 cancer genes encoding membrane and secreted proteins..
 Manuscript submitted."

ORIGIN

Query Match 17.8%; Score 646.8; DB 6; Length 864;
 Best Local Similarity 94.4%; Pred. No. 2,9e-128;
 Matches 668; Conservative 0; Mismatches 33; Indels 1; Gaps 1;

QY 2894 GGGCTTCTACCGTCCCTACCTGACGATCTTGGGAGATTTCCAGAGAGACATGACG 2953
 DB 1 GGGCTTCTACCGTCCCTACCTGACGATCTTGGGAGATTTCCAGAGAGACATGACG 60

QY 2954 TGGCCCTATGAGAGACAGCAACTGCTGTGAGACCCGGCTTCTGGGACACCTCTCG 3013
 DB 61 TGGCCCTATGAGAGACAGCAACTGCTGTGAGACCCGGCTTCTGGGACACCTCTCG 120

QY 3014 GGGCCAGGCGGAGCACTGCGCTTCCAGTATGCAATGCTGTGAGTGTGCTCTCG 3073
 DB 121 GGGCCAGGCGGAGCACTGCGCTTCCAGTATGCAATGCTGTGAGTGTGCTCTCG 180

QY 3074 TCATCTTCTGCTGTCGCAACATCTGCTGTCACCTGCTCACTTGCATGTCAGTT 3133
 DB 181 TCATCTTCTGCTGTCGCAACATCTGCTGTCACCTGCTCACTTGCATGTCAGTT 240

QY 3134 ACAATTTGGGAAATACAGGCAACAGCATCTTCTAGAGAGCGGACGCTTACCGCC 3193
 DB 241 ACAATTTGGGAAATACAGGCAACAGCATCTTCTAGAGAGCGGACGCTTACCGCC 300

QY 3194 TCATCCGGAAATTCACCTCTGAGCCGCGCTGAGCCCGCTTATGCTATCTCCACT 3253
 DB 301 TCATCCGGAAATTCACCTCTGAGCCGCGCTGAGCCCGCTTATGCTATCTCCACT 360

QY 3254 TGGGCTCTCTGCTCAGGCAATTTGTCAGGCGACCCCGAGGCCCGAGCGTCTCCCGG 3313
 DB 361 TGGGCTCTCTGCTCAGGCAATTTGTCAGGCGACCCCGAGGCCCGAGCGTCTCCCGG 420

QY 3314 CCTGAGACATTTCCGGGTTTACCTTTCTAAGAGAGCGGAGAGCTGCTAAGTGG 3373
 DB 421 CCTGAGACATTTCCGGGTTTACCTTTCTAAGAGAGCGGAGAGCTGCTAAGTGG 480

QY 3374 AATGGTGATTAAGAGAACTTTCTGCTGAGCAGCGCTAGAGGACAGGCGGAGAGCT 3433
 DB 481 AATGGTGATTAAGAGAACTTTCTGCTGAGCAGCGCTAGAGGACAGGCGGAGAGCT 540

QY 3434 CCGAGCTGTGAAGCGCAGTCCAGAGGTGACTTGGCACTGAACAGCTGGAGACA 3493

Db 541 CCGAGCGCTGTAAGCGCAGCTCCAGAAAGTGACTTGCACTGAAGAGCTGGAGCA 600
 Qy 3494 TCCGGAGTACGAAGAAGCGCCCTGAAGTCT-GAGCGGGAGAGTCCAGAGTGTACCGC 3552
 Db 601 TCCGGAGTACGAAGAAGCGCCCTGAAGTCTTGAGAGCGGAGTCCAGAGTGTACGCGC 660
 Qy 3553 GTCCGTGGGTGGGTGGCGAGGCGCTGAGCGCGCTGCTGCTGCTGCC 3600
 Db 661 TCCCTGGGGGTGTTGNN 708

RESULT 9
 LOCUS BF311909
 DEFINITION 1090 bp mRNA linear EST 21-NOV-2000
 601897749F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:4126764 5',
 mRNA sequence.
 ACCESSION BF311909
 VERSION BF311909.1 GI:11259680
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 1090)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
 Plate: L1CM1017 row: b column: 13
 High quality sequence stop: 633.
 Location/Qualifiers
 1..1090
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4126764"
 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_1lb="NIH_MGC_19"
 /note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dt priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 17.5%; Score 637.4; DB 2; Length 1090;
 Best Local Similarity 89.6%; Pred. No. 3.1e-126;
 Matches 757; Conservative 0; Mismatches 71; Indels 17; Gaps 6;

Qy 1713 GGCACAGATGACATGACTTCTGGAGATGGGTTCCATGACAGTTTCTCAGCTTTGG 1772
 Db 182 GGCACAGATGACATGACTTCTGGAGATGGGTTCCATGACAGTTTCTCAGCTTTGG 241
 Qy 1773 GGCCTGTTGCTCTCCGGGTGATGACAGCGCTTGAGCTTACGCTTGAGAGGACAGC 1832
 Db 242 GGCCTGTTGCTCTCCGGGTGATGACAGCGCTTGAGCTTACGCTTGAGAGGACAGC 301
 Qy 1833 GAGGAAAGACCTGGCGTTCAAGTTTGAAGGGATGGGCTTGAACCTTTGGCGAGTGTCTA 1892
 Db 302 GAGGAAAGACCTGGCGTTCAAGTTTGAAGGGATGGGCTTGAACCTTTGGCGAGTGTCTA 361
 Qy 1893 TCGCAGCAGTGAAGGAGGCTGCGCGCTCTCTCGTGCCTGCGCTTGAGGAGGA 1952
 Db 362 TCGCAGCAGTGAAGGAGGCTGCGCGCTCTCTCGTGCCTGCGCTTGAGGAGGA 421
 Qy 1953 TGCACATTGCTTCCAGCTGAGCATGACAGTGAAGCGCGCTTCTTTGGCCAGAGATG 2012
 Db 422 TGCACATTGCTTCCAGCTGAGCATGACAGTGAAGCGCGCTTCTTTGGCCAGAGATG 481
 Qy 2013 GTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATGTGGCCAGCACTACACCATCTG 2072
 Db 482 GTACAGTCTCTGCTGACACAGAAAGTGTGGGAGATGTGGCCAGCACTACACCATCTG 541
 Qy 2073 GGCCTGTTGCTGCGCTTCTTTGGCGCTTCACTATCACCGCGCTTACCTTGG 2132
 Db 542 GGCCTGTTGCTGCGCTTCTTTGGCGCTTCACTATCACCGCGCTTACCTTGG 601
 Qy 2133 GAAATCAGAAAGAGAGCCACACAGGAGAGCTA--GAGTTTGAATGATAT--GTGT 2186
 Db 602 GAAATCAGAAAGAGAG--CCACACGAGAGAGCTAAGAGTTTGAATGATATGAGTCA 660
 Qy 2187 CATTAATGGGAGAGGCGCTGTGCGGACGCGGGA---CCAGCCGAAAGAGCGCTGG 2243
 Db 661 TTAATGAGGCGCAAGGCGGTGTCCGGAGCGGAGACCAAGCCGAGAGAGCGCTGG 720
 Qy 2244 GATCCCGCGG-----CAAGTGGGCGGTGCGGCTTGTGCGGCGGCGG--GCTGCGGCGGCG 2296
 Db 721 GATCCCGCGGCGCAACCGGCGCGGCGGCGGAGCGCATGAGGCGCGGCGGCGG 780
 Qy 2297 GCGGATGCTACGCGCGCTGTGCTTCCACTTGTGGGCGCGCGCGGTGACCATTTTCATGAGCA 2356
 Db 781 CCGGCGGCGCAAGCGGATGAGGTCACTTGAAGGCGGCGCATGACCATCTCGGCGGCA 840
 Qy 2357 ACGTG 2361
 Db 841 ACGG 845

RESULT 10
 LOCUS BF159746
 DEFINITION 672 bp mRNA linear EST 25-SEP-2001
 603045620F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5185949 5',
 mRNA sequence.
 ACCESSION BF159746
 VERSION BF159746.1 GI:15751324
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 672)
 NIH-MGC http://mgs.nci.nih.gov/.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

OY		2888	TGCGCCGGCTTTCTTACAGTCCTCCTTACGTGCACATCTTGCGGCAAGATTCCCCAAGAAGACA	294
Db		361	TGCGCCGGCTTTCTTACAGTCCTCCTTACGTGCACATCTTGCGGCAAGATTCCCCAAGAAGACA	420
OY		2948	TGACGTGAGCCCTCATGAGCACAGCAACTGCTGTCGAGAGCCCGGCTTCTGGGACACC	3007
Db		421	TGACGTGAGCCCTCATGAGCACAGCAACTGCTGTCGAGAGCCCGGCTTCTGGGACACC	480
OY		3008	CTCCTGGGGGCCAGGCGGACACCTGCTGCTCCAGTAATGCCAACTGGCTGTGTGCTGC	3067
Db		481	CTCCTGGGGGCCAGGCGGACACCTGCTGCTCCAGTAATGCCAACTGGCTGTGTGCTGC	540
OY		3068	TCCTGCTGATCTTCTGCTGCGGGCAACATCCTGCTGGTCAACTTGCTATTGTCATGT	3122
Db		541	TCCTGCTGATCTTCTGCTGCGGGCAACATCCTGCTGGTCAACTTGCTATTGTCATGT	600
OY		3128	TCAGTTACACATT	3140
Db		601	TCAGTTACACATT	613
RESULT_12				
LOCUS		BE905591	804 bp	mRNA linear EST 20-OCT-2000
DEFINITION		601495244P1 NIH_MGC_70 Homo sapiens CDNA clone IMAGE:3897275 5',		
ACCESSION		BE905591		
VERSION		BE905591.1 GI:10398932		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL		1 (bases 1 to 804)		
COMMENT		NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgsabbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN). DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.llnl.gov Plate: LLM9691 row: h column: 12 High quality sequence stop: 566. Location/Qualifiers 1..804 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone_image="IMAGE:3897275" /tissue_type="epithelioid carcinoma" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH MGC 70" /note="Organ: pancreas; Vector: pCMV-Sport6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.1 kb. Library constructed by Life Technologies."		
FEATURES				
source				
ORIGIN				
Query Match		16.3%	Score 595.4;	DB 2; Length 804;
Best Local Similarity		91.0%;	Pred. No. 3.3e-117;	
Matches 694;		Conservative 0;	Mismatches 51;	Indels 18; Gaps 5;
OY		1310	GGCCTGAATTGCTGCGCTTGCTCATTTCCACAGGCTCAGCCTGAGCACTTCTGACCC	1369
Db		1	GGCCTGAATTGCTGCGCTTGCTCATTTCCACAGGCTCAGCCTGAGCACTTCTGACCC	60
OY		1370	CGATGCGCCTTGCCCACTTCAACAGCGCGGCCCTTCCAACCTGCTATCCGCAACTTT	14299

Db	61	CGATGCGCTG6CCCAACTTACAGCGGGGCGCCTTCCACTGCGTCAATCCGCACTTT	120
QY	1430	TGAGACAGGCGTCCCAACAGCGGACCAAGCCCAAGCCCTAAAGGGGAGCTGCGG	148
Db	121	TGACACAGGCGTCCCAACAGCGGACCAAGCCCAAGCCCTAAAGGGGAGCTGCGG	180
QY	1430	AGCTCGGCGCTTGAAGTGGGAGCTGTGTGAGGATGTGTGTGGGGAAGATGTGCGCG	154
Db	181	AGCTCGGCGCTTGAAGTGGGAGCTGTGTGAGGATGTGTGTGGGGAAGATGTGCGCG	240
QY	1550	CGAGGTACCCCTCGGGGGGCGCTGGGAGCCCTACCCAGGCGCAGGGCTTGGGAGAGCA	160
Db	241	CGAGGTACCCCTCGGGGGGCGCTGGGAGCCCTACCCAGGCGCA-GGCTTGGGAGAGCA	299
QY	1610	TGTATCTGCTCTCGGACAAAGGCACTTGCGGCTCTCGGTGATGCTGAGCTCGGAGAG	166
Db	300	TGTATCTGCTCTCGGACAAAGGCACTTGCGGCTCTCGGTGATGCTGAGCTCGGAGAG	359
QY	1670	CCCCCTGAGGAGCACTGCTTTCTTTGGGACATGTGTGCTGAACAGGCAAGATGGCATGT	172
Db	360	CCCCCTGAGGAGCACTGCTTTCTTTGGGACATGTGTGCTGAACAGGCAAGATGGCATGT	419
QY	1730	ACTTCTGGGAGATGGGATTCGAATGAGTTGCTCAGCTCTTGGGGCTGTTGCTGCTCC	178
Db	420	ACTTCTGGGAGATGGGATTCGAATGAGTTGCTCAGCTCTTGGGGCTGTTGCTGCTCC	479
QY	1790	GGGTGATGGACGCTTGAGGCTTGACGCTGAGAGGAGGACAGCAGAGAAAGCATGGGCT	184
Db	480	GGGTGATGGACGCTTGAGGCTTGACGCTGAGAGGAGGACCCGAGAGAAAGCATGGGCT	539
QY	1850	TCAGATTGAGGGAGTGGGCGTTGACCTCTTTGGGAGTGCT-----ATGCAGC	189
Db	540	TCAGATTGAGGGAGTGGGCGTTGACCTCTTTGGGAGTGGCTTTCCGACAGCACGGAG	599
QY	1900	AGTAGGTGAGGGGCTGCCCCGCTCTCC--TCGTCGCTGCCGCTTGGGGGAGTAGCA	195
Db	600	GTTAGGGGCTG3CCGCTTCTCTCTCCGTCGCTGCGCCGCTTG3GGGGAGTAGCA	659
QY	1958	CTTG--CCTCAGCTGGCCATGCAAGCTGACGCCGCTCTTCTTTG---CCAGAGTAG	201
Db	660	CTTGCCCTTCGAATGGGCAATGCACTTGAAGCCCGTCTCTTTTGCCCCCGGTGTGG	719
QY	2013	GGTACAGTCTCTGTCACACAGAAAGTGTGGGAGAGATATGGCC	2055
Db	720	GGTACAGTCTCTGTCGCGCCCAACATGAGGGGCGGATGGC	762

RESULT 13

AK035197

LOCUS

DEFINITION

AK035197

3449 bp

mRNA

linear

HTC 03-APR-2004

AK035197

Mus musculus 12 days embryo embryonic body between diaphragm region16

and neck cDNA, RIKEN full-length enriched library, clone 943099A16

product:transient receptor potential cation channel, subfamily M,

member 5, full insert sequence.

AK035197

AK035197.1

GI:26330491

HTC; CAP trapper.

AK035197

Mus musculus (house mouse)

AK035197

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Garnicci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Wech. Enzymol. 303, 19-44 (1999)

2

Garnicci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

TITLE

JOURNAL MEDLINE
20499374
PUBMED
11042159
REFERENCE
AUTHORS
3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komoto,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watanabe,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL MEDLINE
20530913
PUBMED
11078661
REFERENCE
AUTHORS
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL MEDLINE
20530913
PUBMED
11078661
REFERENCE
AUTHORS
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL MEDLINE
20530913
PUBMED
11078661
REFERENCE
AUTHORS
6
(Bases 1 to 3449)
Fukuchi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Akiyama,J., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Komoto,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Nunazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail:genome-res@gscc.riken.jp, URL:htp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

JOURNAL MEDLINE
20530913
PUBMED
11078661
REFERENCE
AUTHORS
7
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:htp://genome.gsc.riken.jp/
URL:htp://fantom.gsc.riken.jp/.
Location/Qualifiers
1. 3449
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1. 3094
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QY 656 ACGGGGTCAGTTTCCCTGGACTAACACTACTCGGCTTCTTCTGTGTGACGACGCA 715
DB 132 AGGGACCCCTCGCCCTCGGACACCAATCTCTCCACTTCACTTGTGTGAGTGAGCG 191
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REFERENCE	1	Carninci, P. and Hayashizaki, Y.	
AUTHORS	1	Carninci, P. and Hayashizaki, Y.	
TITLE	1	High-efficiency full-length cDNA cloning	
JOURNAL	1	Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE	1	99279253	
PUBMED	1	10349636	
REFERENCE	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
AUTHORS	2	Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
TITLE	2	Normalization and subtraction of cap-trapper-selected cDNAs to	
JOURNAL	2	prepare full-length cDNA libraries for rapid discovery of new genes	
MEDLINE	2	Genome Res. 10 (10), 1617-1630 (2000)	
PUBMED	2	20499374	
REFERENCE	3	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,	
AUTHORS	3	Kono, H., Akiyama, J., Nishi, K., Katsunaka, T., Teshiro, H., Itoh, M.,	
TITLE	3	Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,	
JOURNAL	3	Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kasai, K.,	
MEDLINE	3	Fujimaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,	
PUBMED	3	Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,	
REFERENCE	4	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
AUTHORS	4	RIKEN integrated sequence analysis (RISA) system--384-format	
TITLE	4	sequencing pipeline with 384 multicapillary sequencer	
JOURNAL	4	Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE	4	20530913	
PUBMED	4	11076861	
REFERENCE	5	The RIKEN Genome Exploration Research Group Phase II Team and the	
AUTHORS	5	PANTOM Consortium.	
TITLE	5	Functional annotation of a full-length mouse cDNA collection	
JOURNAL	5	Nature 409, 685-690 (2001)	
MEDLINE	5	11076861	
PUBMED	5	11076861	
REFERENCE	6	The FANTOM Consortium and the RIKEN Genome Exploration Research	
AUTHORS	6	Group Phase I & II Team.	
TITLE	6	Analysis of the mouse transcriptome based on functional annotation	
JOURNAL	6	Nature 420, 563-573 (2002)	
MEDLINE	6	11076861	
PUBMED	6	11076861	
REFERENCE	7	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,	
AUTHORS	7	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,	
TITLE	7	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,	
JOURNAL	7	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,	
MEDLINE	7	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,	
PUBMED	7	Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,	
REFERENCE	8	Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N.,	
AUTHORS	8	Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,	
TITLE	8	Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shitaki, T.,	
JOURNAL	8	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S.,	
MEDLINE	8	11076861	
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REFERENCE	9	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,	
AUTHORS	9	Muramatsu, M. and Hayashizaki, Y.	
TITLE	9	Submitted (16-JUL-2001) Yoshinori Hayashizaki, The Institute of	
JOURNAL	9	Physical and Chemical Research (RIKEN), Laboratory for Genome	
MEDLINE	9	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	
PUBMED	9	RIKEN Yokohama Institute, 1-7-22 Suenho-cho, Tsukuba-Ku, Yokohama,	
REFERENCE	10	Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,	
AUTHORS	10	URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,	
TITLE	10	Fax: 81-45-503-9216)	
JOURNAL	10	cDNA library was prepared and sequenced in Mouse Genome	
MEDLINE	10	Encyclopedia Project of Genome Exploration Research Group in Riken	
PUBMED	10	Genomic Sciences Center and Genome Science Laboratory in RIKEN.	
REFERENCE	11	Division of Experimental Animal Research in Riken contributed to	
AUTHORS	11	prepare mouse tissues.	
TITLE	11	Tissues were provided by Dr. Tomohiro Kono (Department of Animal	
JOURNAL	11	Science, Tokyo University of Agriculture, 1737 Huroko Atsugi City,	
MEDLINE	11	Kanagawa Prefecture, Japan) whose assistance we gratefully	
PUBMED	11	acknowledge.	
REFERENCE	12	Please visit our web site for further details.	
AUTHORS	12	URL: http://genome.gsc.riken.jp/	
TITLE	12	URL: http://fantom.gsc.riken.jp/	
JOURNAL	12	Location/Qualifiers	
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PUBMED	14	evidence: BLASTN, 99%, match=3363]"	
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AUTHORS	15	16.3%; Score 594.4; DB 3; Length 3998;	
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AUTHORS	16	397 TGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 456	
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AUTHORS	17	577 AGTGTCTCTTGGAGACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 636	
TITLE	17	QY 1070 GGAGAGCTCTCTGACAGCTTATTTCTGCT--AGATGAGGCTGAGGAGATTCGAGACCA 1126	

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Db	697	TCATCTCAGAGCACTTGTGAAGGCTGTGAAGGCAACGCCAAGAAAGCCCAAGACTAC	756
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Db	1113	CGCGACTCAAAAGACTTCCTGATGACGCGCTGCGTGGCTTCTACAGAGAGCGGCGCAG	1172
Oy	1597	TTCCGGGAGAGATATATCTGCTCTCGACAAAGGCACTCGCGGCTCTCGTGTGATGCT	1656
Db	1173	ATGAGAGAGAGAGGCGCACTTAAGCGGCGCCGACGAGCCAGAAATGGCTCCAGACTCACT	1232
Oy	1657	GAGCTCGGAGAGGCGCCCTGTGAGCACTGCTCTTTGAGGCACTGTGTCTGAACAGGAGCA	1716
Db	1233	AGGAAGATGAAGACCTTGTGAAGGACCTGTTCCTCTGGGCTGTGTCTGCAAGATGTTAT	1292
Oy	1717	CAGATGACCATGTACTTCTGGAGATGGGATTCCAATGCAATTTCTCACTCTTGGGGCC	1776
Db	1293	GAGATGGCCACATTACTTCGTGGGCCATGGGCGGAGGGGTGGCGTGTCTCTGTGCTCC	1350
Oy	1777	TGTTTGTCTGCTCCGGGTATGCGACGCTTGAAGCTTGAACGCTGAGAGAGGCAACGAGG	1836
Db	1353	TGCAAGATCATAAAGAAATGTCCACCTTGAGAAAGGACAGAGTGGCCCGCACATG	1412
Oy	1897	AAAGACCTGGGCTCAAGTTTGAAGGGAGATGGGCGTGTGACTCTTTGGAGAGTGCATATGC	1896
Db	1413	CGTGA-----GGCCAATGATGAGAGCTGGGCTCGAATCTTTTCTCAAGAGTCAAGGCGC	1466
Oy	1897	AGCAGTAGTGAAGGCTGCGCCGCTCTCTCTCCGCTCCGCTCTGGGGGATATCC	1956
Db	1467	AAACGTAGGAAACCGTGTCTTGGCTCTGTGTGTGCGAAGAACCAAGCTGAGACGAGAC	1526
Oy	1957	ACTTGGCTCCAGCTGGCCATGCAAGCTACGCGCGGTCTTTTGGCCAGAGTGGGTA	2016
Db	1527	ACGTGTCCGTGACCTGGCCACTGAAAGCTGATGCAAGGCGCTTCTTGGCCATGACGATGTG	1586
Oy	2017	CAGTCTGCGTGAACAGAAATGTGTGGGGAATATGCGCAAGCACTAACCCATCTGGGCC	2076
Db	1587	CAAAGATTCCTGACCAAGATCTGTGTGGGGAAGCATGGCCACAGGACACCAATCTTACGG	1646
Oy	2077	CTGGTCTCGGCTTCTTTTGGCCCTTCATCTTACACCGGCTCATACCTTCAGAAA	2136
Db	1647	CTTCTGGGTGCTTCACTGCTCCAGCCCTCATCTACCAAACTCATCTCTTCACTAGTAG	1706
Oy	2137	TCAGAGAGAGGCCACACAGGAGGAGCTTAAGTTGAATGATGATGTCATTATAGGG	2196
Db	1707	GATGCCCCCGCAGAGGATGAACCTAGAAATCTGCGAGAGGCCAGACAGCTTGGAATGGAA	1766

QY	2197	GAGGGCCCTGTTCGGAGCGGCGGAGCCAGCCAGAAAGACGCCGCTGGGGGTCCCGCGGAC	2256
Db	1767	AAGAGCTTCCATATGACAGCCGGGTGGCCAAATTGAGAGAACTTCAAGAGGCCAAGGGCT	1826
QY	2257	TGCGGCGCGCTCCGGGTGTGTCGGGGGGCGCGTCGGGGGGGGCGCGGTGCTACGCGCGCTGG	2316
Db	1827	CCAGGCGCATGAGGCGCGGAAGTGCCTTC-----CTGCTACACGGTGG	1871
QY	2317	TTCCACTCTGCGGGGCGCGCGGTAGACATCTTCAATGGGCAACGTCAGCTACCTGCTG	2376
Db	1872	AGGAAGTCTGGGGGCGCTCTGTACTGTCTTCCTGGGGAAATGTGTACTTTCGCA	1931
QY	2377	TTCTGCTGCTTTTCTCGGGGTCTGTCGTGAAATTTCAAGCGCGCGCGCCGCTCC	2436
Db	1932	TTCCCTCTTCCTGTTACCTATGTCTGTGGTGAATTTCAAGGCCACACCCCAAGGGCGG	1991
QY	2437	CTG-----GAGCTGCTGCTTATTTTCTGGGCTTTCAAGCTGCTGTGAGAACTGCGC	2490
Db	1992	TCGTGATCCGAGGTACCTCTATTTTCTGGGTGTTCACACTGTGCTGAGAAATCCGA	2051
QY	2491	CAGGCGCTGACCGAGGCGGGGGAGCGCTCCGACCGGGGGCGCCGGGCTGGCATGCC	2550
Db	2052	CAGGCGCTTCTCAAGATGAGAGAACGAC-----	2081
QY	2551	TCACTGAGCCAGCGCGCTGCGCTTACCTCGCCAGACCTGGAACAGTGGACTATGTG	2610
Db	2082	---CTGGTGAAGAAATTCATCTGTATGTGAAACAACTGGAACATGTGTGACATGTG	2138
QY	2611	GCTCTCACCTGCTTCTCTCTGGGCGTGGGCTGCCGCTGACCCCGGGTTGTACACCTG	2670
Db	2139	GCCATCTTCTCGTTTCATATGTGGAGTACACCTGTGAATGTGGCCCTCGGTGTGAAGCT	2198
QY	2671	GGCGGACTGTCTCTGTGATGACCTTATGAGTTTTCAGGTGGGCTCTTACATGTTTC	2730
Db	2199	GGCAGAGCCGTTCTGGCCATTGACTTCAATGGTGTTCACCTTGGCTCATTCACATCTTT	2258
QY	2731	ACGGTCAACAAACAGCTGGGGCCCAAGATCGTCACTGTGAGCAAGATGATGAAGAGCTG	2790
Db	2259	GCTATTCAACAAAGATTGGGCTCTTAAGTATCATTTGTAAAGCAATGATGAAGATGTC	2318
QY	2791	TTCTTTCTCTCTTCTTCTCTCTGGCGTGTGCTGTGACCTATGGCGTGGCCACGAGAGGG	2850
Db	2319	TTCTTTTTCCTCTTCTCTCTGAGCGTATGGCTTGTGCTATGTGTGACACATCAGGCC	2378
QY	2851	CTCCTGAGGCCAGCGGACAGTGAATTTCCCAAGTATCTGTGGCGCGCTTCTACACCTGCC	2910
Db	2379	CTGTGTGATCCCAAGATGGCGGCTTGTGAAGTATTTTCGCGCGTGTGCTAATACAGCTT	2438
QY	2911	TACCTGAGATCTTCGGGACAGATTCCCGAGAGAGACATGACGTGGCCCTCATGGAGCAC	2970
Db	2439	TACCTGAGATCTTTGGGCAATCTCTCTGTGATGAATGATGAGGCTCGTGTGAATCG-	2497
QY	2971	AGCAATGCTCTGTGAGGCCGCGCTTGTGGACACACCTCCTGGGAGCCAGCGGAGCA-C	3029
Db	2498	-----TTCTTTACCCCTGTGTGTGAAGAGCTGGCTTC	2533
QY	3030	CTGGGTCTCCAGATATGCCACTGTGCTGTGTGTGTCTCTGTATCTTCTGTCTGT	3089
Db	2534	CTGGCTTAATCTCATATGCAACATGGCGTGTGATCTTCTCTGTGTATCTTCTCGTGTGT	2593
QY	3090	GGCAACATCTGTGTGACACTTGTGCATTTGGCAATGTAGTTAGTTACATTTCCGCAAGT	3149
Db	2594	CACTAATGTGTGTCTATGAACCTTCTGTATGTGCATTTACGCTACCAATTTCAAGTGT	2653
QY	3150	ACAGGCGAACAGCGCATCTTACTGGAAGGCGAGCGTTACCGGCTCATCCGGGAAATTC	3209
Db	2654	GCAAGGCAATGACAACTATTTGTGAAGTTTCAACGCTACCACTCATCTGTGAATTC	2713
QY	3210	CTCTGGCGCGCTGGCGCCCGCTTATATGTATCTTCCACTTGTGCTCTCTGTCA	3269
Db	2714	TGGAAGACAGCTCTGGCGCCCGCTTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2773

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: June 12, 2005, 04:57:16 ; Search time 1216.46 Seconds
(without alignments)
17723.358 Million cell updates/sec

Title: US-09-869-486b-29_COPY_73_3714
Perfect score: 3642
Sequence: 1 atgctgctgcgcgagaaga.....acctgcctgcggtccaagac 3642

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_16Dec04:*
2: geneseqn1980s:*
3: geneseqn1990s:*
4: geneseqn2000s:*
5: geneseqn2001as:*
6: geneseqn2001bs:*
7: geneseqn2002as:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3642	100.0	4061	3	AAA49923 Human cal
2	3642	100.0	4061	10	ADH62711 Ca activa
3	3642	100.0	4061	13	ADR73511 Human TRP
4	3642	100.0	4061	13	ADSL2774 Transient
5	3640.4	100.0	4061	13	ADSL2774 Human Trp
6	3498	96.0	3501	6	ABK92224 Prostate
7	3498	96.0	3501	11	ADN39597 Cancer/an
8	3498	96.0	4641	11	ADN39239 Cancer/an
9	3473.8	95.4	3898	12	ADL06463 Human tum
10	3421.2	93.9	3810	6	ABK92167 Prostate
11	3421.2	93.9	3810	13	ADR66772 Human pro
12	3421.2	93.9	3810	13	ADR65869 Human pro
13	3421.2	93.9	3810	13	ADSL2778 Human TRP
14	3374.4	92.7	3900	5	AAH76383 Human TLC
15	3374.4	92.7	3900	8	ABK58941 Human tira
16	3374.4	92.7	3900	12	ADH51622 Human 186
17	3373.8	92.6	3387	5	AAH76384 Human TLC
18	3373.8	92.6	3390	12	ADH51624 Human 186
19	3253.4	89.3	3599	6	ABK28677 Human CDN
20	3199.8	87.9	3676	12	ADQ83682 Human tum

21	3199.8	87.9	3676	13	ADQ85834	Adq85834 Human tum
22	3199.8	87.9	3676	13	ADQ86998	Adq86998 Human tum
23	3196.6	87.8	3701	13	ADSL2776	Adsl2776 Transient
24	3052	83.8	3583	11	ADL33391	Adl33391 Human tira
25	2269.4	62.3	2695	5	AAH76383	AAH76383 Human Trp
26	2073.4	56.9	2459	12	ADL06424	ADL06424 Human tum
27	1911	52.5	2393	3	AAV26656	AAV26656 Human PSI
28	1911	52.5	2393	3	AAA64090	AAA64090 Consensus
29	1892.2	52.0	2180	3	AAA49921	AAA49921 Human cal
30	1240.8	34.1	2176	12	ADQ96621	Adq96621 Human PSI
31	1158	31.8	1524	2	AAV58585	AAV58585 Prostate
32	1158	31.8	1524	2	AAV61200	AAV61200 Full leng
33	1158	31.8	1524	3	AAA06348	AAA06348 Human imm
34	1158	31.8	1524	3	ABK71253	ABK71253 Human pro
35	1158	31.8	1524	4	AAH93464	AAH93464 Human pro
36	1158	31.8	1524	4	AAH63556	AAH63556 Human pro
37	1158	31.8	1524	4	AAH02529	AAH02529 Prostate
38	1158	31.8	1524	4	AAH84778	AAH84778 Human pro
39	1158	31.8	1524	5	ACA59365	ACA59365 Prostate
40	1158	31.8	1524	5	AAH10107	AAH10107 Human pro
41	1158	31.8	1524	6	ABL94928	ABL94928 Human J1-
42	1158	31.8	1524	6	ABK58637	ABK58637 Prostate
43	1158	31.8	1524	8	ACC95092	ACC95092 Prostate
44	1158	31.8	1524	10	ADBL3559	ADBL3559 Human pro
45	1158	31.8	1524	10	ADG25975	Adg25975 Human pro

ALIGNMENTS

RESULT 1
ID AAA49923 standard; CDNA; 4061 BP.
AC AAA49923;
DT 10-OCT-2000 (first entry)
XX Human calcium channel SOC-3/CRAC-2 CDNA.
DE SOC-2/CRAC-1; calcium channel; human; store operated channel;
KW calcium release activated channel; therapy; diagnosis;
XX lymphocyte proliferative disorder; ss.
XX
OS Homo sapiens.
FH
FH Key Location/Qualifiers
FT CDS 382..5979 /*tag= a
FT
XX
XX W0200040614-A2.
XX
XX 13-JUL-2000.
XX
XX 20-DEC-1999; 99WO-US029996.
XX
XX 30-DEC-1998; 98US-0114220P.
XX 29-JAN-1999; 99US-0120018P.
XX 22-JUN-1999; 99US-0140415P.
XX
XX (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
XX Scharenberg AM;
XX WPI; 2000-465957/40.
XX P-PSDB; AAY95436.
XX
XX New SOC/CRAC calcium channel polynucleotides and polypeptides used to
XX diagnose and treat proliferative disorders associated with the channel,
XX and to screen for novel modulators of the channel.
XX
XX Claim 1(a); Page 99-100; 108pp; English.

QY	1741	ATGGGTCCTCAAGCAGTTTCCCACTCTCTGGGGGCTGTGGCTCCGGGTATATGCA	1800
Db	1813	ATGGGTTCCATATCAGATTTCCTCACTCTTGGGGCTGTGTCTCCGGGTATATGCA	1872
QY	1801	CGCCTGAGACCTGACGCTGAGAGGACGACAGGAGAAAGACTTGGCTTCAATTTAG	1866
Db	1873	CGCCTGAGAGCTGACGCTGAGAGGACGACAGGAGAAAGACTTGGCTTCAATTTAG	1933
QY	1861	GGGATGGGCGTTGACCTCTTTGGCGATGCTATCGACAGTGAAGTGAAGGCTGCCG	1920
Db	1933	GGGATGGGCGTTGACCTCTTTGGCGATGCTATCGACAGTGAAGTGAAGGCTGCCG	1992
QY	1921	CTCCCTCCGCGGTGCGCCGCTCTGGGGGGATGCGACCTTGGCTCACTGGCCATGCA	1988
Db	1993	CTCCCTCCGCGGTGCGCCGCTCTGGGGGGATGCGACCTTGGCTCACTGGCCATGCA	2052
QY	1981	GCTGACGCCCGTGCCTTCTTTGGCCAGAGTGGGGATACAGTCTCTCTGACACAGATGG	2044
Db	2053	GCTGACGCCCGTGCCTTCTTTGGCCAGAGTGGGGATACAGTCTCTCTGACACAGATGG	2112
QY	2041	TGGGGAGATATAGCCAGCACTACACCCATCTTGGGCGCTTGTCTTCGCTTCTTTGCCCT	2100
Db	2113	TGGGGAGATATAGCCAGCACTACACCCATCTTGGGCGCTTGTCTTCGCTTCTTTGCCCT	2172
QY	2101	CCACTCATCTTACACCCGCTCATCATCTTTCAGAGAAATAGAAAGAGAGCCACAGGAG	2166
Db	2173	CCACTCATCTTACACCCGCTCATCATCTTTCAGAGAAATAGAAAGAGAGCCACAGGAG	2232
QY	2161	GAGCTAGAGTTTGAATGATAGTGTCAATTATGGGAGAGGGCGCTGTGGGACCGCGAG	2220
Db	2233	GAGCTAGAGTTTGAATGATAGTGTCAATTATGGGAGAGGGCGCTGTGGGACCGCGAG	2292
QY	2221	CCAGCCGAGAAAGACGCGCTGGGGGTCCCGCGCAGTGGGCGCGTCCGGTTTGTCTGCGG	2288
Db	2293	CCAGCCGAGAAAGACGCGCTGGGGGTCCCGCGCAGTGGGCGCGTCCGGTTTGTCTGCGG	2352
QY	2281	GGCCGCTTGGGGGGGGCGCGGTGCTACGCGCTGTGTTCACCTTCTGGGGCGCGCGGTG	2340
Db	2353	GGCCGCTTGGGGGGGGCGCGGTGCTACGCGCTGTGTTCACCTTCTGGGGCGCGCGGTG	2412
QY	2341	ACCATCTTCAATGGGCAAGTGAATGAGTCAAGCTGATCCAGCTGCTTTTCTCCGCGGTG	2400
Db	2413	ACCATCTTCAATGGGCAAGTGAATGAGTCAAGCTGATCCAGCTGCTTTTCTCCGCGGTG	2472
QY	2401	CTGCTCGTGATTTTCCAGCCGAGCGCGCGCTCCCTGAGACTGTGCTTCAATTTCTGG	2460
Db	2473	CTGCTCGTGATTTTCCAGCCGAGCGCGCGCTCCCTGAGACTGTGCTTCAATTTCTGG	2532
QY	2461	GCTTTCAAGCTGTGTGTGAGAGAACTGTGGCAGAGGCGCTGAGCGAGCGGGGCAAGCTC	2520
Db	2533	GCTTTCAAGCTGTGTGTGAGAGAACTGTGGCAGAGGCGCTGAGCGAGCGGGGCAAGCTC	2592
QY	2521	GCCAGCGGAGGCGCCCGGGGCTGGGCAATGSCCTCATAGGCGAGCGGCTCTCACTC	2580
Db	2593	GCCAGCGGAGGCGCCCGGGGCTGGGCAATGSCCTCATAGGCGAGCGGCTCTCACTC	2652
QY	2581	GCCGACAGCTGGAACCAAGTGGCACTAGTGGCTCTCACTGCTTCTCTTGGGCGTGGG	2640
Db	2653	GCCGACAGCTGGAACCAAGTGGCACTAGTGGCTCTCACTGCTTCTCTTGGGCGTGGG	2712
QY	2641	TGCGGGCTGACCCCGGGGTTTGTACCACTGGGGCGCACTGTCTCTGTGATGACTTCAATG	2700
Db	2713	TGCGGGCTGACCCCGGGGTTTGTACCACTGGGGCGCACTGTCTCTGTGATGACTTCAATG	2772
QY	2701	GTTTTCACGGGCGGAGCTTCAATCTTTCACGGTCAACAAACAGCTGGGGCCCAAGATC	2760
Db	2773	GTTTTCACGGGCGGAGCTTCAATCTTTCACGGTCAACAAACAGCTGGGGCCCAAGATC	2832
QY	2761	GTCATCTGAGCAAGATGATAGAGACGTGTCTTCTTCTCTCTTCTTCTGCGGCTGTGG	2820
Db	2833	GTCATCTGAGCAAGATGATAGAGACGTGTCTTCTTCTCTCTCTTCTTCTGCGGCTGTGG	2892
QY	2821	CTGGTAGCTTATGCGGTGGCCACGAGAGGGCTCTGAGGCGACGGGACAGTGACTTCCCA	2880

Db	2893	CTGGTAGCCCTAATGGCGTGGCCACGAGGAGGAGCTCTCTGAGGCCACGAGACATGACTTCCCA	2952
Qy	2881	AGTATCCCTGACCCCGCGGTCTTCTAACCGTCCCTACCTGACAGATCTTCGGGACAGATTCGCCAG	2940
Db	2993	AGTATCCCTGACCCCGCGGTCTTCTAACCGTCCCTACCTGACAGATCTTCGGGACAGATTCGCCAG	3012
Qy	2941	GAGGACATGACGTGGCCCTCATGAGACACAGACTGCTGCTGGAGCCCGGCTTCGG	3000
Db	3013	GAGGACATGACGTGGCCCTCATGAGACACAGACTGCTGCTGGAGCCCGGCTTCGG	3072
Qy	3001	GCAACCCCTCTGGGGGCCAGCGGACCTGCGCTTCCAGTATGCCAATTGGCTGTG	3066
Db	3073	GCAACCCCTCTGGGGGCCAGCGGACCTGCGCTTCCAGTATGCCAATTGGCTGTG	3132
Qy	3061	GTGCTGCTCCTCGTCACTTCTCTGCTGGGCAACAATCCTGCTGATCAATTGCTCATTT	3120
Db	3133	GTGCTGCTCCTCGTCACTTCTCTGCTGGGCAACAATCCTGCTGATCAATTGCTCATTT	3192
Qy	3121	GCCATGTTCACTTACATCAATTCGGGAAAGTACAGGGCAACAGCATCTTACTGAGAGCG	3180
Db	3193	GCCATGTTCACTTACATCAATTCGGGAAAGTACAGGGCAACAGCATCTTACTGAGAGCG	3252
Qy	3181	CAGGTTAACCGCTCATTCGGGAAATTCACCTCTGGGCCCGGCTGGGCCCTTTATC	3240
Db	3253	CAGGTTAACCGCTCATTCGGGAAATTCACCTCTGGGCCCGGCTGGGCCCTTTATC	3312
Qy	3241	GTCAATCTCCCACTTGGCGCTCTGCTCAGGCAATTTGTGACAGCCGAGGCCCGCAG	3300
Db	3313	GTCAATCTCCCACTTGGCGCTCTGCTCAGGCAATTTGTGACAGCCGAGGCCCGCAG	3372
Qy	3301	CCGTCCTCCCGCGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGAG	3360
Db	3373	CCGTCCTCCCGCGCCCTCGAGCATTTCCGGGTTTACCTTTCTAAGGAAGCCGAGAG	3432
Qy	3351	CTGCTTAACGTGGGAATGGGTGCATTAAGAGAACTTTCTGCTGCAACGCGCTAGGGAAG	3420
Db	3433	CTGCTTAACGTGGGAATGGGTGCATTAAGAGAACTTTCTGCTGCAACGCGCTAGGGAAG	3492
Qy	3421	CGGAGAGACGACTCGAGACGCTGTAACGGACCGCTCCAGAAAGTGGACTTGGCACTGAA	3480
Db	3493	CGGAGAGACGACTCGAGACGCTGTAACGGACCGCTCCAGAAAGTGGACTTGGCACTGAA	3552
Qy	3481	CAGCTGGGACATCCGCGAGTACGAAACAGCGCTGTAAGTGTGTGAGCGGAGGTCCAG	3540
Db	3553	CAGCTGGGACATCCGCGAGTACGAAACAGCGCTGTAAGTGTGTGAGCGGAGGTCCAG	3612
Qy	3541	CAGTGTAGCCGCGTCTCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTTGCCTTGTGCC	3600
Db	3613	CAGTGTAGCCGCGTCTCTGGGGTGGGTGGCCGAGGCCCTGAGCCGCTTGCCTTGTGCC	3672
Qy	3601	CCAGGTGGGCGCGACCCCGCTGACCTGCGCTGGGCTCCAAAGAC	3642
Db	3673	CCAGGTGGGCGCGACCCCGCTGACCTGCGCTGGGCTCCAAAGAC	3714
RESULT 2			
ADH62711			
ID	ADH62711	standard; cDNA; 4061 BP.	
AC	ADH62711;		
XX	25-MAR-2004	(first entry)	
DT			
XX			
DE	Ca activated nonselective transmembrane channel protein TRPM4b cDNA.		
XX			
XX	bioactive agent; monovalent cation permeability; TRPM4b channel; human;		
KW	calcium activated nonselective transmembrane channel; gene; ss.		
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers		
CT	73..3717		
CDS			

QY 1501 CCTGACGTGGGCGATGTGCTGATGAGATGCTGCTGGGGAAGATGTGCGCCGACGATACCCC 1560
Db 1573 CCTGACGTGGGCGCATGTGCTGAGATGTGCTGGGGAAGATGTGCGCCGACGATACCCC 1632
QY 1561 TCCGGGGGCGCTGGGGAACCTCAACGAGGCGCTTGGGAGAGAGATATATCTGTCTC 1620
Db 1633 TCCGGGGGCGCTGGGGAACCTCAACGAGGCGCTTGGGAGAGAGATATATCTGTCTC 1692
QY 1621 TGGGACAAGGCGACCTCGCGCTCTGCTGATGTGAGCTCGGGCAGAGCCCTCGAGC 1680
Db 1693 TCGGACAAGGCGACCTCGCGCTCTGCTGATGTGAGCTCGGGCAGAGCCCTCGAGC 1752
QY 1681 GACCTGCTCTTGGGACAAGCTGTGTAACAGGCGACAGATGGCCATGTACTTCTGGAG 1740
Db 1753 GACCTGCTCTTGGGACAAGCTGTGTAACAGGCGACAGATGGCCATGTACTTCTGGAG 1812
QY 1741 ATGGGTTCCATGCAAGTTTCTCACTCTTGGGCGCTGTGTGCTCGGGGTGATGCA 1800
Db 1813 ATGGGTTCCATGCAAGTTTCTCACTCTTGGGCGCTGTGTGCTCGGGGTGATGCA 1872
QY 1801 CGCGTGGAGCTGACGCTGAGAGGACGACGAGGGAAGAACTGGGCGTTGAAGTTTGG 1860
Db 1873 CGCGTGGAGCTGACGCTGAGAGGACGACGAGGGAAGAACTGGGCGTTGAAGTTTGG 1932
QY 1861 GGGATGGGCGTTGACCTCTTGGGCGAGTCTATGCGACAGTGAAGTGAAGGCTGCCGC 1920
Db 1933 GGGATGGGCGTTGACCTCTTGGGCGAGTCTATGCGACAGTGAAGTGAAGGCTGCCGC 1992
QY 1921 CTCTCTCTCTCGCTCGCTGCGCTCTGGGGGAGATGCACTTGCTTCAGCTGGCCATGCA 1980
Db 1993 CTCTCTCTCTCGCTCGCTGCGCTCTGGGGGAGATGCACTTGCTTCAGCTGGCCATGCA 2052
QY 1981 GCTGACGCGCGTGTCTTGTGCCAGGATGGGGGATGATGCTGCTGTAACAAGAGTGG 2040
Db 2053 GCTGACGCGCGTGTCTTGTGCCAGGATGGGGGATGATGCTGCTGTAACAAGAGTGG 2112
QY 2041 TGGGGAAGTATGGGACAGACTACCCCATCTGGGCGCTGTCTCGCTCTTGTGGCCT 2100
Db 2113 TGGGGAAGTATGGGACAGACTACCCCATCTGGGCGCTGTCTCGCTCTTGTGGCCT 2172
QY 2101 CCACCTCATCTACACCCGCTCATCACTTCAAGAAATCAGAAAGAGAGCCCAACGAGAG 2160
Db 2173 CCACCTCATCTACACCCGCTCATCACTTCAAGAAATCAGAAAGAGAGCCCAACGAGAG 2232
QY 2161 GAGCTAAGATTGACATGAGATAGTCTATTATGGGGAAGGCGCTGTGGGACGCGGAC 2220
Db 2233 GAGCTAAGATTGACATGAGATAGTCTATTATGGGGAAGGCGCTGTGGGACGCGGAC 2292
QY 2221 CCAGCCGAGAAAGCGCGCTGGGGGTCCGCGCAAGTGGGCGGTCCGGGTTGTGGGGG 2280
Db 2293 CCAGCCGAGAAAGCGCGCTGGGGGTCCGCGCAAGTGGGCGGTCCGGGTTGTGGGGG 2352
QY 2281 GGGCGCTGCGGGGGGCGCGGTGCTACGCGCTGTGTTCACCTTCTGGGGCGCGCGGTG 2340
Db 2353 GGGCGCTGCGGGGGGCGCGGTGCTACGCGCTGTGTTCACCTTCTGGGGCGCGCGGTG 2412
QY 2341 ACCATCTTCAATGGGCAACGTGTGAGCTAAGCTGTCTTCTGTGCTTTTCTCGGGGTG 2400
Db 2413 ACCATCTTCAATGGGCAACGTGTGAGCTAAGCTGTCTTCTGTGCTTTTCTCGGGGTG 2472
QY 2401 CTGCTCGGATTTCCAGCGGGGCGCGCGGCTCCCTGGAGCTGTGCTTATTTTCTGG 2460
Db 2473 CTGCTCGGATTTCCAGCGGGGCGCGCGGCTCCCTGGAGCTGTGCTTATTTTCTGG 2532
QY 2461 GCTTTACGCTGTGTGGAAGAACTGCGCAAGGCGCTGACGAGGCGGGGAGAGCTC 2520
Db 2533 GCTTTACGCTGTGTGGAAGAACTGCGCAAGGCGCTGACGAGGCGGGGAGAGCTC 2592
QY 2521 GCGACGGGGGCGCGCGGCTGGGCGATGCTTCACTGACCGCGCTTGCGCTTACTC 2580
Db 2593 GCGACGGGGGCGCGCGGCTGGGCGATGCTTCACTGACCGCGCTTGCGCTTACTC 2652
QY 2581 GCCGACAGCTGGAAACAGATGGACCTAAGTGTCTCACTGTCTTCTTGGGGGTGGG 2640

Db 2653 GCCGACAGCTGGAAACAGATGGACCTAAGTGTCTCACTGTCTTCTTGGGGGTGGG 2712
QY 2641 TGGCGGCGAACCCCGGGTTTGTACACCTGGGGCGGCACTGTCCCTGTGATGACTTACG 2700
Db 2713 TGGCGGCGAACCCCGGGTTTGTACACCTGGGGCGGCACTGTCCCTGTGATGACTTACG 2772
QY 2701 GTTTTACGCGTGCAGCTCTTCACTCTTCAAGGTCAACAAGAGTGGGCGCAAGATC 2760
Db 2773 GTTTTACGCGTGCAGCTCTTCACTCTTCAAGGTCAACAAGAGTGGGCGCAAGATC 2832
QY 2761 GTCATCTGAGCAAGATGATGAAGAGAGTGTCTTCTTCTTCTTCTTCTGCGGTGG 2820
Db 2833 GTCATCTGAGCAAGATGATGAAGAGAGTGTCTTCTTCTTCTTCTTCTGCGGTGG 2892
QY 2821 CTGGTACCTTATGGCGGTGGCCACGGAAGGGCTCTTGAGGCGCACGGGACATGATCCCA 2880
Db 2893 CTGGTACCTTATGGCGGTGGCCACGGAAGGGCTCTTGAGGCGCACGGGACATGATCCCA 2952
QY 2881 AGTATCCGCGCGCGCTTCTTCAACGCTTCACTGACAGATCTTGGGCAAGATCCCGAG 2940
Db 2953 AGTATCCGCGCGCGCTTCTTCAACGCTTCACTGACAGATCTTGGGCAAGATCCCGAG 3012
QY 2941 GAGGACATGACGATGGCCCTATGAGACACAGCAACTGTCTGTGAGAGCCCGGCTTGG 3000
Db 3013 GAGGACATGACGATGGCCCTATGAGACACAGCAACTGTCTGTGAGAGCCCGGCTTGG 3072
QY 3001 GCACACCTCTCTGGGGCGCCAGGGCGGACCTGTGCTTCCAGATATGCCAATGGCTGTG 3060
Db 3073 GCACACCTCTCTGGGGCGCCAGGGCGGACCTGTGCTTCCAGATATGCCAATGGCTGTG 3132
QY 3061 GTGCTGCTCTCTGATCTTCTGCTGTGTGCGCAACATCCGCTGTGCAACTTGTCTCAT 3120
Db 3133 GTGCTGCTCTCTGATCTTCTGCTGTGTGCGCAACATCCGCTGTGCAACTTGTCTCAT 3192
QY 3121 GCCATGTTCAATTACATATTCGAGAAAGTACAGGGCAACAGCGATCTTCACTGGAAGCG 3180
Db 3193 GCCATGTTCAATTACATATTCGAGAAAGTACAGGGCAACAGCGATCTTCACTGGAAGCG 3252
QY 3181 CAGCGTTACCGGCTCATTCGGGAAATTCGACTCTGGCGCGGCTGCGCCGCTTATTC 3240
Db 3253 CAGCGTTACCGGCTCATTCGGGAAATTCGACTCTGGCGCGGCTGCGCCGCTTATTC 3312
QY 3241 GTCATCTTCCCACTTGGCGCTCTGTCTAGGCAATTGTGCAAGGCGACCCCGGAGCCCCAG 3300
Db 3313 GTCATCTTCCCACTTGGCGCTCTGTCTAGGCAATTGTGCAAGGCGACCCCGGAGCCCCAG 3372
QY 3301 CCGTCTCTCCCGGCGCTCGAGCAATTCGGGTTTACCTTCTAAGAAAGCGAGCGGAG 3360
Db 3373 CCGTCTCTCCCGGCGCTCGAGCAATTCGGGTTTACCTTCTAAGAAAGCGAGCGGAG 3432
QY 3361 CTGTAAAGTGGAAATGATGATTAAGAGAACTTGTGTGCGACGCGTGGGACAG 3420
Db 3433 CTGTAAAGTGGAAATGATGATTAAGAGAACTTGTGTGCGACGCGTGGGACAG 3492
QY 3421 CGGGAAGCGAATTCGAGCGCTGTGAAGCGCACTGCCAAGAAAGTGTGAAGCTTGA 3480
Db 3493 CGGGAAGCGAATTCGAGCGCTGTGAAGCGCACTGCCAAGAAAGTGTGAAGCTTGA 3552
QY 3481 CAGCTGGGACACATTCGCGAGTACGAAGAGGCGCTGAAGGTGAGCGGGAGGTCCAG 3540
Db 3553 CAGCTGGGACACATTCGCGAGTACGAAGAGGCGCTGAAGGTGAGCGGGAGGTCCAG 3612
QY 3541 CAGTGTAGCGCGCTCTGGGGGTGGTGGCGAGGCGCTGAGCGGCTGTGCTTGTGCCC 3600
Db 3613 CAGTGTAGCGCGCTCTGGGGGTGGTGGCGAGGCGCTGAGCGGCTGTGCTTGTGCCC 3672
QY 3601 CCAAGTGGGCGCGCACTTCTGACCTGTGCTGTGCTTCAAGAC 3642
Db 3673 CCAAGTGGGCGCGCACTTCTGACCTGTGCTGTGCTTCAAGAC 3714

RESULT 3

ADNR73511
 ID ADR73511 standard; DNA; 4061 BP.
 AC ADR73511;
 DT 02-DEC-2004 (first entry)
 DE Human TRPM4, gene.
 XX
 XX TRPM4; apoptosis; inhibitor; tumour; cytostatic; cancer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX
 FT CDS Location/Qualifiers
 FT 73..3717
 FT /tag= a
 FT /product= "Human TRPM4"
 FT
 PN WO2004076682-A2.
 XX
 PD 10-SEP-2004;
 XX
 PF 26-FEB-2004; 2004WO-US006020.
 XX
 PR 26-FEB-2003; 2003US-0450886P.
 XX
 PA (SURR-) SURROMED INC.
 XX
 PI Axenovich SA, Stull R, Gelman M, Chui K, Ng D;
 XX
 DR WPI; 2004-653428/63.
 DR P-PSDB; ADR73512.
 XX
 PT Identifying a compound for inducing apoptosis, useful for diagnosing and
 PT treating cancer, comprises identifying an inhibitor of a target.
 XX
 PS Example 1; SEQ ID NO 79; 2555p; English.
 CC The invention relates to a novel method for identifying a compound for
 CC inducing apoptosis comprising identifying an inhibitor of a target.
 CC Examples of an inhibitor of a target include: angio-associated, migratory
 CC cell protein (AAMP), disintegrin and metalloproteinase domain 8 (ADAM8),
 CC disintegrin-like and metalloprotease (reporlysin type) with
 CC thrombospondin type 1 motif, 17 (ADAMTS17), adenylate cyclase 3 (ADCY3),
 CC adrenergic beta receptor kinase 1 (ADBRK1), bladder cancer associated
 CC protein (BLCAP), chromosome 22 open reading frame 5 (C22orf5), CD81
 CC antigen (target of anti-proliferative antibody 1 (CD81), CD9 antigen (p24)
 CC (CD9), claudin 4 (CLDN4), chloride intracellular channel 1 (CLIC1),
 CC collagen, type VI, alpha 2 (COL6A2), CTL2, endothelin converting enzyme 1
 CC (ECE1), ephrinB1 (EFNB1), flotillin 2 (FLOT2), intercellular adhesion
 CC molecule 3 (ICAM3), iduronate 2-sulfatase (Hunter syndrome) (IDS), jagged
 CC 2 (JAG2), junctional adhesion molecule 1 (JAM1), lectin, galactoside-
 CC binding soluble 3 binding protein (LGALS3BP), similar to possible G-
 CC protein receptor (LOC146330), GGI-78 protein (LOC51107), lipoprotein
 CC lipase (LPL), low density lipoprotein receptor-related protein 5 (LRP5),
 CC Lutheran blood group (Auberger b antigen included) (LU), membrane
 CC component, chromosome11, surface marker 1 (ML1S), serum constituent
 CC protein (MSE55), neuropathy target esterase (NTE), Homo sapiens CDNA
 CC FL31043 fls, clone HSYRA200248 (PLEXIN A1) or Homo sapiens CDNA FLJ44113
 CC fls, clone TES114046487, highly similar to Mus musculus plexin A1
 CC (PLXNA1), protein tyrosine phosphatase, receptor type, f polypeptide
 CC (PTPRF), interacting protein1 (liprin), alpha 3 (PPF13), Homo sapiens
 CC peptide-histidine transporter 4 (PRR4), mRNA (PRR4), solute carrier
 CC family 16 (monocarboxylic acid transporters) member 3 (SLC16A3), solute
 CC carrier family 1 (neutral amino acid transporter) member 5 (SLC1A5),
 CC solute carrier family 39 (zinc transporter) member 3 (SLC39A1), serine
 CC protease inhibitor, Kunitz type 2 (SPINT2), stanniocalcin 2 (STC2),
 CC tumour necrosis receptor superfamily member 21 (TNFRSF21), tumour
 CC rejection antigen (gp96) 1 (TRA1), or transient receptor potential cation
 CC channel, subfamily M member 4 (TRPM4), respectively comprising any of the
 CC 40 sequences of 87-1615 amino acids (the even numbers selected from SEQ
 CC ID:2-80), shown in the specification. The invention further comprises a
 CC method for inducing apoptosis and a method for diagnosing a tumour. The

CC novel compounds have cytostatic activity. The method is useful for
 CC identifying a compound for inducing apoptosis. The methods and compounds
 CC are useful for diagnosing and treating cancer, and in determining the
 CC prognosis for cancer in the patient or the susceptibility of the patient
 CC to a therapeutic treatment. This polynucleotide sequence represents a
 CC gene encoding one of the 40 protein targets of the invention.

XX Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match 100.0%; Score 3642; DB 13; Length 4061;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3642; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTGTGTGCGGAGAGACAGAGCTGATGCCCAAGATCTTCAAGAGAAGACTGCG 60
 DB ATGTGTGTGCGGAGAGAGACAGAGCTGATGCCCAAGATCTTCAAGAGAAGACTGCG 132
 61 ACGACGTTCAATGTTGATCCACAGATCCGGAGAGGACCTTGTGCAAGTGGGCGCC 120
 DB ACGACGTTCAATGTTGATCCACAGATCCGGAGAGGACCTTGTGCAAGTGGGCGCC 192
 121 CGGACCGCCCAACCCCGAGTGGGCAATGGAGATGCTTGGGGGACCGGTGGTACG 180
 DB CGGACCGCCCAACCCCGAGTGGGCAATGGAGATGCTTGGGGGACCGGTGGTACG 252
 193 CGGACCGCCCAACCCCGAGTGGGCAATGGAGATGCTTGGGGGACCGGTGGTACG 252
 181 TGGGACAGCGATGACACACACCGAGAGAGCCCAACCGATGCTTACGAGACTGGACTTC 240
 DB TGGGACAGCGATGACACACACCGAGAGAGCCCAACCGATGCTTACGAGACTGGACTTC 312
 253 TGGGACAGCGATGACACACACCGAGAGAGCCCAACCGATGCTTACGAGACTGGACTTC 312
 241 ACGGGGGCGCGCCGAGACACAGCAAGCAATTTCTCGGCTCTTGAACCGAAGATCCAGCT 300
 DB ACGGGGGCGCGCCGAGACACAGCAAGCAATTTCTCGGCTCTTGAACCGAAGATCCAGCT 372
 313 ACGGGGGCGCGCCGAGACACAGCAAGCAATTTCTCGGCTCTTGAACCGAAGATCCAGCT 372
 301 GCAGTTTATGCTGTGTGTACACAGCAATGGGGCTTCCGTCGCCGGAACCTGTGGTGTCA 360
 DB GCAGTTTATGCTGTGTGTACACAGCAATGGGGCTTCCGTCGCCGGAACCTGTGGTGTCA 432
 373 GCAGTTTATGCTGTGTGTACACAGCAATGGGGCTTCCGTCGCCGGAACCTGTGGTGTCA 432
 361 GTGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 420
 DB GTGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 492
 433 GTGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 492
 421 GGGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 480
 DB GGGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 552
 493 GGGCTGTGGGGGATCGGGGGGGCCCGTCTCCAGACTGGCTGACAGACTCTGCGTGTGT 552
 481 GGCATCGGCGCGCATGTTGT 540
 DB GGCATCGGCGCGCATGTTGT 612
 553 GGCATCGGCGCGCATGTTGT 612
 541 ACCAAGGT 600
 DB ACCAAGGT 672
 613 ACCAAGGT 672
 601 ATCAAACCCCAAGGCTGTCTCTGAGAGTACCGGTGGCGCGGTGACCCGAGAGACGGG 660
 DB ATCAAACCCCAAGGCTGTCTCTGAGAGTACCGGTGGCGCGGTGACCCGAGAGACGGG 732
 673 ATCAAACCCCAAGGCTGTCTCTGAGAGTACCGGTGGCGCGGTGACCCGAGAGACGGG 732
 721 GTCCAGTTTCCCTGTGAGATCAACATCTGCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGT 720
 DB GTCCAGTTTCCCTGTGAGATCAACATCTGCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGT 792
 733 GTCCAGTTTCCCTGTGAGATCAACATCTGCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGT 792
 721 GGGCTGCTGGGGGGGAGAGACCGCTTCCGCTTGGCGCTGAGTCTCAATCTCAAGAG 780
 DB GGGCTGCTGGGGGGGAGAGACCGCTTCCGCTTGGCGCTGAGTCTCAATCTCAAGAG 852
 793 GGGCTGCTGGGGGGGAGAGACCGCTTCCGCTTGGCGCTGAGTCTCAATCTCAAGAG 852
 781 AAGACGGGCGT 840
 DB AAGACGGGCGT 912
 853 AAGACGGGCGT 912
 841 GATGAGAGATGT 900
 DB GATGAGAGATGT 972
 913 GATGAGAGATGT 972

Qy 901 GTGCTGAGCTAGAGGGAGCTGCGGACTGCTGCGGAGACCTGGAAGACACTCTGCGC 960
Db 973 GTGGCTGAGCTAGAGGGAGCTGCGGACTGCTGCGGAGAGACCTGGAAGACACTCTGCGC 1032
Qy 961 CCAGGGAATGGGGAGGCGAGGCGAAGCCGAGATCGAATAGAGCGTTTCTTTCC 1020
Db 1033 CCAGGGAATGGGGAGGCGAGGCGAAGCCGAGATCGAATAGAGCGTTTCTTTCC 1092
Qy 1021 AAAGGGAGCTTGAAGGTCTGCAAGGCGAGGTGAGAGATTTATGACCCGGAAGAGCTC 1080
Db 1093 AAAGGGAGCTTGAAGGTCTGCAAGGCGAGGTGAGAGATTTATGACCCGGAAGAGCTC 1152
Qy 1081 CTGACAGTCTATTTCTTCTGAGGATGGGTCTGAGGAAATCGAGACCATAGTTTGAAGGCC 1140
Db 1153 CTGACAGTCTATTTCTTCTGAGGATGGGTCTGAGGAAATCGAGACCATAGTTTGAAGGCC 1212
Qy 1141 CTTGTGAAGGCGCTGAGGAGCTCGAGAGCCTTCAGCTTACTGTGATGAGCTGCGTTGAGCT 1200
Db 1213 CTTGTGAAGGCGCTGAGGAGCTCGAGAGCCTTCAGCTTACTGTGATGAGCTGCGTTGAGCT 1272
Qy 1201 GTGGCTTGGAAACCGGCTGGAGCAATGGCCGAGTGAATCTTTTCGGGGGGAGCATCCAAATGG 1260
Db 1273 GTGGCTTGGAAACCGGCTGGAGCAATGGCCGAGTGAATCTTTTCGGGGGGAGCATCCAAATGG 1332
Qy 1261 CGGTCTCTTCATCTCGAAGCTTCCCTCATGGAAGCGCCCTGTGAATGACCGGCTGAGTTTC 1320
Db 1333 CGGTCTCTTCATCTCGAAGCTTCCCTCATGGAAGCGCCCTGTGAATGACCGGCTGAGTTTC 1392
Qy 1321 GTGGCTTGTCTCATTTTCCAGGCGCTCAGCGTGGGCGCATTTCTGAGCCCGAGTGGCGCTG 1380
Db 1393 GTGGCTTGTCTCATTTTCCAGGCGCTCAGCGTGGGCGCATTTCTGAGCCCGAGTGGCGCTG 1452
Qy 1381 GCCCAACTCTACAGGCGGCGCCCTTCCAATCTGCTCATACCCGAACCTTTTGGACCAAGGCG 1440
Db 1453 GCCCAACTCTACAGGCGGCGCCCTTCCAATCTGCTCATACCCGAACCTTTTGGACCAAGGCG 1512
Qy 1441 TCCCAACAGCGAGGCGACCAAAAGCCCGAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGCGCC 1500
Db 1513 TCCCAACAGCGAGGCGACCAAAAGCCCGAGCCCTAAAAGGGGGAGCTGCGGAGCTCCGCGCC 1572
Qy 1501 CCGTGAAGGGGAGCATGATGCTGAGAGATGCTGCTGAGGGAAGATGTGCGCGCGAGTACC 1560
Db 1573 CCGTGAAGGGGAGCATGATGCTGAGAGATGCTGCTGAGGGAAGATGTGCGCGCGAGTACC 1632
Qy 1561 TCCGGGGAGCGCTGGGAGACCTTCACCCAGGCGGCTTTCGGGGAGAGCATGATGTGCTC 1620
Db 1633 TCCGGGGAGCGCTGGGAGACCTTCACCCAGGCGGCTTTCGGGGAGAGCATGATGTGCTC 1692
Qy 1621 TCGGACAAAGGCGACCTGCGCGCTCGCTGAGATGCTGAGCTCGGGCAGAGCCCGCTGAGG 1680
Db 1693 TCGGACAAAGGCGACCTGCGCGCTCGCTGAGATGCTGAGCTCGGGCAGAGCCCGCTGAGG 1752
Qy 1681 GACCTGCTTTCTTTGGGCACTGTTGCTGAACAAGGCGACAGATGAGCCATGACTTTGAGAG 1740
Db 1753 GACCTGCTTTCTTTGGGCACTGTTGCTGAACAAGGCGACAGATGAGCCATGACTTTGAGAG 1812
Qy 1741 ATGGTTCGAATGCACTTTCTCACTGCTTGGGCGCTGTTGCTGCTCGGGTGATGCA 1800
Db 1813 ATGGTTCGAATGCACTTTCTCACTGCTTGGGCGCTGTTGCTGCTCGGGTGATGCA 1872
Qy 1801 GCGCTGAGCGCTGAGCGTGAAGGAGCAGAGAGGAAGAAGCTGGCGTTCAAGTTTGA 1860
Db 1873 GCGCTGAGCGCTGAGCGTGAAGGAGCAGAGAGGAAGAAGCTGGCGTTCAAGTTTGA 1932
Qy 1861 GGGATGGGCGTTGACCTTTTGGCGAGTGTATCGACAGTGAAGTGAAGGAGTGGCCGC 1920
Db 1933 GGGATGGGCGTTGACCTTTTGGCGAGTGTATCGACAGTGAAGTGAAGGAGTGGCCGC 1992
Qy 1921 CTCTCTCTTCGCTCGTGGCGCGCTCTGGGGGAGATGCACTTGTCTCACTGAGCCATGCA 1980
Db 1993 CTCTCTCTTCGCTCGTGGCGCGCTCTGGGGGAGATGCACTTGTCTCACTGAGCCATGCA 2052
Qy 1981 GCTACGCGCGTCTTTTGGCCAGAGATGGGGTGAAGTCTCTGTCAACACAGAGTGG 2040

Db 2053 GCTACGCGCGTCTTTTGGCCAGAGATGGGGTGAAGTCTCTGTCAACACAGAGTGG 2112
Qy 2041 TGGGGAATATGCGACACACTACACCATCTGGGCGCTGGTTCTCGGCTTTTGCCCT 2100
Db 2113 TGGGGAATATGCGACACACTACACCATCTGGGCGCTGGTTCTCGGCTTTTGCCCT 2172
Qy 2101 CCACTCATCTACACCGCGCTCATCACTTCAAGAAATCAGAAGAGAGCCACAGGAG 2160
Db 2173 CCACTCATCTACACCGCGCTCATCACTTCAAGAAATCAGAAGAGAGCCACAGGAG 2232
Qy 2161 GAGCTAAGTTTGACATGATAGTGTATTAAATGGGGAAGGAGCTGTGAGAGCGGAG 2220
Db 2233 GAGCTAAGTTTGACATGATAGTGTATTAAATGGGGAAGGAGCTGTGAGAGCGGAG 2292
Qy 2221 CCAGCCAGAAAGAGCGCGCTGGGGGTCCCGGCCAGTGGCGCTCCGGGTTGCTGGGG 2280
Db 2293 CCAGCCAGAAAGAGCGCGCTGGGGGTCCCGGCCAGTGGCGCTCCGGGTTGCTGGGG 2352
Qy 2281 GCGCGCTGCGGGGGGCGCGGCTGCTAGCGCGCTGTTCCACTTCTGGGGGCGCGG 2340
Db 2353 GCGCGCTGCGGGGGGCGCGGCTGCTAGCGCGCTGTTCCACTTCTGGGGGCGCGG 2412
Qy 2341 ACGATCTTCAATGGGCAAGTGTGAGCTACCTGCTGTTCTGCTGCTTTCTCGCGG 2400
Db 2413 ACGATCTTCAATGGGCAAGTGTGAGCTACCTGCTGTTCTGCTGCTTTCTCGCGG 2472
Qy 2401 CTGCTCTGGAATTTCCAGCGGCGCGCGCTCGGCTCTCGGAGCTGCTCATTTCTGG 2460
Db 2473 CTGCTCTGGAATTTCCAGCGGCGCGCGCTCGGCTCTCGGAGCTGCTCATTTCTGG 2532
Qy 2461 GCTTTCAGCTGCTGCTGCTGAGGAACTGGCGAGGGCGCTGAGCGGAGCGGGGAGGCTC 2520
Db 2533 GCTTTCAGCTGCTGCTGCTGAGGAACTGGCGAGGGCGCTGAGCGGAGCGGGGAGGCTC 2592
Qy 2521 GCCAGCGGGGGCGCGGCGCTGCGCATGCTCACTGAGCGAGCGCTGCGCTTACTC 2580
Db 2593 GCCAGCGGGGGCGCGGCGCTGCGCATGCTCACTGAGCGAGCGCGCTGCGCTTACTC 2652
Qy 2581 GCCGACAGCTGGAACAGTGGGACCTAGTGCTCTCACTGCTGCTTCTTCTGGCGTGG 2640
Db 2653 GCCGACAGCTGGAACAGTGGGACCTAGTGCTCTCACTGCTGCTTCTTCTGGCGTGG 2712
Qy 2641 TGGCGGCTGAGCCCGGGTTTGTACACTGGGCGGCACTGGCTCTGCACTGATGATG 2700
Db 2713 TGGCGGCTGAGCCCGGGTTTGTACACTGGGCGGCACTGGCTCTGCACTGATGATG 2772
Qy 2701 GTTTTCAGGCTGCGGCTGCTTCACTTCAAGGCTCAACAAACAGCTGGGGCCAGAT 2760
Db 2773 GTTTTCAGGCTGCGGCTGCTTCACTTCAAGGCTCAACAAACAGCTGGGGCCAGAT 2832
Qy 2761 GTCATGCTGAGCAAGATGATGAGAGAGCTGTTCTTCTTCTTCTTCTTCTGCGGTGG 2820
Db 2833 GTCATGCTGAGCAAGATGATGAGAGAGCTGTTCTTCTTCTTCTTCTTCTTCTGCGGTGG 2892
Qy 2821 CTGGTACCTTATGGCGTGGGCGCAGGAGGGCTCCTGAGGCGCAGGGAAGTATTTCCA 2880
Db 2893 CTGGTACCTTATGGCGTGGGCGCAGGAGGGCTCCTGAGGCGCAGGGAAGTATTTCCA 2952
Qy 2881 AGTATCTGCGCGCGCTTCTTCACTGCTTCAAGTCTTCAAGTCTTGGGAGATTTCC 2940
Db 2953 AGTATCTGCGCGCGCTTCTTCACTGCTTCAAGTCTTCAAGTCTTGGGAGATTTCC 3012
Qy 2941 GAGGACATGAGAGCTGGCGCTTATGAGCAGAGCAAGCTGCTGCTGAGGCGCGGCTTGG 3000
Db 3013 GAGGACATGAGAGCTGGCGCTTATGAGCAGAGCAAGCTGCTGCTGAGGCGCGGCTTGG 3072
Qy 3001 GCACACCTCTCTGGGGCGCAGGCGGAGCAGTGGGTCTTCCAGTATGCAACTGGCTGG 3060
Db 3073 GCACACCTCTCTGGGGCGCAGGCGGAGCAGTGGGTCTTCCAGTATGCAACTGGCTGG 3132
Qy 3061 GTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3120

Db	3133	GTGCGGCTCCCTGCGATCTTCTGTGTGGCCAAACCTGTCGTGCAATTGTCAATT	3192
Qy	3121	GCCATGTTCAATTACACTTTGGCAAGTAACGGCCAAACAGCATCTTACTGGAAGCG	3180
Db	3193	GCCATGTTCAATTACACTTTGGCAAGTAACGGCCAAACAGCATCTTACTGGAAGCG	3252
Qy	3181	CAGGTTAACCGCCATCCGGGAATTCACCTCGGCCCCGGGCGAGCCGCCCTTATC	3240
Db	3253	CAGGTTAACCGCCATCCGGGAATTCACCTCGGCCCCGGGCGAGCCGCCCTTATC	3312
Qy	3241	GTCATCTCCCACTTGGCGCTCTGCTCAGGCATTTGTCAGAGCCACCAGAGCCCGAC	3300
Db	3313	GTCATCTCCCACTTGGCGCTCTGCTCAGGCATTTGTCAGAGCCACCAGAGCCCGAC	3372
Qy	3301	CCGTCCTCCCGGCCCTTCGAGCATTTCCGGGTTTACTTTCTAAGAAACCGAGCGAAG	3360
Db	3373	CCGTCCTCCCGGCCCTTCGAGCATTTCCGGGTTTACTTTCTAAGAAACCGAGCGAAG	3432
Qy	3361	CTGCTTAACGTGGGAATCGGTGCTAATGAAGAACTTTCTGTGCGACCGGCTAAGGACAAG	3420
Db	3433	CTGCTTAACGTGGGAATCGGTGCTAATGAAGAACTTTCTGTGCGACCGGCTAAGGACAAG	3492
Qy	3421	CGGGAGAGCGCACTCCGAGCGCTCTGAAGCGCAAGTCCAGAAAGGTGGACTTGGCACTGAAA	3480
Db	3493	CGGGAGAGCGCACTCCGAGCGCTCTGAAGCGCAAGTCCAGAAAGGTGGACTTGGCACTGAAA	3552
Qy	3481	CAGCTGGGACACATCCGCGAGTACGAAACAGCGCCTTGAAAGTCTGAGCGGGAAGTCCAG	3540
Db	3553	CAGCTGGGACACATCCGCGAGTACGAAACAGCGCCTTGAAAGTCTGAGCGGGAAGTCCAG	3612
Qy	3541	CAGTGTAGCCCGCGTCTTGGGGTGGGTGGCCGAGGCCCTGAGCGGCTTGTGCTGCGCC	3600
Db	3613	CAGTGTAGCCCGCGTCTTGGGGTGGGTGGCCGAGGCCCTGAGCGGCTTGTGCTGCGCC	3672
Qy	3601	CCAGTGTAGCCCGCACCCCTTGACCTGTGCTGGGTCCAAAGAC	3642
Db	3673	CCAGTGTAGCCCGCACCCCTTGACCTGTGCTGGGTCCAAAGAC	3714

RESULT 4	
ADSI2774	
ID	ADSI2774 standard; cDNA; 4061 BP.
XX	
AC	ADSI2774;
XX	
DT	16-DEC-2004 (first entry)
XX	
DE	Transient receptor potential cation channel, subfamily M member 4b cDNA.
XX	
KW	transient receptor potential cation channel; subfamily M; member 4;
KW	TRPM4; phospholipase A1-A; PLA1A; butyryl coenzyme A synthetase 1; BUCS1;
KW	prostate cancer; TRPM4b; gene; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	73..3717
FT	/*tag= a
FT	/product= "Human TRPM4b protein"
XX	
PN	JP2004267118-A.
XX	
PD	30-SEP-2004.
XX	
PF	10-MAR-2003; 2003JP-00063578.
XX	
PR	10-MAR-2003; 2003JP-00063578.
XX	
PA	(SANTO) SANTO CO LTD.
XX	
WI	WI; 2004-693915/68.
DR	P-PSDB; ADSI2775.
XX	

PT Detecting prostatic cancer, comprises extracting RNA fractions from test
 PT substance of subject and normal human, measuring and analyzing the
 PT difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
 PT expression levels.
 XX
 XX
 PS Claim 1; SEQ ID NO 1; 126bp; Japanese.
 XX
 CC The invention comprises a method for detecting prostatic cancer in a
 CC subject. The method involves measuring the expression levels of specific
 CC genes: transient receptor potential cation channel, subfamily M, member 4
 CC (TRPM4); phospholipase A1-A (PLA1A); and butyryl coenzyme A synthetase 1
 CC (BUCS1). The method of the invention is useful for the detection and
 CC treatment of prostate cancer. The present cDNA sequence encodes the human
 CC TRPM4b protein of the invention.
 XX
 SQ Sequence 4061 BP; 697 A; 1268 C; 1306 G; 790 T; 0 U; 0 Other;

Query Match	100.0%	Score 3642;	DB 13;	Length 4061;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 3642; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

OY	1	ATGTGTGTGCGGAGAAAGAGACAGAGCTGTGATATCCCAAGATCTTCAAGAAAGACCTGC	60
Db	73	ATGTGTGTGCGGAGAAAGAGACAGAGCTGTGATATCCCAAGATCTTCAAGAAAGACCTGC	132
OY	61	ACGACGTTCAATGATGTGACTCCACAGATCCGGAGGAGACTTGTGCACTGTGTGGCGCCC	120
Db	133	ACGACGTTCAATGATGTGACTCCACAGATCCGGAGGAGACTTGTGCACTGTGTGGCGCCC	192
OY	121	CGGACCGGCGACCCCGGAGTGGCCATGAGAGATGCTTCCGGGGGAGCGGTGTGTGACCGTG	180
Db	193	CGGACCGGCGACCCCGGAGTGGCCATGAGAGATGCTTCCGGGGGAGCGGTGTGTGACCGTG	252
OY	181	TGGGACAGCGATGACACACACGAGAGAGCCACCGATGTGCTTA CGGAGAGCTGTGACTTTC	240
Db	253	TGGGACAGCGATGACACACACGAGAGAGCCACCGATGTGCTTA CGGAGAGCTGTGACTTTC	312
OY	241	ACGGGGGCGGGCGGACGACACGAAATTTCTCCGGCTCTTGACCGAA CGGATCOAGCT	300
Db	313	ACGGGGGCGGGCGGACGACACGAAATTTCTCCGGCTCTTGACCGAA CGGATCOAGCT	372
OY	301	GCAGTTTATAGTCCTGTGTGACACGACATATGGGGCTTCGAGCCCGGAA CTTGTGTGTGTA	360
Db	373	GCAGTTTATAGTCCTGTGTGACACGACATATGGGGCTTCGAGCCCGGAA CTTGTGTGTGTA	432
OY	361	GTGCTGGGGGGGATCGGGGGGCCCGCTCTCCAGACCTTGAGTGCAGAGACTTGCTGTGCT	420
Db	433	GTGCTGGGGGGGATCGGGGGGCCCGCTCTCCAGACCTTGAGTGCAGAGACTTGCTGTGCT	492
OY	421	GCGCTGTGTGCGGGCTGCCAGAGACAGAGAGCTGATTTGTCACTGGGGGTCTGCACACG	480
Db	493	GCGCTGTGTGCGGGCTGCCAGAGACAGAGAGCTGATTTGTCACTGGGGGTCTGCACACG	552
OY	481	GGCATTCGGCCGGGACATGTTGT	540
Db	553	GGCATTCGGCCGGGACATGTTGT	612
OY	541	ACCAAGTGTGTGACCATGATGTGTGACCCCTCGGGGTGTGTGTGTGTGTGTGTGTGTGTGT	600
Db	613	ACCAAGTGTGTGACCATGATGTGTGACCCCTCGGGGTGTGTGTGTGTGTGTGTGTGTGTGT	672
OY	601	ATCAACCCCAAGGGCTGTGTTCCCTGTGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG	660
Db	673	ATCAACCCCAAGGGCTGTGTTCCCTGTGAGGTACCGGTGGCGCGGTGACCCGGAGGACGGG	732
OY	661	GTCCAGTTTCCCTGTGACTACACTACTGTGGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGT	720
Db	733	GTCCAGTTTCCCTGTGACTACACTACTGTGGCTTCTTCTGTGTGTGTGTGTGTGTGTGTGT	792
OY	721	GCGTCCCTGTGGGGGGGAGAACCGCTTCGGCTTGGCGCTGTGAGTCTTAATCTCAAGACAG	780
Db	793	GCGTCCCTGTGGGGGGGAGAACCGCTTCGGCTTGGCGCTGTGAGTCTTAATCTCAAGACAG	852

QY	781	AAGACGGGCGTGGGAGGGACCTGGAAATTGACATCCCTGTCCTGCTCTCTGATTTAGTGT	840
Db	853	AAGACGGGCGTGGGAGGGACCTGGAAATTGACATCCCTGTCCTGCTCTCTGATTTAGTGT	912
QY	841	GATGAGAAAGATTGACCGCGAATAGAGAACGCCAACCCGAGCTCAGCTCCATGTCCTCTC	900
Db	913	GATGAGAAAGATTGACCGCGAATAGAGAACGCCAACCCGAGCTCAGCTCCATGTCCTCTC	972
QY	901	GTGGCTGGCTCAAGGGGAGCTTGCAGACTGCTGGCGAGAACCTTGGAAAGACACTCTGGCC	960
Db	973	GTGGCTGGCTCAAGGGGAGCTTGCAGACTGCTGGCGAGAACCTTGGAAAGACACTCTGGCC	1032
QY	961	CCAGGGAATGGGGGGAGCCGAGGCAAGGGCAACCCGAGATCGAATCAGGCGTTTCTTCCC	1020
Db	1033	CCAGGGAATGGGGGGAGCCGAGGCAAGGGCAACCCGAGATCGAATCAGGCGTTTCTTCCC	1092
QY	1021	AAAGGGGACCTTGAAGTCTCTCAGGCCCCAGGTGGAGAGATTATGACCCGGAAAGAGCTC	1080
Db	1093	AAAGGGGACCTTGAAGTCTCTCAGGCCCCAGGTGGAGAGATTATGACCCGGAAAGAGCTC	1152
QY	1081	CTGACAGCTTATTTCTTCTGAGAGATGGTCTGAGGAATTCAGACCATAGTTTGAAGGCC	1140
Db	1153	CTGACAGCTTATTTCTTCTGAGAGATGGTCTGAGGAATTCAGACCATAGTTTGAAGGCC	1212
QY	1141	CTTGTGAAGGCTGTGGGAGCTTCGAGGGCTCAGGCTACCTGATAGACTGCTTTGGCT	1200
Db	1213	CTTGTGAAGGCTGTGGGAGCTTCGAGGGCTCAGGCTACCTGATAGACTGCTTTGGCT	1272
QY	1201	GTGGCTTTGAACCGCGTGGACATTTGCCAGAGTGAACCTTTCGGGGGGGACATCCAAATGG	1260
Db	1273	GTGGCTTTGAACCGCGTGGACATTTGCCAGAGTGAACCTTTCGGGGGGGACATCCAAATGG	1332
QY	1261	CGGTCCTTCCATCTGAAAGCTTCCCTCAATGAGACGCCCTGCTGAATGACCGGCTGAGTTC	1320
Db	1333	CGGTCCTTCCATCTGAAAGCTTCCCTCAATGAGACGCCCTGCTGAATGACCGGCTGAGTTC	1392
QY	1321	GTGGGCTTGTCTCATTTTCCCAAGGCTCAGCTCTGGGGCACCTTCTCAGCCCGATGCGCTG	1380
Db	1393	GTGGGCTTGTCTCATTTTCCCAAGGCTCAGCTCTGGGGCACCTTCTCAGCCCGATGCGCTG	1452
QY	1381	GCCCAACCTCTACAGGCGCGGCGCCCTCCCAACTCGGCTCATCGGCMAACCTTTTGAACAAGCG	1440
Db	1453	GCCCAACCTCTACAGGCGCGGCGCCCTCCCAACTCGGCTCATCGGCMAACCTTTTGAACAAGCG	1512
QY	1441	TCCCAACAGCGAGGCAACCAAAAGCCCAAGCCCTTAAAGGGGGAGCTGCGAGACTCCGCGCC	1500
Db	1513	TCCCAACAGCGAGGCAACCAAAAGCCCAAGCCCTTAAAGGGGGAGCTGCGAGACTCCGCGCC	1572
QY	1501	CCTGACGTGGGGGCACTGTGCTGAGATGTGCTGGGGAAGATGTGCGCGCCGAGGTATCCC	1560
Db	1573	CCTGACGTGGGGGCACTGTGCTGAGATGTGCTGGGGAAGATGTGCGCGCCGAGGTATCCC	1632
QY	1561	TCCGGGGGCGGCTGGGAAACCTCAACCAAGGGGAGCTTCCGGGGAGAGATGTATCTGCTC	1620
Db	1633	TCCGGGGGCGGCTGGGAAACCTCAACCAAGGGGAGCTTCCGGGGAGAGATGTATCTGCTC	1692
QY	1621	TCCGACAAAGGCCACTCGCGCTGCTGCTGATCTGGGCTCGGGACAGGCCCTCCCTGAGC	1680
Db	1693	TCCGACAAAGGCCACTCGCGCTGCTGCTGATCTGGGCTCGGGACAGGCCCTCCCTGAGC	1752
QY	1681	GACCTGCTTCTTTGGGCACTGTGCTGTAACAGGCGACAGATGCGCATGTACTTTGCGAG	1740
Db	1753	GACCTGCTTCTTTGGGCACTGTGCTGTAACAGGCGACAGATGCGCATGTACTTTGCGAG	1812
QY	1741	ATGGGTTTCCAAATGAGTTTCTCTCAGCTCTTGGGGGCTGTTTGTCTCCGGGTGATGGCA	1800
Db	1813	ATGGGTTTCCAAATGAGTTTCTCTCAGCTCTTGGGGGCTGTTTGTCTCCGGGTGATGGCA	1872
QY	1801	CGCTGTGAGCGCTGAGGAGGAGGACAGACGAGAGAAAGACCTGGCGTTCAAGTTTGAG	1860
Db	1873	CGCTGTGAGCGCTGAGGAGGAGGACAGACGAGAGAAAGACCTGGCGTTCAAGTTTGAG	1932
QY	1861	GGGATGGGCTTGAACCTTTTGGCGAGTGTATCGACAGAGTGAAGTGAAGGCTGCCGC	1920

Db	1933	GGGATGGGCGCTTGACCTCTTTGGCGAGTGCCTATGCGACAGTAGAGTGAAGGCTGCCGC	1992
OY	1921	CTCCTCCTCGCTCGCTGCCCTCTCGGAGGAGATGCCATTGGCTTCAGCTGGCCATGCAA	1980
Db	1993	CTCCTCCTCGGCTCGCTCGCCGCTCTGGAGGAGATGCCATTGGCTTCAGCTGGCCATGCAA	2052
OY	1981	GCTGACGCCGCTGCTCTTTTGGCCAGAGATGGGTACAGTCTGTCTGACACAGAAATGG	2040
Db	2053	GCTACGCGCCCTGCTCTTTTGGCCAGAGATGGGTACAGTCTGTCTGACACAGAAATGG	2112
OY	2041	TGGGAGAGATATGCGCAGACCTACACCCATCGGGCCCTGGTTCTCGCTCTTTTGGCCT	2100
Db	2113	TGGGAGAGATATGCGCAGACCTACACCCATCGGGCCCTGGTTCTCGCTCTTTTGGCCT	2172
OY	2101	CCACTCATCTTACACCCGCTCATCACTTGAGAAATCAGAAAGAGACCACACGGAG	2160
Db	2173	CCACTCATCTTACACCCGCTCATCACTTGAGAAATCAGAAAGAGACCACACGGAG	2232
OY	2161	GAGCTTAAAGTTTGACATGATAGTGTCAATTAATGGGAAAGGCTGTGGGAGCGGAC	2220
Db	2233	GAGCTTAAAGTTTGACATGATAGTGTCAATTAATGGGAAAGGCTGTGGGAGCGGAC	2292
OY	2221	CCACCCGAGAAAGACGCGCTGGGGGTCCCGCAGTGGGCGCTCCGGGTTCGTGGG	2280
Db	2293	CCACCCGAGAAAGACGCGCTGGGGGTCCCGCAGTGGGCGCTCCGGGTTCGTGGG	2352
OY	2281	GGCGCTGGGGGGGGCCGGGTGCTACGCGCTGAGTTCACATCTTGGGGCGGCGGCTG	2340
Db	2353	GGCGCTGGGGGGGGCCGGGTGCTACGCGCTGAGTTCACATCTTGGGGCGGCGGCTG	2412
OY	2341	ACCATCTTCAATGGGCAACGTGTCAAGCTATGCTGTTCCTGCTCTTTTCTGGGGGTG	2400
Db	2413	ACCATCTTCAATGGGCAACGTGTCAAGCTATGCTGTTCCTGCTCTTTTCTGGGGGTG	2472
OY	2401	CTGCTCGTAGATTTTCCAGCCGGCGCCGCGCTCCCTGGAGCTGCTCTTATTTCTGG	2460
Db	2473	CTGCTCGTAGATTTTCCAGCCGGCGCCGCGCTCCCTGGAGCTGCTCTTATTTCTGG	2532
OY	2461	GCTTTCACAGCTGCTGTGCGAGAACTGCGCAGGGCTTGGAGCGGAGCGGGGAGGCTCT	2520
Db	2533	GCTTTCACAGCTGCTGTGCGAGAACTGCGCAGGGCTTGGAGCGGAGCGGGGAGGCTCT	2592
OY	2521	GCCAGCGGGGGCCCCGGGCTTGGCATGCTCACTAGACAGCGCTTGGCTCTTACCTC	2580
Db	2593	GCCAGCGGGGGCCCCGGGCTTGGCATGCTCACTAGACAGCGCTTGGCTCTTACCTC	2652
OY	2581	GCCGACAGCTGGAAACCATGTGCACTTAGTGGCTTCACTGTCTTCTCTGGGCGTGGGCG	2640
Db	2653	GCCGACAGCTGGAAACCATGTGCACTTAGTGGCTTCACTGTCTTCTCTGGGCGTGGGCG	2712
OY	2641	TGCGGGCTGACCCCCGGGCTTTGTACACCTGGGGCGGACCTGCTCTGTCATCGACTTCATG	2700
Db	2713	TGCGGGCTGACCCCCGGGCTTTGTACACCTGGGGCGGACCTGCTCTGTCATCGACTTCATG	2772
OY	2701	GTTTTCACGGTGCGGCTGTTCACATCTTCAACGGTCAACAAACAGCTGGGCGCCAAAGTC	2760
Db	2773	GTTTTCACGGTGCGGCTGTTCACATCTTCAACGGTCAACAAACAGCTGGGCGCCAAAGTC	2832
OY	2761	GTATTCGTGACCAAGATGATGAAAGAGCTGTTCTTCTCTCTTCTTCTCGGCGTGTGG	2820
Db	2833	GTATTCGTGACCAAGATGATGAAAGAGCTGTTCTTCTCTCTTCTTCTCGGCGTGTGG	2892
OY	2821	CTGGTATCCATATGGCCGTGGGACAGAGAGGGCTCTGAGGCGACAGGGACATGTGACTTCCCA	2880
Db	2893	CTGGTATCCATATGGCCGTGGGACAGAGAGGGCTCTGAGGCGACAGGGACATGTGACTTCCCA	2952
OY	2881	AGTATCCTGGCGCGGCTCTTCTTACACCGTCCCTTACCTGACAGATCTTGGGCGAGATTCGCCAG	2940
Db	2953	AGTATCCTGGCGCGGCTCTTCTTACACCGTCCCTTACCTGAGATCTTGGGCGAGATTCGCCAG	3012
OY	2941	GAGGACATGACGTGGCTTCAATGAGACACAGCACTGCTGTGGAGCCCGGCTTCTGG	3000

Db 3013 GAGGATCATGACGTGGCCCTCATGAGACAGCAACCTGCTGTCGAGCCCGGCTTCTGG 3072
 Qy 3001 GCAACACCTCTCTGGGGCCCAAGCGGGCACTGCTCTCCAGTATGCAACCTGGCTGGT 3060
 Db 3073 GCAACACCTCTCTGGGGCCCAAGCGGGCACTGCTCTCCAGTATGCAACCTGGCTGGT 3132
 Qy 3061 GTGCTGCTCTGTCATCTTCTGCTGTCGTCGCAACATCTGCTGTCGCACTTGTCTCAT 3120
 Db 3133 GTGCTGCTCTGTCATCTTCTGCTGTCGTCGCAACATCTGCTGTCGCACTTGTCTCAT 3192
 Qy 3121 GCCATGTCATTTACATTTGGGCAAGTATAGAGGCAACACCATCTCTACTGGAAGCG 3180
 Db 3193 GCCATGTCATTTACATTTGGGCAAGTATAGAGGCAACACCATCTCTACTGGAAGCG 3252
 Qy 3181 CAGGCTTACCCGCTCATCCGGGAATTCCACTCTGGGCGCGGCTGGGCCCCGCTTATC 3240
 Db 3253 CAGGCTTACCCGCTCATCCGGGAATTCCACTCTGGGCGCGGCTGGGCCCCGCTTATC 3312
 Qy 3241 GTCATCTCCCACTTGGCGCTCTCTGTCAGGCAATTTGTGCAAGGCAACCCCGAGCCCCCAG 3300
 Db 3313 GTCATCTCCCACTTGGCGCTCTCTGTCAGGCAATTTGTGCAAGGCAACCCCGAGCCCCCAG 3372
 Qy 3301 CCGTCTCTCCCGGCTCTGAGCAATTTCCGGGTTTACCTTTCTAAGAAAGCCGAGCGAG 3360
 Db 3373 CCGTCTCTCCCGGCTCTGAGCAATTTCCGGGTTTACCTTTCTAAGAAAGCCGAGCGAG 3432
 Qy 3361 CTGCTAAGTGGGAATCGGTGATTAAGGAATTTCTGTCGACGCGCTAAGGAACAG 3420
 Db 3433 CTGCTAAGTGGGAATCGGTGATTAAGGAATTTCTGTCGACGCGCTAAGGAACAG 3492
 Qy 3421 CGGAGAGCGAATCCGAGCGTCTGTAAGCGCACTGTCGCAAGAGTGAATTGGCACTGAAA 3480
 Db 3493 CGGAGAGCGAATCCGAGCGTCTGTAAGCGCACTGTCGCAAGAGTGAATTGGCACTGAAA 3552
 Qy 3481 CAGCTGGGACATTCGCGGAATTAAGAACAGGCGCTGAAAGTGTGAGCGGAGAGTCCAG 3540
 Db 3553 CAGCTGGGACATTCGCGGAATTAAGAACAGGCGCTGAAAGTGTGAGCGGAGAGTCCAG 3612
 Qy 3541 CAGTGTAGCCGCTGCTGGGGTGGGTGGCGAGGCGCTGAGCGCTGCTGCTGCTGCC 3600
 Db 3613 CAGTGTAGCCGCTGCTGGGGTGGGTGGCGAGGCGCTGAGCGCTGCTGCTGCTGCC 3672
 Qy 3601 CCAAGTGGGCGGCAACCCCTGACCTGCTGGGTTCCAAAGAC 3642
 Db 3673 CCAAGTGGGCGGCAACCCCTGACCTGCTGGGTTCCAAAGAC 3714

RESULT 5
 AAD32372
 ID AAD32372 standard; cDNA; 4042 BP.

AC AAD32372;
 XX
 DT 18-JUN-2002. (first entry)
 DE Human Trp9 protein encoding cDNA.
 XX
 XX Human: prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
 KW transient receptor potential; calcium channel protein; Trp8; Trp8b;
 KW molecular marker; endometrial cancer; uterine carcinoma; melanoma; gene;
 KW tumour; chorion carcinoma; lung cancer; antisense therapy; ss.
 XX
 OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT CDS 42..3686
 FT /*tag= a
 FT /product= "Human Trp9 protein"

XX
 XX
 XX
 XX
 XX
 PD 07-FEB-2002.

PF 18-JUL-2001; 2001WO-EP008309.
 XX
 XX 28-JUL-2000; 2000US-0221513P.
 XX
 PA (WISS/) WISSENBAACH U.
 XX
 XX Wissenbach U;
 XX PI
 XX DR WPI; 2002-269013/31.
 XX P-PSDB; AAE20283.
 PT Novel isolated nucleic acid encoding human prostate carcinoma associated
 PT protein such as transient receptor potential 8a, 8b, 10a, 10b proteins,
 PT useful as molecular markers for diagnosing prostate cancer.
 PS Claim 1; Fig 9a; 70pp; English.
 XX
 XX The invention relates to human prostate carcinoma associated proteins
 CC such as transient receptor potential (Trp8a, Trp8b, Trp9, Trp10a and
 CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8, Trp9,
 CC Trp10 are novel calcium channel proteins. Sequences of the invention are
 CC useful as molecular markers for diagnosing prostate cancer. Sequences of
 CC the invention, their antibodies, inhibitors and antisense molecules are
 CC useful for preventing, treating or ameliorating a prostate tumour,
 CC endometrial cancer (uterine carcinoma), tumour, a chorion carcinoma,
 CC cancer of the lung or melanoma. Polynucleotides of the invention are used
 CC in antisense therapy. The present sequence is human Trp9 protein encoding
 CC cDNA
 XX
 SQ Sequence 4042 BP; 703 A; 1260 C; 1290 G; 789 T; 0 U; 0 Other;
 Query Match 100.0%; Score 3640.4; DB 6; Length 4042;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3641; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGTGTGTCGCGAAGAGAGAGAGTGGATCCCAAGTCTTCAAGAAAGACCTGC 60
 Db 42 ATGGTGTGTCGCGAAGAGAGAGAGTGGATCCCAAGTCTTCAAGAAAGACCTGC 101
 Qy 61 ACAGACGTTCAATGATGATCTCCACAGATCCGGGAGGAGCTTGCCAGTGTGGGCGCCC 120
 Db 102 ACAGACGTTCAATGATGATCTCCACAGATCCGGGAGGAGCTTGCCAGTGTGGGCGCCC 161
 Qy 102 ACAGACGTTCAATGATGATCTCCACAGATCCGGGAGGAGCTTGCCAGTGTGGGCGCCC 161
 Db 121 CGGACCGCCACCCCGAGTGGCCATGAGAGATGCTTCGAGGCGAGCCGCTGTGACCTG 180
 Qy 162 CGGACCGCCACCCCGAGTGGCCATGAGAGATGCTTCGAGGCGAGCCGCTGTGACCTG 221
 Db 181 TGGGACAGCATGACACACACGAGAGAGCCACCGATGCTTACGAGAGCTGACCTTC 240
 Qy 222 TGGGACAGCATGACACACACGAGAGAGCCACCGATGCTTACGAGAGCTGACCTTC 281
 Db 241 ACGGGGGCGGGCGGCAAGACACAGATTTCTCCGCTCTGACCGGAACGATCCAGCT 300
 Qy 282 ACGGGGGCGGGCGGCAAGACACAGATTTCTCCGCTCTGACCGGAACGATCCAGCT 341
 Db 301 GCAGTTATATGCTGTGTCACACGACATGAGGCTTCGAGCCCGGACCTGTGATGTC 360
 Qy 342 GCAGTTATATGCTGTGTCACACGACATGAGGCTTCGAGCCCGGACCTGTGATGTC 401
 Db 361 GTGCTGGGGGATGCGGGGGGCGCTGCTCAGACCTGCTGAGAGACCTGCTGCTGCT 420
 Qy 402 GTGCTGGGGGATGCGGGGGGCGCTGCTCAGACCTGCTGAGAGACCTGCTGCTGCT 461
 Db 421 GGGCTGTGGGGCTCCCAAGACACAGAGCCTGATGTCATCTGGGGGCTGCAACAG 480
 Qy 462 GGGCTGTGGGGCTCCCAAGACACAGAGCCTGATGTCATCTGGGGGCTGCAACAG 521
 Db 481 GGCATCGGCGGATGTTGTTGCTGTACGAGGACATCATGATGTCGACATCTGGGGGC 540
 Qy 522 GGCATCGGCGGATGTTGTTGCTGTACGAGGACATCATGATGTCGACATCTGGGGGC 581
 Db 541 ACCAAGTGTGCGCATGGGTGTGCCCCCTGGGGTGTGGTCCGGAATAGACACCTTC 600

Dh 582 ACCAAGGTGATGTCATGAGTGTGCCCCCTGAGGTGTGTCCGGAATAGACACCCCTC 641
Qy ATCAACCCCAAGGGGCTGTTCCCTGCGAGGTACCGGTGGCGGGTGACCCCGAGAGACGGG 660
Dh 661 ATCAACCCCAAGGGGCTGTTCCCTGCGAGGTACCGGTGGCGGGTGACCCCGAGAGACGGG 701
Qy 661 GTCCAGTTTCCCTGGAATCAACTACTGCGCTTCTTCTGTGTGAAGACGGGACACAC 720
Dh 702 GTCCAGTTTCCCTGGAATCAACTACTGCGCTTCTTCTGTGTGAAGACGGGACACAC 761
Qy 721 GGTGCTGTTGGGGGGGAGAACCGCTTCCGCTTGGCTGAGTCTTACATCTCACAGCAG 780
Dh 762 GGTGCTGTTGGGGGGGAGAACCGCTTCCGCTTGGCTGAGTCTTACATCTCACAGCAG 821
Qy 781 AAGAGGGGCTGAGGAGGAGTGAATTGACATCCCTGTCTCTCTCTCTGATGTGT 840
Dh 822 AAGAGGGGCTGAGGAGGAGTGAATTGACATCCCTGTCTCTCTCTCTGATGTGT 881
Qy 841 GATGAGAGATGTGTACCGGAATAGAGAACGCGACCCAGGCTCAGCTCCCATGTCTCTC 900
Dh 882 GATGAGAGATGTGTACCGGAATAGAGAACGCGACCCAGGCTCAGCTCCCATGTCTCTC 941
Qy 901 GTGCTGTGCTCAGGGGGAGCTGCGGACTGCTGTGGCGAGACCCGTGAAGACACTGTGCG 960
Dh 942 GTGCTGTGCTCAGGGGGAGCTGCGGACTGCTGTGGCGAGACCCGTGAAGACACTGTGCG 1001
Qy 961 CCAAGGATGTGGGGAGGCCAGGAGCCAGACCCGAGATCGAATCAGGCGTTTCTTTCC 1020
Dh 1002 CCAAGGATGTGGGGAGGCCAGGAGCCAGACCCGAGATCGAATCAGGCGTTTCTTTCC 1061
Qy 1021 AAAAGGGACCTTGAAGTCTGTGAGGCGCCAGGTGAGAGGATTAATGACCCGAGAGAGCTC 1080
Dh 1062 AAAAGGGACCTTGAAGTCTGTGAGGCGCCAGGTGAGAGGATTAATGACCCGAGAGAGCTC 1121
Qy 1081 CTGACAGTCTAATCTTCTGAGGATGAGTCTGAGAAATTCAGAACCATAGTTTGAAGGCC 1140
Dh 1122 CTGACAGTCTAATCTTCTGAGGATGAGTCTGAGAAATTCAGAACCATAGTTTGAAGGCC 1181
Qy 1141 CTTGTGAGAGGCTGTGGAGACTCGGAGGCTTACGCTTACCTGTAGTGTGCTTGTGCT 1200
Dh 1182 CTTGTGAGAGGCTGTGGAGACTCGGAGGCTTACGCTTACCTGTAGTGTGCTTGTGCT 1241
Qy 1201 GTGCTTGAAGCCGAGGTGAGACATGCGAGAGTGAATCTTTGGGGGGGACATCCAAATG 1260
Dh 1242 GTGCTTGAAGCCGAGGTGAGACATGCGAGAGTGAATCTTTGGGGGGGACATCCAAATG 1301
Qy 1261 CGGTCTTCAATCTCTGAGAGTTCCTCTCATGAGCGCTGTGTAATGACCGGCTGAGTTC 1320
Dh 1302 CGGTCTTCAATCTCTGAGAGTTCCTCTCATGAGCGCTGTGTAATGACCGGCTGAGTTC 1361
Qy 1321 GTGCTTGTCTCATTTTCCACGAGCTTCAAGCTGTGGGCCATTTCTGACCCCGATGTGCGCTG 1380
Dh 1362 GTGCTTGTCTCATTTTCCACGAGCTTCAAGCTGTGGGCCATTTCTGACCCCGATGTGCGCTG 1421
Qy 1381 GCCCAACTCTACAGGCGGCGCCCTCCCACTGTGCTCATCCGCAACTTTTGAACCAAGGCG 1440
Dh 1422 GCCCAACTCTACAGGCGGCGCCCTCCCACTGTGCTCATCCGCAACTTTTGAACCAAGGCG 1481
Qy 1441 TCCCAACAGGAGGACCAAAAGCCCAAGCCCTAAAGAGGGAGCTGCGAGCTCGGCGCC 1500
Dh 1482 TCCCAACAGGAGGACCAAAAGCCCAAGCCCTAAAGAGGGAGCTGCGAGCTCGGCGCC 1541
Qy 1501 CTTGACGTGGGAGCATGTCTGAGAGTGTCTGTGGGAAAGATGTGCGGCGCAAGGTACCC 1560
Dh 1542 CTTGACGTGGGAGCATGTCTGAGAGTGTCTGTGGGAAAGATGTGCGGCGCAAGGTACCC 1601
Qy 1561 TCCCGGGGCGCTGGGAGCCCTCAACCAAGGCGAGGCTTCCGAGAGAGATGATGTGCTC 1620
Dh 1602 TCCCGGGGCGCTGGGAGCCCTCAACCAAGGCGAGGCTTCCGAGAGAGATGATGTGCTC 1661
Qy 1621 TCGGACAGGAGGACCTCGCTCTCGCTGAGTGTGAGCTTGGGAGAGCCCTGTGAGC 1680
Dh 1662 TCGGACAGGAGGACCTCGCTCTCGCTGAGTGTGAGCTTGGGAGAGCCCTGTGAGC 1721

Qy 1681 GACCTGCTTCTTTGGGGACCTGTGTGTAACAGGGACAGATGGGCCATGTACTTTCGGGAG 1740
Dh 1722 GACCTGCTTCTTTGGGGACCTGTGTGTAACAGGGACAGATGGGCCATGTACTTTCGGGAG 1781
Qy 1741 ATGGGTTCCAAATGACAGTTTCTTCCAGCTTGTGGGGCTGTTTGTCTGTCCGGGTGATGCA 1800
Dh 1782 ATGGGTTCCAAATGACAGTTTCTTCCAGCTTGTGGGGCTGTTTGTCTGTCCGGGTGATGCA 1841
Qy 1801 GCGCTGAGCTGACGCTGAGAGGACAGACGAGAGAAAGACCTGCGCTTCAAGTTTGA 1860
Dh 1842 GCGCTGAGCTGACGCTGAGAGGACAGACGAGAGAAAGACCTGCGCTTCAAGTTTGA 1901
Qy 1861 GGGATGGGCGTTGACCTTGTGGGAGTGTGATGAGCAGTGAAGTGAAGGCTGCGCCG 1920
Dh 1902 GGGATGGGCGTTGACCTTGTGGGAGTGTGATGAGCAGTGAAGTGAAGGCTGCGCCG 1961
Qy 1921 CTCTCTCTCGCTGCTGCGCTCTGAGGGGAGATGCACTTGTCTGCACTGAGCCATGCA 1980
Dh 1962 CTCTCTCTCGCTGCTGCGCTCTGAGGGGAGATGCACTTGTCTGCACTGAGCCATGCA 2021
Qy 1981 GCTGACGCGGCTGCTTCTTGTCCAGAGATGAGGTACAGTCTGTGACACAGAGTGG 2040
Dh 2022 GCTGACGCGGCTGCTTCTTGTCCAGAGATGAGGTACAGTCTGTGACACAGAGTGG 2081
Qy 2041 TGGGAGATATGGCTGACACTACACCATCTGGGCGCTGTGCTTCTTGTGCGCT 2100
Dh 2082 TGGGAGATATGGCTGACACTACACCATCTGGGCGCTGTGCTTCTTGTGCGCT 2141
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Dh 2142 CCACTCATCTACACCGGCTCATCACCTTCAAGAAATCAGAAAGAGAGCCACAGGGAG 2201
Qy 2161 GAGCTAGATTGACATGATAGTGTCTTAATGAGGAGAGGCGCTGTGGAGCGGAGC 2220
Dh 2202 GAGCTAGATTGACATGATAGTGTCTTAATGAGGAGAGGCGCTGTGGAGCGGAGC 2261
Qy 2221 CCAAGCCGAGAGAGCGCGCTGTGGGGTCCCGGCCACAGTGTGGGCTGTGCGGG 2280
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Qy 2281 GAGCGCTGCGGGGGGCGCGGCTGACGCGCTGAGTTCACCTTCTGAGGAGCGCGGCTG 2340
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Dh 2562 GCCAGCGGGGGCGCGGCGCTGTGCAATGCTCACTGAGCCAGCGCTGTGCTTACTC 2621
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Dh 2622 GCCGACAGCTGGAACCAAGTGTGACCTTGTGCTTCACTGTCTTCTGTGGGCTGAGG 2681
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Dh 2682 TGGCGGCTGACCCGCGGTTGTACACCTGTGGGCGGCACTGTCTGTGATGACTTATG 2741
Qy 2701 GTTTTCAGGCTGCGCTGCTTCACTTTCAGGCTTCAAAACAGCTGGGGCCCAAGATC 2760
Dh 2742 GTTTTCAGGCTGCGCTGCTTCACTTTCAGGCTTCAAAACAGCTGGGGCCCAAGATC 2801

QY	2761	GTCAATCGGACCAAGATATGATGAAGAAGTGTTCTTCTTCCTTCCTTCCTTCGAGGTGG	2820
Db	2802	GTCAATCGGACCAAGATATGATGAAGAAGTGTTCTTCTTCCTTCCTTCCTTCGAGGTGG	2861
QY	2821	CTGGTAGCCTATGAGCGTGGCCACGAGAGGAGCTCTCTGAGGCCACGAGCACTGACTTCCCA	2880
Db	2862	CTGGTAGCCTATGAGCGTGGCCACGAGAGGAGCTCTCTGAGGCCACGAGCACTGACTTCCCA	2921
QY	2881	AGTATCCCTGGGCGCGCTTCTTCTACCGTCCCTACCTGACGATCTTCGGGCGAGATTCCCCAG	2940
Db	2922	AGTATCCCTGGGCGCGCTTCTTCTACCGTCCCTACCTGACGATCTTCGGGCGAGATTCCCCAG	2981
QY	2941	GAGGACATGACGATGGCCCTCATGAGACACAGCAACTGCTGTGAGACCCTGGCTTCTGG	3000
Db	2982	GAGGACATGACGATGGCCCTCATGAGACACAGCAACTGCTGTGAGACCCTGGCTTCTGG	3041
QY	3001	GCACACCTCTCTGGGGGCCACGAGCGGACCTTGGCTTCTCCAGTATGCCAACTGGCTGGT	3060
Db	3042	GCACACCTCTCTGGGGGCCACGAGCGGACCTTGGCTTCTCCAGTATGCCAACTGGCTGGT	3101
QY	3061	GTGCTGCTCCTCGTCACTCTTCTGTGCTGAGCACAACCTGAGTGTCAACTTTCCTCAT	3120
Db	3102	GTGCTGCTCCTCGTCACTCTTCTGTGCTGAGCACAACCTGCTGTGTCAACTTTCCTCAT	3161
QY	3121	GCCATGTTCAATTACACTTTCGGCAAAATGACAGGCAACAGCGATCTCTACTGGAAGCG	3180
Db	3162	GCCATGTTCAATTACACTTTCGGCAAAATGACAGGCAACAGCGATCTCTACTGGAAGCG	3221
QY	3181	CAGGGTTACCGCTCATCCGGGAATTCACACTCTGGGCCGGGCGTGGCCGCCCTTATTC	3240
Db	3222	CAGGGTTACCGCTCATCCGGGAATTCACACTCTGGGCCGGGCGTGGCCGCCCTTATTC	3281
QY	3241	GTCAATCTTCCAATTGCGGCTCTCTGTACGAGCAATTGTGACAGCGACCCCGAGGCCCG	3300
Db	3282	GTCAATCTTCCAATTGCGGCTCTCTGTACGAGCAATTGTGACAGCGACCCCGAGGCCCG	3341
QY	3301	CCGTCTCTCCCGGCTCTGAGCAATTTCCGGGTTTAACTTTTAAAGAAAGCCGACCGGAG	3360
Db	3342	CCGTCTCTCCCGGCTCTGAGCAATTTCCGGGTTTAACTTTTAAAGAAAGCCGACCGGAG	3401
QY	3361	CTGCTAAAGTGGGAATCGTGCAATTAAGAGAACTTTCTGCTGAGCACGCGCTAGGAGCAAG	3420
Db	3402	CTGCTAAAGTGGGAATCGTGCAATTAAGAGAACTTTCTGCTGAGCACGCGCTAGGAGCAAG	3461
QY	3421	CGGAGAGACGACTCCGAGCGTGTGAAGCGCACGTTCCAGAAAGTGTGAATTGTGGCACTGAAA	3480
Db	3462	CGGAGAGACGACTCCGAGCGTGTGAAGCGCACGTTCCAGAAAGTGTGAATTGTGGCACTGAAA	3521
QY	3481	CAGCTGGAGCAATCCGAGGATGCGAAACAGGCGCTGAAAGTGTGAGCGGAGAGTCCAG	3540
Db	3522	CAGCTGGAGCAATCCGAGGATGCGAAACAGGCGCTGAAAGTGTGAGCGGAGAGTCCAG	3561
QY	3541	CAGTGTAGCCGCGCTCTGGAGGTGGGTGGCCGAGGCGCTGAGCCGCTGCTTGTCTGCCC	3600
Db	3582	CAGTGTAGCCGCGCTCTGGAGGTGGGTGGCCGAGGCGCTGAGCCGCTGCTGCTTGTCTGCCC	3641
QY	3601	CCAGGTGGGCGGCAACCCCTTGACCTGTGCTGTGATCAAAAGC	3642
Db	3642	CCAGGTGGGCGGCAACCCCTTGACCTGTGCTGTGATCAAAAGC	3683

XX	RESULT 6
XX	ABK92224
ID	ABK92224 standard; DNA; 3501 BP.
XX	
AC	ABK92224;
XX	
DT	15-AUG-2002 (first entry)
XX	
DE	Prostate cancer-associated DNA sequence #110.
XX	
XX	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW	gene therapy; gene; ds.

XX	Mammalia.
XX	
XX	WO200230268-A2.
XX	
PD	18-APR-2002.
XX	
PF	12-OCT-2001; 2001WO-US032045.
XX	
XX	13-OCT-2000; 2000US-00687576.
PR	08-DEC-2000; 2000US-00733288.
PR	08-DEC-2000; 2000US-00733742.
PR	24-JAN-2001; 2001US-0263957P.
PR	16-MAR-2001; 2001US-0276791P.
PR	16-MAR-2001; 2001US-0276888P.
PR	06-APR-2001; 2001US-0281922P.
PR	24-APR-2001; 2001US-0286214P.
PR	30-APR-2001; 2001US-00847046.
PR	04-MAY-2001; 2001US-0288589P.
XX	(E0SB-)EOS BIOTECHNOLOGY INC.
PA	
P1	Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX	
DR	WPI; 2002-471335/50.
DR	P-PSDB; ABG61907.
XX	
PT	Detecting a prostate cancer-associated transcript in a cell in a patient,
PT	useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT	by determining if prostate cancer-associated genes are expressed in a
PT	prostate tissue.
PS	Claim 22; Page 390-391; 436pp; English.
XX	
XX	The present invention relates to methods of detecting a prostate cancer-
CC	associated transcript in a cell from a patient. The method comprises
CC	associating a biological sample from the patient with prostate cancer-
CC	associated polynucleotides (designated PC genes) that selectively
CC	hybridize to a sequence that is at least 80% identical to them. The
CC	prostate cancer-associated polynucleotide sequences are differentially
CC	expressed in prostate tumour tissue or in prostate cancer and are derived
CC	from the tissues of various organisms such as humans or other mammals
CC	(e.g. mice, sheep and dogs). The methods of the invention are useful for
CC	diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC	associated genes are useful for diagnosing or treating prostate cancer,
CC	as well as for identifying modulators of prostate cancer or agents that
CC	inhibit prostate cancer. The nucleic acid sequences are particularly
CC	useful in gene therapy, as a vaccine or in antisense applications.
CC	ABX32115-ABK92263 represent prostate cancer-associated polynucleotide
CC	sequences
SQ	Sequence 3501 BP; 579 A; 1094 C; 1131 G; 697 T; 0 U; 0 Other:
Query Match	96.0%; Score 3498; DB 6; Length 3501;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 3498; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	145 ATGGAGGATGCGCTTCGGGGGCACGCGGTGAACCGTGTGGACAGGATGACACACACG 204
Db	1 ATGGAGGATGCGCTTCGGGGGCACGCGGTGAACCGTGTGGACAGGATGACACACACG 60
OY	205 GAGAAGCCCAACCATGACTTACGAGAGCTGACATTACGCGGGGCCGCGCAGAACAGACG 264
Db	61 GAGAAGCCCAACCATGACTTACGAGAGAGTGACATTACGCGGGGCCGCGCAGAACAGACG 120
OY	265 AATTTCCTCGGACTTCTGACCAGAAAGGATCCAGCTGACATTATAGTCTGGTCAACGCG 324
Db	121 AATTTCCTCGGACTTCTGACCAGAAAGGATCCAGCTGACATTATAGTCTGGTCAACGCG 180
OY	325 ACATGGGGCTTCGCGCCCCGCAACCTGTGGTGTAGAGCTGGGGGGATCCGGGGGGCCCC 384
Db	181 ACATGGGGCTTCGCGCCCCGCAACCTGTGGTGTAGAGCTGGGGGGATCCGGGGGGCCCC 240

Qy 385 GTCCCTCAGAACCTGAGAGGACCTGCTCGTGGGCTGCTGCGGGCTGCCAGAGC 444
|
|
Db 241 GTCCCTCAGAACCTGAGAGGACCTGCTCGTGGGCTGCTGCGGGCTGCCAGAGC 300
|
|
Qy 445 ACAGAGGCTTGAGATTGTCACTGAGGGGTCTGCAACGGGATGAGCGGATGTTGGTGTG 504
|
|
Db 301 ACAGAGGCTTGAGATTGTCACTGAGGGGTCTGCAACGGGATGAGCGGATGTTGGTGTG 360
|
|
Qy 505 GCTGACGGGACCAATCAATATGCGACATGAGGGGACCAAGGTGTGGCCATGGGTGTG 564
|
|
Db 361 GCTGACGGGACCAATCAATATGCGACATGAGGGGACCAAGGTGTGGCCATGGGTGTG 420
|
|
Qy 565 GCCCCTGAGGGGTGTGTGCTCGGAAATAGAGACACCTCATCAACCCCAAGGGCTGTTCCT 624
|
|
Db 421 GCCCCTGAGGGGTGTGTGCTCGGAAATAGAGACACCTCATCAACCCCAAGGGCTGTTCCT 480
|
|
Qy 625 GCGAGGTACCGGTGCGCGGTGACCCGAGAGAGGGGTCTCAATTTCCCTGAGCTTACAC 684
|
|
Db 481 GCGAGGTACCGGTGCGCGGTGACCCGAGAGAGGGGTCTCAATTTCCCTGAGCTTACAC 540
|
|
Qy 685 TACTGCGCTTCTTCTGTGTGAGACGCGACACACGCGTGTGCTGGGGGCGAGAACCGC 744
|
|
Db 541 TACTGCGCTTCTTCTGTGTGAGACGCGACACACGCGTGTGCTGGGGGCGAGAACCGC 600
|
|
Qy 745 TTCCGCTTGCGGCTGAGATCTACATCTACAGAGAAAGACGGGGGTGGAGGAGCTGGA 804
|
|
Db 601 TTCCGCTTGCGGCTGAGATCTACATCTACAGAGAAAGACGGGGGTGGAGGAGCTGGA 660
|
|
Qy 805 ATTGACATCCCTGTCTCTCTCTCTGATTTGATGATGAGAGATGTTGACGGAAAT 864
|
|
Db 661 ATTGACATCCCTGTCTCTCTCTCTGATTTGATGATGAGAGATGTTGACGGAAAT 720
|
|
Qy 865 GAGAACGCGACCCAGAGGCTCAGTCCCATGTCTCTGTGGCTGCTCAGGGGAGAGCTGC 924
|
|
Db 721 GAGAACGCGACCCAGAGGCTCAGTCCCATGTCTCTGTGGCTGCTCAGGGGAGAGCTGC 780
|
|
Qy 925 GACTGCTTGAGGAGAGACCTGGAGAGACCTGAGGCCAGGGAGTGGGGAGAGCGAGAA 984
|
|
Db 781 GACTGCTTGAGGAGAGACCTGGAGAGACCTGAGGCCAGGGAGTGGGGAGAGCGAGAA 840
|
|
Qy 985 GCGGAGGCCGAGATCGAATGAGGCGTTCCTTCCCAAAGGGAGCTTGAAGTCTCTGAG 1044
|
|
Db 841 GCGGAGGCCGAGATCGAATGAGGCGTTCCTTCCCAAAGGGAGCTTGAAGTCTCTGAG 900
|
|
Qy 1045 GCCCAGGTGAGAGAGATTATGACCCGAGAGAGCTCTGACAGTCTATTCTTGAAGAT 1104
|
|
Db 901 GCCCAGGTGAGAGAGATTATGACCCGAGAGAGCTCTGACAGTCTATTCTTGAAGAT 960
|
|
Qy 1105 GGGTCTGAGGAATTGAGACCATAGTTTGAAGGCCCTTGAAGGCCCTGTGGAGCTGC 1164
|
|
Db 961 GGGTCTGAGGAATTGAGACCATAGTTTGAAGGCCCTTGAAGGCCCTGTGGAGCTGC 1020
|
|
Qy 1165 GAGGCTCAGGCTACCTGATAGAGTGTGCTGTGGCTTGGACCCGCTGAGACATT 1224
|
|
Db 1201 GAGGCTCAGGCTACCTGATAGAGTGTGCTGTGGCTTGGACCCGCTGAGACATT 1080
|
|
Qy 1225 GCCCAGAGTGAATCTTTTGGGGGAGACATCCAAATGCGGCTCTTCCATCTGAGACTTCC 1284
|
|
Db 1081 GCCCAGAGTGAATCTTTTGGGGGAGACATCCAAATGCGGCTCTTCCATCTGAGACTTCC 1140
|
|
Qy 1285 CTCATGAGCGGCTGCTGAATGACCGGCTGATGTCGGCTTGGCTGCTATTTCCACGGC 1344
|
|
Db 1141 CTCATGAGCGGCTGCTGAATGACCGGCTGATGTCGGCTTGGCTGCTATTTCCACGGC 1200
|
|
Qy 1345 CTCAGCCTGGGCACTTCTCTGACCCGATGCGCTGAGCCCAACTACAGCGCGCGCC 1404
|
|
Db 1201 CTCAGCCTGGGCACTTCTCTGACCCGATGCGCTGAGCCCAACTACAGCGCGCGCC 1260
|
|
Qy 1405 TCCAACTGCTCATTCGCAACTTTTGGACCAAGGCGTCCACAGCGAGGACCAAAAGCC 1464
|
|
Db 1261 TCCAACTGCTCATTCGCAACTTTTGGACCAAGGCGTCCACAGCGAGGACCAAAAGCC 1320
|
|
Qy 1465 CCAAGCCCTAAAGGGGAGCTGCGGAGCTCCGAGCCCTGACGTGGGCAATGTGTAAG 1524
|
|
|

Db 1321 CCAAGCCCTAAAGGGGAGCTGCGGAGCTCCGAGCCCTTGAAGTGGGCAATGTGTAAG 1380
|
|
Qy 1525 ATGCTGCTGGGAAAGATGTGCGCGAGGTAACCTCTCGGGGCGCTGGAGCCCTCAC 1584
|
|
Db 1381 ATGCTGCTGGGAAAGATGTGCGCGAGGTAACCTCTCGGGGCGCGCTGGAGCCCTCAC 1440
|
|
Qy 1585 CCAAGCCGAGGCTTGGGGAAGCATGTATGCTCTTGGACAAAGCCACTTGGCGCTC 1644
|
|
Db 1441 CCAAGCCGAGGCTTGGGGAAGCATGTATGCTCTTGGACAAAGCCACTTGGCGCTC 1500
|
|
Qy 1645 TCGCTGATGTGCGCTGAGGCAAGCCCTGAGAGCACTGCTTCTTGGGCACTGTTG 1704
|
|
Db 1501 TCGCTGATGTGCGCTGAGGCAAGCCCTGAGAGCACTGCTTCTTGGGCACTGTTG 1560
|
|
Qy 1705 CTGAACAGGAGCAAGATGGCCATGTACTTCTGGAGATGGGTTCCATGACAGTTTCTCA 1764
|
|
Db 1561 CTGAACAGGAGCAAGATGGCCATGTACTTCTGGAGATGGGTTCCATGACAGTTTCTCA 1620
|
|
Qy 1765 GCTCTTGGGGCTCTTGTGCTGCTCGGGTATGCGACGCTGAGACCTGAGCGTGAAGAG 1824
|
|
Db 1621 GCTCTTGGGGCTCTTGTGCTGCTCGGGTATGCGACGCTGAGACCTGAGCGTGAAGAG 1680
|
|
Qy 1825 GCAGCAGGAGAAAGACCTGAGCTTCAAGTTTGAAGGGATGGGGTTGACCTTTGGC 1884
|
|
Db 1681 GCAGCAGGAGAAAGACCTGAGCTTCAAGTTTGAAGGGATGGGGTTGACCTTTGGC 1740
|
|
Qy 1885 GAGTGTATCGCAGCAGTGAAGTGAAGGCTCCGCGCTCTCTCGTGTGCTCCGCTC 1944
|
|
Db 1741 GAGTGTATCGCAGCAGTGAAGTGAAGGCTCCGCGCTCTCTCGTGTGCTCCGCTC 1800
|
|
Qy 1945 TGGGGGATGCGCATTTGCTTCACTGCGCATGCGACCTGACGCGCTTCTTTGCC 2004
|
|
Db 1801 TGGGGGATGCGCATTTGCTTCACTGCGCATGCGACCTGACGCGCTTCTTTGCC 1860
|
|
Qy 2005 CAGATGGGATGACGTCTGCTGACAGAAAGTGTGGGAGATATGAGCCAGACTACA 2064
|
|
Db 1861 CAGATGGGATGACGTCTGCTGACAGAAAGTGTGGGAGATATGAGCCAGACTACA 1920
|
|
Qy 2065 CCAATCTGGGCTGCTGCTTCTGCTTCTTGGCCCTCACTCATCTACACCGCTCATC 2124
|
|
Db 1921 CCAATCTGGGCTGCTGCTTCTGCTTCTTGGCCCTCACTCATCTACACCGCTCATC 1980
|
|
Qy 2125 ACCTTCAAGGAATAGAAAGAGAGCCACAGGAGAGAGCTTAGAGTTGACATGATAGT 2184
|
|
Db 1981 ACCTTCAAGGAATAGAAAGAGAGCCACAGGAGAGAGCTTAGAGTTGACATGATAGT 2040
|
|
Qy 2185 GTCAATTAATGGGAAAGGCGCTGTGAGAGCGGCGGACCCAGCGGAGAAAGACCGCTGGGG 2244
|
|
Db 2041 GTCAATTAATGGGAAAGGCGCTGTGAGAGCGGCGGACCCAGCGGAGAAAGACCGCTGGGG 2100
|
|
Qy 2245 GTCCCGCGCAGTGGGCGGTGCTGCGGGGTTGCTGCGGGGCGCTGCGGGGCGCGGATG 2304
|
|
Db 2101 GTCCCGCGCAGTGGGCGGTGCTGCGGGGTTGCTGCGGGGCGCTGCGGGGCGCGGATG 2160
|
|
Qy 2305 CTACGCGCTGTGTTCACTTGTGAGGCGCGCGGTGACCATCTTCAATGAGCAAGTGTG 2364
|
|
Db 2161 CTACGCGCTGTGTTCACTTGTGAGGCGCGCGGTGACCATCTTCAATGAGCAAGTGTG 2220
|
|
Qy 2365 AGCTAACGCTGCTGCTGCTGCTTCTGCGGGGTGCTGCGGAGATTTCACGCGGCG 2424
|
|
Db 2221 AGCTAACGCTGCTGCTGCTGCTTCTGCGGGGTGCTGCGGAGATTTCACGCGGCG 2280
|
|
Qy 2425 CCGCGCGGCTCTGAGAGCTGCTGCTTCTGAGGCTTTCACGCTGCTGTGAGAGAA 2484
|
|
Db 2281 CCGCGCGGCTCTGAGAGCTGCTGCTTCTGAGGCTTTCACGCTGCTGTGAGAGAA 2340
|
|
Qy 2485 CTGCGCAAGGCTGAGCGAGGCGGAGGAGCTTCCGACAGGGGAGCCCGGCGCTGGC 2544
|
|
Db 2341 CTGCGCAAGGCTGAGCGAGGCGGAGGAGCTTCCGACAGGGGAGCCCGGCGCTGGC 2400
|
|
Qy 2545 CATGCTCATGAGCCAGCGCGCTGCGCTCACTCCGCAACACTGGAACCAATGAGAC 2604
|
|
|

Db 1981 ACCTTAGAGAAATCAGAGAGAGAGCCACACAGGAGAGACTGAGTTGATGATGATGAT 2040
Qy 2185 GTCAATTAATGAGGAGAGGAGGCTGTGCGGAGACGCGGAGCCAGCCGAGAGAGAGCGCGCTGAGG 2244
Db 2041 GTCAATTAATGAGGAGAGGAGGCTGTGCGGAGACGCGGAGCCAGCCGAGAGAGAGCGCGCTGAGG 2100
Qy 2245 GTCCGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGG 2304
Db 2101 GTCCGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGG 2160
Qy 2305 GTACGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGG 2364
Db 2161 GTACGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGGAGGCTGTGCGG 2220
Qy 2365 AGCTACCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2424
Db 2221 AGCTACCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2280
Qy 2425 CCGCGCGGAGGCTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2484
Db 2281 CCGCGCGGAGGCTGTGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 2340
Qy 2485 CTGCGCGAGAGGCTGTGAGGAGGCGGAGGAGGCTGTGCGAGGCGGAGGCGGAGGCGGAGGCGG 2544
Db 2341 CTGCGCGAGAGGCTGTGAGGAGGCGGAGGAGGCTGTGCGAGGCGGAGGCGGAGGCGGAGGCGG 2400
Qy 2545 CATGCTCTCACTAGGACGAGGCGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2604
Db 2401 CATGCTCTCACTAGGACGAGGCGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2460
Qy 2605 CTAGTGGCTCTGACCTGTCTCTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2664
Db 2461 CTAGTGGCTCTGACCTGTCTCTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2520
Qy 2665 GACCTGTGGGCGGAGCTGTCTCTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2724
Db 2521 GACCTGTGGGCGGAGCTGTCTCTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2580
Qy 2725 ATCTTCACTGATCAAGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGT 2784
Db 2581 ATCTTCACTGATCAAGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGT 2640
Qy 2785 GACGTGTCTTCT 2844
Db 2641 GACGTGTCTTCT 2700
Qy 2845 GAGGGGCTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2904
Db 2701 GAGGGGCTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2760
Qy 2905 CGTCCCTCACTGAGATCTTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2964
Db 2761 CGTCCCTCACTGAGATCTTCTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAG 2820
Qy 2965 GAGCAAGCAAGCTGTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 3024
Db 2821 GAGCAAGCAAGCTGTCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 2880
Qy 3025 GGCACCTGTGCTCTCCAGATAGCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3084
Db 2881 GGCACCTGTGCTCTCCAGATAGCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2940
Qy 3085 CTGCTGTGCAATCTGT 3144
Db 2941 CTGCTGTGCAATCTGT 3000
Qy 3145 AAAGTACAGAGGCAAGCAGATCTTCTGAAAGGCGCAGCGTTCACGCTCAATCCGAGGAA 3204
Db 3001 AAAGTACAGAGGCAAGCAGATCTTCTGAAAGGCGCAGCGTTCACGCTCAATCCGAGGAA 3060
Qy 3205 TTTCACCTCTGCGGCGCGGCTGTGCGGCGGCTGTGCGGCGGCTGTGCGGCGGCTGTGCGGCGG 3264
Db 3061 TTTCACCTCTGCGGCGCGGCTGTGCGGCGGCTGTGCGGCGGCTGTGCGGCGGCTGTGCGGCGG 3120

Qy 3265 CTCAGGCAATTGTGAGGCGAGCCCGAGAGCCCGAGGCGGCTCTCTCCCGGCTGTGAGCAT 3324
Db 3121 CTCAGGCAATTGTGAGGCGAGCCCGAGAGCCCGAGGCGGCTCTCTCCCGGCTGTGAGCAT 3180
Qy 3325 TTCCGGGTTTACCTTCTTAAGAGAGCGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3384
Db 3181 TTCCGGGTTTACCTTCTTAAGAGAGCGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3240
Qy 3385 AAGAGAACTTCTCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3444
Db 3241 AAGAGAACTTCTCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3300
Qy 3445 AAGCGACGCTCCAGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGG 3504
Db 3301 AAGCGACGCTCCAGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGG 3360
Qy 3505 GAAACAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAG 3564
Db 3361 GAAACAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAG 3420
Qy 3565 GTGGCGAGGCGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3624
Db 3421 GTGGCGAGGCGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAG 3480
Qy 3625 CTGCTGTGGGTCCAAAGAC 3642
Db 3481 CTGCTGTGGGTCCAAAGAC 3498

RESULT 8
ADN39239
ID ADN39239 strand; cDNA; 4641 BP.
XX
AC ADN39239;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:57.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularisation syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
XX
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397757P.
PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX Afar D, Aziz N, Ginsburg WM, Gish KC, Glyme R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX WPI; 2003-468649/44.
DR P-PSDB; ADN39240.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
PS
PS Claim 8; SEQ ID NO 557; 1385bp; English.
XX
XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularization syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 4641 BP; 808 A; 1459 C; 1432 G; 942 T; 0 U; 0 Other;
Query Match 96.0%; Score 3498; DB 11; Length 4641;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 ATGAGAGTGCCTTGGGGGACCGGTGTGACCGTGTGGACAGGATGCACACACAGC 204
Db 769 ATGAGAGTGCCTTGGGGGACCGGTGTGACCGTGTGGACAGGATGCACACACAGC 828
QY 205 GAGAGGCCACCGATGCTTACGAGAGAGCTGACCTTACAGGGGGCCGGCCGACAGCAGC 264
Db 829 GAGAGGCCACCGATGCTTACGAGAGAGCTGACCTTACAGGGGGCCGGCCGACAGCAGC 888
QY 265 AATTTCCTCCGAGCTCTGACCGAAGGATCAGCTGAGTTTATGTTGATGTCACAGC 324
Db 889 AATTTCCTCCGAGCTCTGACCGAAGGATCAGCTGAGTTTATGTTGATGTCACAGC 948
QY 325 ACATGGGGCTTCCGTGCCCCGAACTGTGTGTGTCAGTGTGGGGGATTCGGGGGGCCCC 384
Db 949 ACATGGGGCTTCCGTGCCCCGAACTGTGTGTGTCAGTGTGGGGGATTCGGGGGGCCCC 1008
QY 385 GTCTTCAGAGCTGCTGACAGAGCTGCTGTGCTGTGGGCTGTGGGCTGCCAGAGC 444
Db 1009 GTCTTCAGAGCTGCTGACAGAGCTGCTGTGCTGTGGGCTGTGGGCTGCCAGAGC 1068
QY 445 ACAGAGAGCTGATGTCTCACTGGGGGCTGTGCAACAGGGGATCGGGCCGATGTTGATG 504
Db 1069 ACAGAGAGCTGATGTCTCACTGGGGGCTGTGCAACAGGGGATCGGGCCGATGTTGATG 1128
QY 505 GCTGTACGGGACATCAGATGGCCAGCATGTGGGGCACCAAGTGTGTGGCCATGGGTGTG 564
Db 1129 GCTGTACGGGACATCAGATGGCCAGCATGTGGGGCACCAAGTGTGTGGCCATGGGTGTG 1188
QY 565 GCCCGCTGGGGTGTGTGTCGGAATTAAGACACCTTCATCAACCCCAAGGGCTGTTCCCT 624
Db 1189 GCCCGCTGGGGTGTGTGTCGGAATTAAGACACCTTCATCAACCCCAAGGGCTGTTCCCT 1248
QY 625 GCGAGGTACCGGTGGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCTGGAATCAAC 684

Db 1249 GCGAGGTACCGGTGGCGGTGACCCGGAGGACGGGGTCCAGTTTCCCTGGAATCAAC 1308
QY 685 TACTCGGCTTCTTCTGTTGTGACGACGACACAGGCTCTCGGGGGGCGAAGACCCG 744
Db 1309 TACTCGGCTTCTTCTGTTGTGACGACGACACAGGCTCTCGGGGGGCGAAGACCCG 1368
QY 745 TTCCGCTTGGCGCTGAGAGTCTTACATCTCAAGGAGAGACGGGGCTGGAGGAGCTGA 804
Db 1369 TTCCGCTTGGCGCTGAGAGTCTTACATCTCAAGGAGAGACGGGGCTGGAGGAGCTGA 1428
QY 805 ATTGACATCCCTGTCCTGCTCTCTCTGATTTGATGATGATGAAGATTTGACCGGAATA 864
Db 1429 ATTGACATCCCTGTCCTGCTCTCTCTGATTTGATGATGATGAAGATTTGACCGGAATA 1488
QY 865 GAGAACGCCACCCAGAGCTCACTCTCATGTCTCTCTGCTGCTGCTGAGGGAGCTGCG 924
Db 1489 GAGAACGCCACCCAGAGCTCACTCTCATGTCTCTCTGCTGCTGCTGAGGGAGCTGCG 1548
QY 925 GACTGCTGGGGGAGACCTGGAAGACACTGTGGCCCGAGGAGTGGGGGAGCCAGGCA 984
Db 1549 GACTGCTGGGGGAGACCTGGAAGACACTGTGGCCCGAGGAGTGGGGGAGCCAGGCA 1608
QY 985 GCGGAGGCCGAGATCGAATCAGGCGTTTCTTCCAAAGGGGACCTTGAAGTCTGCGAG 1044
Db 1609 GCGGAGGCCGAGATCGAATCAGGCGTTTCTTCCAAAGGGGACCTTGAAGTCTGCGAG 1668
QY 1045 GCCCAGGTGAGAGATTAATGACCCGGAAGAGCTCTGACAGTCTATTTCTTGAGAT 1104
Db 1669 GCCCAGGTGAGAGATTAATGACCCGGAAGAGCTCTGACAGTCTATTTCTTGAGAT 1728
QY 1105 GGGTCTGAGAAATTCGACCATAGTTTGAAGCCCTTGGAAGCCCTGAGGAGCTCG 1164
Db 1729 GGGTCTGAGAAATTCGACCATAGTTTGAAGCCCTTGGAAGCCCTGAGGAGCTCG 1788
QY 1165 GAGGCTTCAGGCTTACCTGATGAGCTGCTGTGCTGTGCTGGAACCGGCTGAGACATT 1224
Db 1789 GAGGCTTCAGGCTTACCTGATGAGCTGCTGTGCTGTGCTGGAACCGGCTGAGACATT 1848
QY 1225 GCCCAGAGTGAATCTTTTGGGGGAGACATCCATAGGGGCTCTTCAATCTGAGAGCTTCC 1284
Db 1849 GCCCAGAGTGAATCTTTTGGGGGAGACATCCATAGGGGCTCTTCAATCTGAGAGCTTCC 1908
QY 1285 CTCAATGACCGCTGCTGAATGAACCGGCTGATGCTGTGCTGCTTATTTCCACGCG 1344
Db 1909 CTCAATGACCGCTGCTGAATGAACCGGCTGATGCTGTGCTGCTTATTTCCACGCG 1968
QY 1345 CTCAGCTGGGCACTTCTGACCCCGATGGGCTGTGGCCCAACTCTACAGGCGGGCGCC 1404
Db 1969 CTCAGCTGGGCACTTCTGACCCCGATGGGCTGTGGCCCAACTCTACAGGCGGGCGCC 2028
QY 1405 TCCAATCTGCTATCCGCAACTTTTGAACCAAGGCTGCCACAGCGAGGACCAAAAGCC 1464
Db 2029 TCCAATCTGCTATCCGCAACTTTTGAACCAAGGCTGCCACAGCGAGGACCAAAAGCC 2088
QY 1465 CCAAGCTTAAAGGGGAGAGCTGCGAGAGCTCGGCGCCCTGACGTTGGGGCATGTGCTAGG 1524
Db 2089 CCAAGCTTAAAGGGGAGAGCTGCGAGAGCTCGGCGCCCTGACGTTGGGGCATGTGCTAGG 2148
QY 1525 ATGCTGTGGGAGAGATGTGCGCGCGAGGTAACCTTCGAGGGGCGCTGGAGACCTTCAC 1584
Db 2149 ATGCTGTGGGAGAGATGTGCGCGCGAGGTAACCTTCGAGGGGCGCTGGAGACCTTCAC 2208
QY 1585 CCAAGGCAAGGCTTTCGGGAGAGAGCATATCTGCTTCGACCAAGGCACTTCGCGCTC 1644
Db 2209 CCAAGGCAAGGCTTTCGGGAGAGAGCATATCTGCTTCGACCAAGGCACTTCGCGCTC 2268
QY 1645 TCGCTGATGCTGGCTCTCGGGCAGAGCCCTTGAAGGCACTGCTTTTGGGCACTGTG 1704
Db 2269 TCGCTGATGCTGGCTCTCGGGCAGAGCCCTTGAAGGCACTGCTTTTGGGCACTGTG 2328
QY 1705 CTGAACAGGCAACAGATGCGCATGTACTTCTGGAGATGAGGTTCAATGAGTTTCTCA 1764

Db 2329 CTGAACAGGGGACAGATGGCCATGTACTTCTGGAGATGGGTTCCAAATGACGTTTCTTCA 2388
Qy 1765 GCTCTTGGGGGCTGTTTGTCTGCTCCGGGATGAGACGCTGGAGCTTGAAG 1824
Db 2389 GCTCTTGGGGGCTGTTTGTCTGCTCCGGGATGAGACGCTGGAGCTTGAAG 2448
Qy 1825 GCAGCAGGAGGAAAGACTGGCTTCAAGTTTGAAGGGATGGCGTTGACCTTTTGGC 1884
Db 2449 GCAGCAGGAGGAAAGACTGGCTTCAAGTTTGAAGGGATGGCGTTGACCTTTTGGC 2508
Qy 1885 GAGTCTATCCGAGAGTGAAGGTGAGGGGTGCGCCCTCTCTCCGTGCGTCCGCTC 1944
Db 2509 GAGTCTATCCGAGAGTGAAGGTGAGGGGTGCGCCCTCTCTCCGTGCGTCCGCTC 2568
Qy 1945 TGGGGGGAATGCACTTGGCTCCAGCTGGCCATGACGAGCTGACCGCCGTCCTTTTGGC 2004
Db 2569 TGGGGGGAATGCACTTGGCTCCAGCTGGCCATGACGAGCTGACCGCCGTCCTTTTGGC 2628
Qy 2005 CAGGATGGGGATCAGTCTCTGCTGACACAGAAAGTGGTGGGATATGGCCACGACTACA 2064
Db 2629 CAGGATGGGGATCAGTCTCTGCTGACACAGAAAGTGGTGGGATATGGCCACGACTACA 2688
Qy 2065 CCCATCTGGGCGCTGGTTCTGCGCTTCTTTTGGCCCTCCATCATGACACCGCCCTGATC 2124
Db 2689 CCCATCTGGGCGCTGGTTCTGCGCTTCTTTTGGCCCTCCATCATGACACCGCCCTGATC 2748
Qy 2125 ACCTTCAGGAATCAGAAAGAGAGCCACACAGGAGAGCTAGAGTTTGAATGATAGT 2184
Db 2749 ACCTTCAGGAATCAGAAAGAGAGCCACACAGGAGAGCTAGAGTTTGAATGATAGT 2808
Qy 2185 GTCAATTAATGGGGAAAGGGCTCTGCGGAGCGGCGAACCCAGAGAAAGCGCGCTGGG 2244
Db 2809 GTCAATTAATGGGGAAAGGGCTCTGCGGAGCGGCGAACCCAGAGAAAGCGCGCTGGG 2868
Qy 2245 GTCCCGCGGCAATCGGGCGCTGCGGGTTCTGCGGGGGCGCTGCGGGGGGGCGCGTGC 2304
Db 2869 GTCCCGCGGCAATCGGGCGCTGCGGGTTCTGCGGGGGCGCTGCGGGGGGGCGCGTGC 2928
Qy 2305 CTACGCGCGTGGTTCCACTTCTGGGGCGGCGGATGACCATCTTCAATGGGCAAGTGTC 2364
Db 2929 CTACGCGCGTGGTTCCACTTCTGGGGCGGCGGATGACCATCTTCAATGGGCAAGTGTC 2988
Qy 2365 AGCTACCTGCTGTTCTGCTGCTTTTCTGCGGGGTCTGCTGTGATTTTCAAGCGGCG 2424
Db 2989 AGCTACCTGCTGTTCTGCTGCTTTTCTGCGGGGTCTGCTGTGATTTTCAAGCGGCG 3048
Qy 2425 CCGCCCGGCTCCCTGAGAGTGTGCTCTTCTTCTGGGCTTTCAAGCTGTGTGCAAGGA 2484
Db 3049 CCGCCCGGCTCCCTGAGAGTGTGCTCTTCTTCTGGGCTTTCAAGCTGTGTGCAAGGA 3108
Qy 2485 CTGGCGCAGGGGCTGAGCGGAGGCGGGGAGGCTTGCAGCGGGGGGCCCGGGCTTGC 2544
Db 3109 CTGGCGCAGGGGCTGAGCGGAGGCGGGGAGGCTTGCAGCGGGGGGCCCGGGCTTGC 3168
Qy 2545 CATGCTCACTAGAGCCAGGCGCTGCGCTTCTACCTTGCAGACAGCTGAAACAGTGCAC 2604
Db 3169 CATGCTCACTAGAGCCAGGCGCTGCGCTTCTACCTTGCAGACAGCTGAAACAGTGCAC 3228
Qy 2605 CTAGTGGCTCTCACTGCTTCTCTCTGGGCGTGGGCTGCGCGGCTTGTAC 2664
Db 3229 CTAGTGGCTCTCACTGCTTCTCTCTGGGCGTGGGCTGCGCGGCTTGTAC 3288
Qy 2665 CACCTGGGCGGACGTCTCTGATGCACTTCAATGTTTTCACGCTGGGCGCTTTCAC 2724
Db 3289 CACCTGGGCGGACGTCTCTGATGCACTTCAATGTTTTCACGCTGGGCGCTTTCAC 3348
Qy 2725 ATCTTCACGCTCAACAAAGAGCTGGGCGCAAGATGATCATGTGAGCAAGATGATGA 2784
Db 3349 ATCTTCACGCTCAACAAAGAGCTGGGCGCAAGATGATCATGTGAGCAAGATGATGA 3408
Qy 2785 GAGGTGTTCTTCTTCTTCTTCTTCTGGGCGTGTGAGCTTGAAGCTTGAAGCTGACG 2844
Db 3409 GAGGTGTTCTTCTTCTTCTTCTTCTGGGCGTGTGAGCTTGAAGCTTGAAGCTGACG 3468

Qy 2845 GAGGGGCTCTGAGGCGACGAGACATGATCTTCCCAATCTTCCGCGCTTCTTAC 2904
Db 3469 GAGGGGCTCTGAGGCGACGAGACATGATCTTCCCAATCTTCCGCGCTTCTTAC 3528
Qy 2905 CGTCCCTACCTGAGATCTTGGGGGAGATTTCCCAAGAGAGCATGAGAGTGGCCCTCAG 2964
Db 3529 CGTCCCTACCTGAGATCTTGGGGGAGATTTCCCAAGAGAGCATGAGAGTGGCCCTCAG 3588
Qy 2965 GAGCACAACAATGCTCGTCCGAGGCGCGGCTTCTGGGACACCTCTTGGGGCCAGGCG 3024
Db 3589 GAGCACAACAATGCTCGTCCGAGGCGCGGCTTCTGGGACACCTCTTGGGGCCAGGCG 3648
Qy 3025 GGCACCTGCTCTCCAGATGCCATGAGCTGGTGTGCTCTCTGTCATCTTCTG 3084
Db 3649 GGCACCTGCTCTCCAGATGCCATGAGCTGGTGTGCTCTCTGTCATCTTCTG 3708
Qy 3085 CTCTGGGCAACATCTGCTGTCATCTTGGCACTTGGCAATGTTAGTTACATTTGGC 3144
Db 3709 CTCTGGGCAACATCTGCTGTCATCTTGGCACTTGGCAATGTTAGTTACATTTGGC 3768
Qy 3145 AAAGTACAGGCGCAAGGATCTTACTGAAAGGCGAGCTTACCGCTCATCCGAGAA 3204
Db 3769 AAAGTACAGGCGCAAGGATCTTACTGAAAGGCGAGCTTACCGCTCATCCGAGAA 3828
Qy 3205 TTCCACTCTGGGCGCGGCTGGCCCGCTTTATGTCATCTCCACTTGGCCTCTG 3264
Db 3829 TTCCACTCTGGGCGCGGCTGGCCCGCTTTATGTCATCTCCACTTGGGCTCTG 3888
Qy 3265 CTCAGGCAATTTGTGAGGCGACCCCGAGAGCCCGGCTCTCCCGGCGCTGAGAT 3324
Db 3889 CTCAGGCAATTTGTGAGGCGACCCCGAGAGCCCGGCTCTCCCGGCGCTGAGAT 3948
Qy 3325 TTCGGGTTTACCTTTCTTAAAGAACCGAGCGGAAGTCTTAACTGGGAAATCGGTGAT 3384
Db 3949 TTCGGGTTTACCTTTCTTAAAGAACCGAGCGGAAGTCTTAACTGGGAAATCGGTGAT 4008
Qy 3385 AAGGAACTTTCTGCTGCAAGGCTTAAAGGACAAAGCGGAGAGCGACTCCGAGGCTTG 3444
Db 4009 AAGGAACTTTCTGCTGCAAGGCTTAAAGGACAAAGCGGAGAGCGACTCCGAGGCTTG 4068
Qy 3445 AAGCGCAGTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGAGATAC 3504
Db 4069 AAGCGCAGTCCCAAGAGTGAATTTGGCACTGAAACAGCTGGGACACATCCGAGATAC 4128
Qy 3505 GAAACGCGCTGAAAGTGTGAGGAGGAGTCCAGCATGTGAGCGGCTCTGGGAGTGG 3564
Db 4129 GAAACGCGCTGAAAGTGTGAGGAGGAGTCCAGCATGTGAGCGGCTCTGGGAGTGG 4188
Qy 3565 GTGGCGAGGCGCTGAGCGGCTTGTGCTTGTGCCCCAGAGTGGCCGACCTTGAC 3624
Db 4189 GTGGCGAGGCGCTGAGCGGCTTGTGCTTGTGCCCCAGAGTGGCCGACCTTGAC 4248
Qy 3625 CTGCTGGGCTCAAAAGAC 3642
Db 4249 CTGCTGGGCTCAAAAGAC 4266

RESULT 9
ADL06463
ID ADL06463 standard; cDNA; 3998 BP.
XX
XX ADL06463;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) cDNA sequence #43.
DE Human: tumour-associated antigenic target; TAT; cell death; tumour;
XX
XX Human: tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic; gene; ss.
XX
XX Homo sapiens.
OS

PN MO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
PA (GETH) GENENTECH INC.
XX
PI Deaauvage FJ, Franz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
XX P-PSDB; ADL06543.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
XX
PS Claim 1; SEQ ID NO 43; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanized antibody. It is conjugated to a growth inhibitory agent or a
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT cDNA sequence of the invention.
XX
SQ Sequence 3898 BP; 685 A; 1207 C; 1235 G; 771 T; 0 U; 0 Other;
Query Match 95.4%; Score 3473.8; DB 12; Length 3898;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 3506; Conservative 0; Mismatches 17; Indels 2; Gaps 2;
QY 118 CCCCCGACCGCCGACCGCCGAGTGCATGAGATGCTTCGCGGACCGCTGTGACC 177
DB 7 CCCCCGACCGCCGACCGCCGAGTGCATGAGATGCTTCGCGGACCGCTGTGACC 65
QY 178 GTGTGGGACAGCGATGACAC-ACACCAAGAGAGCCACCGATGCTACGAGAGCTGGA 236
DB 66 GTGTGGGACAGCGATGACACACACGAGAGAGCCACCGATGCTACGAGAGCTGGA 125
QY 237 CTTACAGGGGGCCCGCCGCAAGACAGCAATTTCTCCGCTCTCTGAACGAGATCC 296
DB 126 CTTACAGGGGGCCCGCCGCAAGACAGCAATTTCTCCGCTCTCTGAACGAGATCC 185
QY 297 AGCTGCAAGTTATATGCTGTGACACAGCAATGGGGCTTCGCTGCCCGGAACCTGTGTGT 356
DB 186 AGCTGCAAGTTATATGCTGTGACACAGCAATGGGGCTTCGCTGCCCGGAACCTGTGTGT 245
QY 357 GTCAAGTGTGGGGGATCGGGGGGCGCGCTCTCCAGACTGTGACAGAGACTGTGCTCG 416
DB 246 GTCAAGTGTGGGGGATCGGGGGGCGCGCTCTCCAGACTGTGACAGAGACTGTGCTCG 305
QY 417 TGTGTGGGCTGTGCGGGGCTGCCAGAGACAGAGAGCTGTGATCTCACTGGGGGTCTGCA 476
DB 306 TGTGTGGGCTGTGCGGGGCTGCCAGAGACAGAGAGCTGTGATCTCACTGGGGGTCTGCA 365
QY 477 CACGGGCTGTGCGGGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 536
DB 366 CACGGGCTGTGCGGGGCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 425
QY 537 GGGGACCAAGGT 596
|||||

DB 426 GGGGACCAAGGT 485
QY 597 CCTATGCAACCCCAAGGCTGT 656
DB 486 CTTATGCAACCCCAAGGCTGT 545
QY 657 CGGGGTCCAGTTTCCCTGAGACTACAACTACTCGGCTCTTCTGCTGTGTGTGTGTGTGTGTGTGT 716
DB 546 CGGGGTCCAGTTTCCCTGAGACTACAACTACTCGGCTCTTCTGCTGTGTGTGTGTGTGTGTGTGT 605
QY 717 ACACGGCTGCTGTGGGGGCGAGAACCGCTTCGCTGTGCGCTGTGAGTCTTACATCTCA 776
DB 606 ACACGGCTGCTGTGGGGGCGAGAACCGCTTCGCTGTGCGCTGTGAGTCTTACATCTCA 665
QY 777 GCAGAAAGCGGGCGGTGGGAGGAGACTGTGAATTGATCCCTGTCTCTCTCTGTATTGGA 836
DB 666 GCAGAAAGCGGGCGGTGGGAGGAGACTGTGAATTGATCCCTGTCTCTCTCTGTATTGGA 725
QY 837 TGTGTATGAGAAAGTGTGACGCGAATPAGAGACGCCACCGAGCTCAGCTCCCATGTCT 896
DB 726 TGTGTATGAGAAAGTGTGACGCGAATPAGAGACGCCACCGAGCTCAGCTCCCATGTCT 785
QY 897 CCTGT 956
DB 786 CTTGT 845
QY 957 GGGCCCAAGGAGTGTGGGGAGCCAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1016
DB 846 GGGCCCAAGGAGTGTGGGGAGCCAGGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 905
QY 1017 TCCCAAGGAGGAGCTGTGAGGCTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1076
DB 906 TCCCAAGGAGGAGCTGTGAGGCTCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 965
QY 1077 GCTCTGTGACACTTATCTTCTGTGAGATGAGTGTGTGAGGATTTGAGACCATAGTTTGA 1136
DB 966 GCTCTGTGACACTTATCTTCTGTGAGATGAGTGTGTGAGGATTTGAGACCATAGTTTGA 1025
QY 1137 GGGCTTGTGAGAGCTGT 1196
DB 1026 GGGCTTGTGAGAGCTGT 1085
QY 1197 GGGCTTGTGAGAGCTGT 1256
DB 1086 GGGCTTGTGAGAGCTGT 1145
QY 1257 ATGGCGGTCTTTCATCTCGAAGCTTCTCTATGAGAGCGCTGTGTGATGACCGGCTGGA 1316
DB 1146 ATGGCGGTCTTTCATCTCGAAGCTTCTCTATGAGAGCGCTGTGTGATGACCGGCTGGA 1205
QY 1317 GTTGT 1376
DB 1206 GTTGT 1265
QY 1377 CTTGGCCCAATCTACAGCGGCGGCGCTTCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1436
DB 1266 CTTGGCCCAATCTACAGCGGCGGCGCTTCCAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1325
QY 1437 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1496
DB 1326 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1385
QY 1497 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1556
DB 1386 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1445
QY 1557 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1616
DB 1446 GGGCTTCCACAGCGCAGGACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1505
QY 1617 GCTCTGTGAGCAAGGAGCACTGT 1676
DB 1506 GCTCTGTGAGCAAGGAGCACTGT 1565
|||||

1677 GAGCACCCTCTCTTTGGGACATGTGTGAACAGGGACAGATGAGCCATGATCTTCTG 1736
1566 GAGCCACCTGCTCTTTTGGGACATGTGTGAACAGGGACAGATGAGCCATGATCTTCTG 1625
1737 GAGAGATGGGTTCCAAATGACAGTTTCTCAGCTCTTGGGGCTGTGTGCTCCGGGTAT 1796
1626 GAGAGATGGGTTCCAAATGACAGTTTCTCAGCTCTTGGGGCTGTGTGCTCCGGGTAT 1685
1737 GGCAGGCTCTGAGGCTGAGAGGCTGAGAGGACACAGAGAGAAAGACTGGGCTTTAAAT 1856
1686 GGCAGGCTCTGAGGCTGAGAGGCTGAGAGGACACAGAGAGAAAGACTGGGCTTTAAAT 1745
1857 TGAGGGGATGAGGCTGAGGCTCTTGTGAGGCTATCGACAGATGAGAGGCTGAGGCTG 1916
1746 TGAGGGGATGAGGCTGAGGCTCTTGTGAGGCTATCGACAGATGAGAGGCTGAGGCTG 1805
1917 CGGCTCTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1976
1806 CGGCTCTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1865
1977 GGAAGCTGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2036
1866 GGAAGCTGACGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1925
2037 GTGTGTGGGAGATATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2096
1926 GTGTGTGGGAGATATGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 1985
2097 CCTCTCACTCATCTACACCGGCTCATACCTCTTCAAGAAATCAGAAAGAGAGCCACAG 2156
1986 CCTCTCACTCATCTACACCGGCTCATACCTCTTCAAGAAATCAGAAAGAGAGCCACAG 2045
2157 GAGAGAGCTAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2216
2046 GAGAGAGCTAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2105
2217 GAGAGAGCTAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2276
2106 GAGAGAGCTAGAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2165
2277 CGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2336
2166 CGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2225
2337 GGTGACATCTTCAATGAGGCAAGTGTGACGTAACCTGCTGCTGCTGCTGCTGCTGCT 2396
2226 GGTGACATCTTCAATGAGGCAAGTGTGACGTAACCTGCTGCTGCTGCTGCTGCTGCT 2285
2397 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2456
2286 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2345
2457 CTGGGCTTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2516
2346 CTGGGCTTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2405
2517 CTGGGCTTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2576
2406 CTGGGCTTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2465
2577 CCTGGCCGACAGCTGAGAACAGTGCAGCTAGTGCCTCACCTGCTTCTCTGAGGAGCT 2636
2466 CCTGGCCGACAGCTGAGAACAGTGCAGCTAGTGCCTCACCTGCTTCTCTGAGGAGCT 2525
2637 GGGCTGCTCCGCTGAGCCCGGGTTTGTACCACTGGGCTGACCTGCTCTGATGATGAT 2696
2526 GGGCTGCTCCGCTGAGCCCGGGTTTGTACCACTGGGCTGACCTGCTCTGATGATGAT 2585
2697 CATGCTTTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2756
2586 CATGCTTTTCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2645

2757 GATGCTCATCTGTGAGCAAGATGATGAGAGAGCTGCTCTTCTCTCTCTCTCTCTCTG 2816
2646 GATGCTCATCTGTGAGCAAGATGATGAGAGAGCTGCTCTTCTCTCTCTCTCTCTCTG 2705
2817 GTGCTGTGTAGCTATGAGGCTGTGAGGCTGAGGAGGCTCTGAGGCTGAGGAGCTGACT 2876
2706 GTGCTGTGTAGCTATGAGGCTGTGAGGCTGAGGAGGCTCTGAGGCTGAGGAGCTGACT 2765
2877 CCCAAGTATCTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2936
2766 CCCAAGTATCTGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2825
2937 CCAGAGAGCAATGAGAGTGTGAGGCTGATGAGGAGCAAGCAATGCTGTGAGAGCCGCTT 2996
2826 CCAGAGAGCAATGAGAGTGTGAGGCTGATGAGGAGCAAGCAATGCTGTGAGAGCCGCTT 2885
2997 CTGGGCAACACCTCTGAGGAGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCT 3056
2886 CTGGGCAACACCTCTGAGGAGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCT 2945
3057 GGTGTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3116
2946 GGTGTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3005
3117 CATTCGCAATGTTCAATGACATTCGAGCAATTCGAGGAGCAAGCAAGATCTTCACTGGA 3176
3006 CATTCGCAATGTTCAATGACATTCGAGCAATTCGAGGAGCAAGCAAGATCTTCACTGGA 3065
3177 GGGCGAGGTTTACCGCTCTCATTCGAGGAGTTTCACTCTGAGGCTGAGGCTGAGGCTGCT 3236
3066 GGGCGAGGTTTACCGCTCTCATTCGAGGAGTTTCACTCTGAGGCTGAGGCTGAGGCTGCT 3125
3237 TATGCTCATCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3296
3126 TATGCTCATCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3185
3297 CCAGGCTGCTCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3356
3186 CCAGGCTGCTCTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3245
3357 GAACTGCTTAACTGTGAGGATGAGTGTGATGAGGAGATTTTCTGCTGAGCAAGGCTGAG 3416
3246 GAACTGCTTAACTGTGAGGATGAGTGTGATGAGGAGATTTTCTGCTGAGCAAGGCTGAG 3305
3417 CAAGGAGGAGAGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3476
3306 CAAGGAGGAGAGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3365
3477 GAAACAGCTGAGGACATTCGAGGATGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGG 3536
3366 GAAACAGCTGAGGACATTCGAGGATGAGGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGG 3425
3537 CCAGAGGTTGAGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3596
3426 CCAGAGGTTGAGGCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 3485
3597 GCCCCAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3641
3486 GCCCTCAAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3530

RESULT 10
ABK92167
ID ABK92167 standard; DNA; 3810 BP.
XX
XX ABK92167;
AC
XX
XX
DT 15-AUG-2002 (first entry)
XX
XX Prostate cancer-associated DNA sequence #53.
DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

XX Mammalia.
 OS WO20020268-A2.
 XX 18-APR-2002.
 XX 12-OCT-2001; 2001WO-US032045.
 XX 13-OCT-2000; 2000US-00687576.
 PR 08-DEC-2000; 2000US-00733288.
 PR 08-DEC-2000; 2000US-00733742.
 PR 24-JAN-2001; 2001US-0263957P.
 PR 16-MAR-2001; 2001US-0276791P.
 PR 16-MAR-2001; 2001US-0276888P.
 PR 06-APR-2001; 2001US-0281922P.
 PR 24-APR-2001; 2001US-0286214P.
 PR 30-APR-2001; 2001US-00847046.
 PR 04-MAY-2001; 2001US-0288589P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Gish KC, Mack DH, Wilson KE, Afari D, Heyezi P;
 DR MPI; 2002-471335/50.
 DR P-PSDB; ABG61852.
 XX
 PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.
 XX
 PS Claim 22; Page 339-340; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridize to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences
 CC
 XX
 SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;
 Query Match 93.9%; Score 3421.2; DB 6; Length 3810;
 Best Local Similarity 99.6%; Pred. No. 0; Mismatches 13; Indels 0; Gaps 0;
 Matches 3429; Conservative 0;

QY 440 AGAGCAGAGAGCCTGATTGTCACTGCGGGGTGCAACAGGGGATCGGCCGATGTG 499
 DB 241 AGAGCAGAGAGCCTGATTGTCACTGCGGGGTGCAACAGGGGATCGGCCGATGTG 300
 QY 500 GTGTGGCTGTACGGGACCATCAGATGATGACAGACTGCGGGGACCAAGGTGTGCGCATG 559
 DB 301 GTGTGGCTGTACGGGACCATCAGATGATGACAGACTGCGGGGACCAAGGTGTGCGCATG 360
 QY 560 GTGTGGCCCCCTGGGGGTGTGTCGGGAATAGAGCACTTCATTAACCCCAAGGGCTGT 619
 DB 361 GTGTGGCCCCCTGGGGGTGTGTCGGGAATAGAGCACTTCATTAACCCCAAGGGCTGT 420
 QY 620 TCCCTGCGAGGTACCGGTGCGCGGTGACCGGAGAGAGGGGTCACTTCCCTGCACT 679
 DB 421 TCCCTGCGAGGTACCGGTGCGCGGTGACCGGAGAGAGGGGTCACTTCCCTGCACT 480
 QY 680 ACAACTACTGCGGCTTCTTCTGTGTGAGCGAGCAGACAGCGGTGCTGTGGGGGCGAGA 739
 DB 481 ACAACTACTGCGGCTTCTTCTGTGTGAGCGAGCAGACAGCGGTGCTGTGGGGGCGAGA 540
 QY 740 ACCGCTTCGCTGCGCTGAGTCTTCACTTCAACAGAGAAACGGGCTGTGGAGGA 799
 DB 541 ACCGCTTCGCTGCGCTGAGTCTTCACTTCAACAGAGAAACGGGCTGTGGAGGA 600
 QY 800 CTGGAATTGACATCCTGTCTGCTCTCTGATTTGATGATGAGAAATGTTGACGC 859
 DB 601 CTGGAATTGACATCCTGTCTGCTCTCTGATTTGATGATGAGAAATGTTGACGC 660
 QY 860 GAATAGAGAGCGCCAGCCAGGCTCAGCTCCCATGCTCTCTGTGCTGCTCAGGGAG 919
 DB 661 GAATAGAGAGCGCCAGCCAGGCTCAGCTCCCATGCTCTCTGTGCTGCTCAGGGAG 720
 QY 920 CTGCGGACTGCTGTGCGAGAGCCTGGAAGACACTGTGCGCCCAAGAGTGGGGAGCCA 979
 DB 721 CTGCGGACTGCTGTGCGAGAGCCTGGAAGACACTGTGCGCCCAAGAGTGGGGAGCCA 780
 QY 980 GGCAAGGGAGAGCCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1039
 DB 781 GGCAAGGGAGAGCCCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 1040 TGCAAGGCCAGGTGAGAGATTAATGACCCCGAGAGAGCTTCTGACAGTATTCTTCTG 1099
 DB 841 TGCAAGGCCAGGTGAGAGATTAATGACCCCGAGAGAGCTTCTGACAGTATTCTTCTG 900
 QY 1100 AGATGGGTCTGAGAAATTCAGACCAATGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 1159
 DB 901 AGATGGGTCTGAGAAATTCAGACCAATGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 960
 QY 1160 GCTGGAGGCTCTAGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATG 1219
 DB 961 GCTGGAGGCTCTAGGCTTACCTGATGATGATGATGATGATGATGATGATGATGATG 1020
 QY 1220 ACATTGCCAGAGAGAACTTTTCGGGGGAGCATCAATGGGCTGCTTCCATCTGAA 1279
 DB 1021 ACATTGCCAGAGAGAACTTTTCGGGGGAGCATCAATGGGCTGCTTCCATCTGAA 1080
 QY 1280 CTTCCTCATAGAGCGCTCTGTGAATGACCGGCTGTGATGATGATGATGATGATGATG 1339
 DB 1081 CTTCCTCATAGAGCGCTCTGTGAATGACCGGCTGTGATGATGATGATGATGATGATG 1140
 QY 1340 ACGGCTCAGCTGAGGCACTTCTGACCCCGAGATGCGGCTGAGCCCACTTCAAGCCGG 1399
 DB 1141 ACGGCTCAGCTGAGGCACTTCTGACCCCGAGATGCGGCTGAGCCCACTTCAAGCCGG 1200
 QY 1400 CGGCTTCAACTGCTCATCTGACCACTTTTGAAGCGGTGCCACAGCGGAGCAACA 1459
 DB 1201 CGGCTTCAACTGCTCATCTGACCACTTTTGAAGCGGTGCCACAGCGGAGCAACA 1260
 QY 1460 AAGCCCAAGCCCTAAAGAGGGAGCTGCGAGCTTCCGCGCCCTGTGACGTGTGGGATGTC 1519
 DB 1261 AAGCCCAAGCCCTAAAGAGGGAGCTGCGAGCTTCCGCGCCCTGTGACGTGTGGGATGTC 1320
 QY 1520 TGAAGATGCTGCTGAGGAGAAATGTGCGCGCCGAGATACCCCTCGGGGGGCGCCCTGGAGCC 1579

1321 TGAGATGCTGCTGGGGAAAGATGTGCGCCGAGGATACCTTCGCGGGGCGCTTGAGACC 1380
1580 CTCACCCAGGCGCAGGGCTTCGCGGAGAGATGATCTGCTCTCGGACAAAGGCACCTGGC 1639
1381 CTCACCCAGGCGCAGGGCTTCGCGGAGAGATGATCTGCTCTCGGACAAAGGCACCTGGC 1440
1640 CGCTCTCGCTGAGTCTGCGCTCGGGCAGGGCCCGTGGAGCGACCTGCTCTTCTTGGGAC 1699
1441 CGCTCTCGCTGAGTCTGCGCTCGGGCAGGGCCCGTGGAGCGACCTGCTCTTCTTGGGAC 1500
1700 TGTTCGTGAACAGGGGACAGATGCGCATGTACTTCCTGGGAGATGGGATTCGAAATGCAATTT 1759
1501 TGTTCGTGAACAGGGGACAGATGCGCATGTACTTCCTGGGAGATGGGATTCGAAATGCAATTT 1560
1760 CCTCAGCTCTTGGGGCGTGTGTTGCTGCTCGGGGTGATGGCAGCGCTGGAGCGCTGACGCG 1819
1561 CCTCAGCTCTTGGGGCGTGTGTTGCTGCTCGGGGTGATGGCAGCGCTGGAGCGCTGACGCG 1620
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1621 AGAGGCGAGCAGCAGAGAAAGACTTGCCTTCAAGTTTGGGGAGATGGGCGTTGACCTCT 1680
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1681 TTGGCGAGTGTATGCGACAGTGAAGTGAAGGCTGCGCTCTCTCTCTCTCTCTCTCTCTCT 1740
1940 CGCTCGGGGGGATGCGACTTGCCTGCGAGCTGGGCAATGCAAGCTGACGCGCTGCTCTCT 1999
1741 CGCTCGGGGGGATGCGACTTGCCTGCGAGCTGGGCAATGCAAGCTGACGCGCTGCTCTCT 1800
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2120 TCATACCTTTCAGAAATAGAAAGAGAGCCACACGGGAGAGCTAGAGTTTGAATGG 2179
1921 TCATACCTTTCAGAAATAGAAAGAGAGCCACACGGGAGAGCTAGAGTTTGAATGG 1980
2180 ATAGTGTCAATTAATGGGAAAGGCGCTGTGCGGACGGCGAGCCAGCCGAGAAAGACGCGC 2239
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2101 GGTGCTAGCGCGCTGCTGCTCTTCTGCGGGCGCGCGCGTGAACATCTTCAATGAGGCAAG 2160
2360 TGTGAGCTACCTGCTGCTCTGCTGCTTCTCTGCGGGTGTGCTGCTGCTGCTGCTGCTGCT 2419
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2420 CGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2479
2221 CGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280
2480 AGGAACTGGGCGCAGGGCTGAGCGAGGCGGGGCGAGCTCGCCAGCGGGGCGCGCGCG 2539
2281 AGGAACTGGGCGCAGGGCTGAGCGAGGCGGGGCGAGCTCGCCAGCGGGGCGCGCGCG 2340
2540 CTGGCATGCTCTCATGAGCCAGCGCTGCGCTCTCACTCGCCGACACACTGGAACAGT 2599
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2461 TGTACCACTTGGGCGCAGCTGCTCTGCTGATCGACTTTCATGAGTTTCACGGTGCGGCTGC 2520
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2521 TTCACTCTTCAACGGTCAACAAACAGCTGGGGGCCCAAGATGTCTATCTGTAGCAAGATGA 2580
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2581 TGAAGAGTGTGTTCTTCT 2640
2840 CCAAGAGGGGCTCTGAGGCGCAGGAGCAGTGAATCTTCCAAATCTCTGCGCGCGCTCT 2899
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2701 TCTACCGTCCCTACCTGAGATCTTTCGGGCAAGATCTCCCAAGAGACATGACGTCGCC 2760
2960 TCAATGAGCAGACAGCACTGCTCTGCGAGCGCGGCTTCTGGGCAACACCTCTCGGGGCGC 3019
2761 TCAATGAGCAGACAGCACTGCTCTGCGAGCGCGGCTTCTGGGCAACACCTCTCGGGGCGC 2820
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2821 AGGCGGGGACCTGCGCTCTCCAGATGCGCAATGGCTGATGCTGCTCTCTCTCTCTCTCT 2880
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2881 TCTGCTGCTGCGCAACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
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2941 TCGGCAAGTACAGGGGCAACAGCGATCTCTTCTGGAAGGCGGAGGTTAACCGGCTCATCC 3000
3200 GGGAAATTCACCTGCGGCGCGCTGCGCGCGCGCTTATGCTCATCTTCCACTTGGCGC 3259
3001 GGGAAATTCACCTGCGGCGCGCTGCGCGCGCGCTTATGCTCATCTTCCACTTGGCGC 3060
3260 TCTGCTCAGGCAATTTGTCAGGCGAGCCCGAGCGCCCAAGCTGCTCTCTCGGCGCTTGC 3319
3061 TCTGCTCAGGCAATTTGTCAGGCGAGCCCGAGCGCCCAAGCTGCTCTCTCGGCGCTTGC 3120
3320 AGCATTTCCGGGTTTACCTTTCTTAAGGAAGCGAGCGGAAGTGTCTAATGTTGGAATTCG 3379
3121 AGCATTTCCGGGTTTACCTTTCTTAAGGAAGCGAGCGGAAGTGTCTAATGTTGGAATTCG 3180
3380 TGCATTAAGGAAGCTTCTGCTGCGACGCGCTAGGGAACAAGCGGAGAGAGCACTCCGAGC 3439
3181 TGCATTAAGGAAGCTTCTGCTGCGACGCGCTAGGGAACAAGCGGAGAGAGCACTCCGAGC 3240
3440 GTCTGAAGCGCAGTCCAGAAAGTGAATTTGCACTGAACAAGCTGGAACATCTCCGCG 3499
3241 GTCTGAAGCGCAGTCCAGAAAGTGAATTTGCACTGAACAAGCTGGAACATCTCCGCG 3300
3500 AGTACGAACAGGCGCTGGAAGTGTGAGCGGGAGAGTCCAGAGTGTAGCCGCGCTCTGCG 3559
3301 AGTACGAACAGGCGCTGGAAGTGTGAGCGGGAGAGTCCAGAGTGTAGCCGCGCTCTGCG 3360
3560 GGTGGGTGGCGAGGCGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3619
3361 GGTGGGTGGCGAGGCGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3420
3620 CTGACCTGCTGGGTCCAAAG 3641
3421 TTGACCTGATGCGTCCAAAG 3442

RESULT 11
ADR66772

ID AD866772 standard; DNA; 3810 BP.
XX
AC AD866772;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human prostatic carcinoma derived DNA SEQ ID 65 #4.
XX
KW human; cytosolic; diagnosis; prostatic cancer;
XX differential expression analysis; ds.
OS Homo sapiens.
XX
XX MO2004076614-A2.
XX
PD 10-SEP-2004.
XX
PF 22-FEB-2004; 2004MO-DE000433.
XX
PR 27-FEB-2003; 2003DE-01009985.
XX 14-MAY-2003; 2003DE-01022134.
XX
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILAR/) PILARSKY C.
XX
PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarczyk C, Specht T,
PI Schmitt A, Beckmann G, Bruemendorf T, Kinnemann H, Roepcke S;
PI Kinzhong L, Staub E;
XX
DR WPI; 2004-653386/63.
XX
PT New nucleic acid, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.
XX
PS Claim 1; Page 1439; 1607pp; German.
XX
XX This invention describes novel cytosolic polynucleotide and polypeptide
XX sequences which can be used in a method for diagnosing prostatic cancer
XX or the risk of developing prostatic cancer. Diagnosis is based on
XX determining over transcription or over expression of the sequences in
XX prostatic tissue. Screening for inhibitors of the sequences or detection
XX of substances involves a binding assay, any compounds that bind are
XX selected, optionally after deconvolution of mixtures. Detection of a
XX predetermined minimum level of the reporter indicates the presence of
XX tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
XX short-interfering RNA or ribozymes; an organic molecule of molecular
XX weight below 5000, preferably 300, that binds to the polypeptide; an
XX aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
XX polypeptide, preferably humanised or human; an anti-idiotypic, non-human
XX (monoclonal) antibody directed against Ab or any of the above derivatised
XX with a reporter group, cell toxin, immunostimulatory molecules and/or
XX radioisotope. The polynucleotides are identified in human prostatic
XX cancer by differential expression analysis, using DNA microarrays,
XX between normal and tumorous tissues, with (over)expression being detected
XX by quantitative PCR. Analysis of prostatic cancer samples showed that
XX CD4 was upregulated in many of them. Sections of tissue, isolated from
XX prostatic cancer patients, or subjects at risk, were incubated
XX sequentially with anti-human CD4 murine monoclonal antibodies;
XX biotinylated second antibody; streptavidin-conjugated horseradish
XX peroxidase and then diaminobenzidine as colour former (brown). The
XX samples were counterstained with hemalum (blue). Malignant cells stained
XX strongly but non-malignant cells only weakly. In 15 of 63 samples of
XX adenocarcinoma, membrane and cytoplasmic staining was very strong, and
XX lymph node metastases were also stained. AD865805-AD866954 represent the
XX polynucleotide and polypeptide sequences used in the method of the
XX invention.
SQ Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 93.9%; Score 3421.2; DB 13; Length 3810;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3429; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 200 CCACGAGAACCCACCGAGTCTTACGAGAGCTTGACCTTCAACGGGGCCGGCCGCAAGC 259
DB 1 CCACGAGAACCCACCGAGTCTTACGAGAGCTTGACCTTCAACGGGGCCGGCCGCAAGC 60
QY 260 ACAGCAATTTCTCCGGCTCTCTGACCGAAGGATCCAGCTGCACTTTATAGTCTGTCA 319
DB 61 ACAGCAATTTCTCCGGCTCTCTGACCGAAGGATCCAGCTGCACTTTATAGTCTGTCA 120
QY 320 CACGCAATGGGGCTTCCGTCCTCCGAACTGTGTGTGTCAGTGTGGGGGATGGGGG 379
DB 121 CACGCAATGGGGCTTCCGTCCTCCGAACTGTGTGTGTCAGTGTGGGGGATGGGGG 180
QY 380 GCCCGTCTTCAGACCTGCTGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
DB 181 GCCCGTCTTCAGACCTGCTGAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 440 AGAGCAGAGAGCTTGATTTGCTACCTGGGGCTTGACACGGGCATCGCGCATTTG 499
DB 241 AGAGCAGAGAGCTTGATTTGCTACCTGGGGCTTGACACGGGCATCGCGCATTTG 300
QY 500 GTGTGGCTGTACGGGACCATGATGAGCAGACCTGGGGGACCAAGGTGGTGGCATGG 559
DB 301 GTGTGGCTGTACGGGACCATGATGAGCAGACCTGGGGGACCAAGGTGGTGGCATGG 360
QY 560 GTGTGGCCCCCTGGGGGTGTGTGTCGGAATGAGACACCTTCATGACCCCAAGGCTTGT 619
DB 361 GTGTGGCCCCCTGGGGGTGTGTGTCGGAATGAGACACCTTCATGACCCCAAGGCTTGT 420
QY 620 TCCCTGGAGGTACCGGTGGCGGGGTGACCCGAGAGACGGGGTCAATTTCCCTGCACT 679
DB 421 TCCCTGGAGGTACCGGTGGCGGGGTGACCCGAGAGACGGGGTCAATTTCCCTGCACT 480
QY 680 ACAACTACTGGGCTTCTTCTGCTGTGACGACGCGACACAGCGCTGCGGGGGCGGA 739
DB 481 ACAACTACTGGGCTTCTTCTGCTGTGACGACGCGACACAGCGCTGCGGGGGCGGA 540
QY 740 ACCGCTTCGCTTGGCTGGCTGAGTCTTACATCTCAGACAGAAACGGGCTGGAGAGGA 799
DB 541 ACCGCTTCGCTTGGCTGGCTGAGTCTTACATCTCAGACAGAAACGGGCTGGAGAGGA 600
QY 800 CTGAATTGACATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 859
DB 601 CTGAATTGACATCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 860 GAATGAGAACCGCACCCAGGCTGACGTCCTCATGCTCTCTCTCTCTCTCTCTCTCTCT 919
DB 661 GAATGAGAACCGCACCCAGGCTGACGTCCTCATGCTCTCTCTCTCTCTCTCTCTCTCT 720
QY 920 CTGCGGACTGCTGGCGGAGACCTTGAAGACACTTGGCCCCAGGAGTGGGGAGCA 979
DB 721 CTGCGGACTGCTGGCGGAGACCTTGAAGACACTTGGCCCCAGGAGTGGGGAGCA 780
QY 980 GCGAAGCGAAGCCCGAGATGAAATCAAGCGCTTTCTTCCCAAGGGAGCCTTGAAGTCC 1039
DB 781 GCGAAGCGAAGCCCGAGATGAAATCAAGCGCTTTCTTCCCAAGGGAGCCTTGAAGTCC 840
QY 1040 TGCAGGCGCCAGTGGAGATTAATGACCCGGAAGAGCTTCCAGCATCTTCTTCTG 1099
DB 841 TGCAGGCGCCAGTGGAGATTAATGACCCGGAAGAGCTTCCAGCATCTTCTTCTG 900
QY 1100 AGATGGGTGAGGAATTTGAGACCAATAGTTTGAAGGCTTGTAAAGGCTGTGGGA 1159
DB 901 AGATGGGTGAGGAATTTGAGACCAATAGTTTGAAGGCTTGTAAAGGCTGTGGGA 960
QY 1160 GCTGGAAGGCTTCACTTCTGATGAGCTGCTTGTGCTGTGGAACCGCGCTGG 1219
DB 961 GCTGGAAGGCTTCACTTCTGATGAGCTGCTTGTGCTGTGGAACCGCGCTGG 1020
QY 1220 ACATGGCCAGATGAATCTTTTGGGGGAGCAATCCATGCGGCTCTTCAATCTGAAG 1279

Db 1021 AATTGGCCAGAGTAACTCTTTCGGGGGAGCATCCAAATGGCGCTCTTCATCTCGAAG 1080
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Db 1141 ACGGCTCAGCCCTGAGGCCACTTCTGACCCCGATGCGCTGAGCCCAACTCTACAGCGCG 1200
QY 1400 CGCCTCCACATCTGCTCATCCGCAACCTTTTGAACAGGCGTTCACAGCGCAGGACCA 1459
Db 1201 CGCCTCCACATCTGCTCATCCGCAACCTTTTGAACAGGCGTTCACAGCGCAGGACCA 1260
QY 1460 AAGCCCAAGCCCTTAAAGGGGGAGCGGAGCTCCGCGCCCTGACGCGGGGCAATGTC 1519
Db 1261 AAGCCCAAGCCCTTAAAGGGGGAGCGGAGCTCCGCGCCCTGACGCGGGGCAATGTC 1320
QY 1520 TGAGATGCTGCTGGGGAGAGATGTGCGCGCGAGGTAACCCCTCCGGGGCGCTGGGAC 1579
Db 1321 TGAGATGCTGCTGGGGAGAGATGTGCGCGCGAGGTAACCCCTCCGGGGCGCTGGGAC 1380
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QY 1760 CCTCAGCTCTTGGGGCTGTGTTTCTGCTTCGGGATGATGCGACGCTGAGCCTGACGCTG 1819
Db 1561 CCTCAGCTCTTGGGGCTGTGTTTCTGCTTCGGGATGATGCGACGCTGAGCCTGACGCTG 1620
QY 1820 AAGAGCGACAGGAGGAGAAAGACTGGGCTTGAAGTTGAGGGGATGGCGTTGACCTCT 1879
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QY 1880 TTGGCGAGTGTATCGCAGCAGTGAAGGTGAGGGCTGCGCCTCTCTCCGCTCGCTGCG 1939
Db 1681 TTGGCGAGTGTATCGCAGCAGTGAAGGTGAGGGCTGCGCCTCTCTCCGCTCGCTGCG 1740
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Db 1741 CGCTCTGGGGGATGCGACTTGCGCTTCAGCTGGCCATGCAAGCTGAACGCGCGTCTCT 1800
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Db 1801 TTGGCCAGGATGGGAGACGCTGCTGCAACAAGAGTGGGGAGATGAGCCAGCA 1860
QY 2060 CTACACCCATCTGGGCCCTGTTCTGCTCTCTTTTCCCTCAGCTCATCTACACCGCC 2119
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QY 2120 TCATCAGCTTCAAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTGAGTTTGAACATG 2179
Db 1921 TCATCAGCTTCAAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTGAGTTTGAACATG 1980
QY 2180 ATAGTGTCTTAAATGGGAAAGGCGCTGTGGGACGGCGGACCCAGCGCGAAGAGCGCCG 2239
Db 1981 ATAGTGTCTTAAATGGGAAAGGCGCTGTGGGACGGCGGACCCAGCGCGAAGAGCGCCG 2040
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Db 2041 TGGGGGTCCCGCGCCAGTGGGGCGGTCCGGGTTTCTGCGGGGGCGCTTCGGGGGGCGCC 2100
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Db 2101 GGTGCTACGCGCTGCTTCACTTCTGGGGCGCGCGGTGACATCTTTCATGGGCAAG 2160
QY 2360 TGTGAGCTACCTGCTGTTCTGCTGCTTTTCTCGGGGCTGCTGCTGATTTTCCAGC 2419
Db 2161 TGTGAGCTACCTGCTGTTCTGCTGCTTTTCTCGGGGCTGCTGCTGATTTTCCAGC 2220
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Db 2221 CGGCGCGCGCGCTGCTGCTGAGAGCTGCTCTAATTTCTGGGCTTTTCAAGCTGCTGCG 2280
QY 2480 AAGAACTGCGCAGAGGCTGAGCGGAGCGGGGAGAGCTGGCGAGCGGGGGCCCCGGGG 2539
Db 2281 AAGAACTGCGCAGAGGCTGAGCGGAGCGGGGAGAGCTGGCGAGCGGGGGCCCCGGGG 2340
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Db 2881 TCTGCTGCTGAGCAACATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2940
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Db 2941 TCGGCAAGTACAGGAGCAACAGCATCTCTAAGAGGAGCGAGCTGTAACCGCTCATCC 3000
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Db 3001 GGGAAATTCACCTTCTGCGCGCGGCTGCGCGCGCGCTTATGTCTATCTTCCACTTGGCG 3060
QY 3260 TCTGCTGAGGCAATTTGAGAGGAGAGCGCGGAGCGCGAGCGCTGCTGCGCGCGCTGCG 3319
Db 3061 TCTGCTGAGGCAATTTGAGAGGAGAGCGCGGAGCGCGAGCGCTGCTGCGCGCGCTGCG 3120
QY 3320 AGCATTTTCGGGTTTACCTTTCTAAGAGGCGAGCGGAGCTGCTAAGCTGAGTACG 3379
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QY 3380 TGCATAGAGAACTTTCTGCTGCGCAGCGCTTAGGAGCAAGCGGAGAGCGCATCTCGAGC 3439
Db 3181 TGCATAGAGAACTTTCTGCTGCGCAGCGCTTAGGAGCAAGCGGAGAGCGCATCTCGAGC 3240

Db 721 CTGCGACCTGCTGCGGAGACCTCTGGAAGACACTCTGCCCCAGGGAGTGGGGAGCA 780
Qy 980 GGGAAAGGAGGAGCCGAGATGGAATCAGGCGCTTCTTCCCAAAGGGAGCTTGAGTCC 1039
Db 781 GCGAAGGGAGAGCCGAGATGGAATCAGGCGCTTCTTCCCAAAGGGAGCTTGAGTCC 840
Qy 1040 TGCAGGCCAGGTGAGAGATTTATGACCCGAGAGAGCTCTGACAGTCTATTTCTTCTG 1099
Db 841 TGCAGGCCAGGTGAGAGATTTATGACCCGAGAGAGCTCTGACAGTCTATTTCTTCTG 900
Qy 1100 AGGATGGGTCTGAGGAATTTGAGACCATAGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 1159
Db 901 AGGATGGGTCTGAGGAATTTGAGACCATAGTTTGAAGGCCCTTGTGAAGGCTGTGGGA 960
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Db 1141 ACGGCTCAGGCTGAGGAGCTTCTGACCCCGATGCGGCTGGCCCACTTACAGCGGG 1200
Qy 1400 CGCCCTCCAACTCGCTCATCCGCAACTTTTGGACAGAGCGTCCCAAGCGGAGCA 1459
Db 1201 CGCCCTCCAACTCGCTCATCCGCAACTTTTGGACAGAGCGTCCCAAGCGGAGCA 1260
Qy 1460 AAGCCCAAGCCCTTAAAGGGGAGAGCTGCGAGACTCCGCGCCCTTACAGTGGGGAGTGGC 1519
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Db 1321 TGAGGATGCTGCTGGGAGAGATGTCGCGCGAGGATCCCTTCGGGGGAGGCTTGGAGC 1380
Qy 1580 CTCAACCAAGGCGAGGCTTTCGGGAGAGAGATGATCTGCTCTCGACAAGGCAACTTGC 1639
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Qy 1640 CGCTCTCGCTGATGCTGAGCTTTCGGGAGAGGCCCCCTGAGAGCACTTGTCTTTGGGAGC 1699
Db 1441 CGCTCTCGCTGATGCTGAGCTTTCGGGAGAGGCCCCCTGAGAGCACTTGTCTTTGGGAGC 1500
Qy 1700 TGTTCCTGAACAGGAGCAAGATGGCCATGTACTTCTGGAGATGGGTTCCAAATGCACTTT 1759
Db 1501 TGTTCCTGAACAGGAGCAAGATGGCCATGTACTTCTGGAGATGGGTTCCAAATGCACTTT 1560
Qy 1760 CCTCAAGCTTTCGGGAGGCTGTTTTCGTCTTCGGGATGAGCAAGCTTGAAGCTTGAAGCTG 1819
Db 1561 CCTCAAGCTTTCGGGAGGCTGTTTTCGTCTTCGGGATGAGCAAGCTTGAAGCTTGAAGCTG 1620
Qy 1820 AGGAGGAGCAAGAGAGAAAGCTTGGGCTTCAAGTTTGAAGGAGTGGGCTTGAAGCTTCT 1879
Db 1621 AGGAGGAGCAAGAGAGAAAGCTTGGGCTTCAAGTTTGAAGGAGTGGGCTTGAAGCTTCT 1680
Qy 1880 TTGGGAGGTCTATGAGCAAGATGAGGTGAGGGGCTCCGAGCTCTCCCTCGCTGCTGCC 1939
Db 1681 TTGGGAGGTCTATGAGCAAGATGAGGTGAGGGGCTCCGAGCTCTCCCTCGCTGCTGCC 1740
Qy 1940 CGCTCTGGGGAGATGCACTTGCCTCAAGCTTGCATGCAAGCTGACCGCGTGTCTTCT 1999
Db 1741 CGCTCTGGGGAGATGCACTTGCCTCAAGCTTGCATGCAAGCTGACCGCGTGTCTTCT 1800
Qy 2000 TTGCCAGAGATGGGATGAGTCTTCTGCTGACACAGAGTGTGGGAGATATGCGCACGA 2059

Db 1801 TTGCCAGAGATGGGATGAGTCTTCTGCTGACACAGAGTGTGGGAGATATGCGCACGA 1860
Qy 2060 CTACACCATCTGGGAGCCCTGGTTCCTGCGCTTCTTTTGGCCCTCACTCATACACCGCC 2119
Db 1861 CTACACCATCTGGGAGCCCTGGTTCCTGCGCTTCTTTTGGCCCTCACTCATACACCGCC 1920
Qy 2120 TCATCACTTCAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTAGAGTTTGAATGG 2179
Db 1921 TCATCACTTCAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTAGAGTTTGAATGG 1980
Qy 2180 ATAGTGTATTAATGGGAGAGGCTGTGGGAGCGGAGACCCAGCGAGAAAGCGCCGC 2239
Db 1981 ATAGTGTATTAATGGGAGAGGCTGTGGGAGCGGAGACCCAGCGAGAAAGCGCCGC 2040
Qy 2240 TGGGGGTCCCGGAGCTGAGGCGGCTCCGGATTCGTGAGGAGGCGCTGCGGGGAGCGCC 2299
Db 2041 TGGGGGTCCCGGAGCTGAGGCGGCTCCGGATTCGTGAGGAGGCGCTGCGGGGAGCGCC 2100
Qy 2300 GGTGCTACGCGCTGTTCCATCTTGGGGGCGCGGATGACATCTTCAATGGGCAAG 2359
Db 2101 GGTGCTACGCGCGCTGTTCCATCTTGGGGGCGCGGATGACATCTTCAATGGGCAAG 2160
Qy 2360 TGGTTCAGCTACCTGCTGTTCTGCGGCTTTCTGCGGGGAGCTGCTGTTGAATTTCCAGC 2419
Db 2161 TGGTTCAGCTACCTGCTGTTCTGCGGCTTTCTGCGGGGAGCTGCTGTTGAATTTCCAGC 2220
Qy 2420 CGGCGCGCGCGGCTCCCTGAGGCTGCTCTATTTCTGGGCTTTCACTGCTGCTGTCG 2479
Db 2221 CGGCGCGCGCGGCTCCCTGAGGCTGCTCTATTTCTGGGCTTTCACTGCTGCTGTCG 2280
Qy 2480 AGGAACTGCGCAGGGCTTGAAGCGAGGCGGGGAGAGCTTGGCCAGCGGGGGCCCCGGGC 2539
Db 2281 AGGAACTGCGCAGGGCTTGAAGCGAGGCGGGGAGAGCTTGGCCAGCGGGGGCCCCGGGC 2340
Qy 2540 CTGGCATGCTCACTGAGCGAGGCGCTGAGCTCTTCACTGCGGAGAGCTGGAACAGT 2599
Db 2341 CTGGCATGCTCACTGAGCGAGGCGCTGAGCTCTTCACTGCGGAGAGCTGGAACAGT 2400
Qy 2600 GCGACTAGTGGCTCTCACTGCTTCTCTTGGGCGTGGGCTGCGCGGCTGACCCCGGCTT 2659
Db 2401 GCGACTAGTGGCTCTCACTGCTTCTCTTGGGCGTGGGCTGCGCGGCTGACCCCGGCTT 2460
Qy 2660 TGTACACCTGGGCGGAGCTGCTCTGATGAGCTTCACTGCTTTCAGCGGTGGGCTGCG 2719
Db 2461 TGTACACCTGGGCGGAGCTGCTCTGATGAGCTTCACTGCTTTCAGCGGTGGGCTGCG 2520
Qy 2720 TTTCACTTCAAGGTCACAAACAGGCTGGGGCCCAAGATGTCATGTCAGAAATGA 2779
Db 2521 TTTCACTTCAAGGTCACAAACAGGCTGGGGCCCAAGATGTCATGTCAGAAATGA 2580
Qy 2780 TGAAGGAGCTGCTTCTTCTCTTCTTCTCTGCGGCTGAGCTGAGCTTATGAGCGTGG 2839
Db 2581 TGAAGGAGCTGCTTCTTCTCTTCTTCTCTGCGGCTGAGCTGAGCTTATGAGCGTGG 2640
Qy 2840 CCAAGGAGGCTCTTGAAGCCAGGAGCAAGTGAATTTCCAAATCTTCTGCGCGCTCT 2899
Db 2641 CCAAGGAGGCTCTTGAAGCCAGGAGCAAGTGAATTTCCAAATCTTCTGCGCGCTCT 2700
Qy 2900 TCTACCGTCCCTACCTGAGATCTTTCGGGAGATTTCCCAAGAGAGCAATGAGCGTGGC 2959
Db 2701 TCTACCGTCCCTACCTGAGATCTTTCGGGAGATTTCCCAAGAGAGCAATGAGCGTGGC 2760
Qy 2960 TCATGAGAGCAGCAACTGCTGTCGAGGCCGCTTCTGGGACACCTCTCTGGGAGCC 3019
Db 2761 TCATGAGAGCAGCAACTGCTGTCGAGGCCGCTTCTGGGACACCTCTCTGGGAGCC 2820
Qy 3020 AGGCGGAGCACTGCGTCTCCAGTATGCAACTGAGCTGAGTGTCTCTCTGCTCATCT 3079
Db 2821 AGGCGGAGCACTGCGTCTCCAGTATGCAACTGAGCTGAGTGTCTCTCTGCTCATCT 2880
Qy 3080 TCTGCTGTGAGCAAACTCTGCTGTCGCACTTGTGCACTTGTGCACTGTTCACTTCACT 3139
Db 2881 TCTGCTGTGAGCAAACTCTGCTGTCGCACTTGTGCACTTGTGCACTGTTCACTTCACT 2940

QY 3140 TCGGCAAGTACAGGGCAACAGCGATCTCTACTGGAAAGGCGGCTTACCGCTCATCC 3199
DB 2941 TCGGCAAGTACAGGGCAACAGCGATCTCTACTGGAAAGGCGGCTTACCGCTCATCC 3000
QY 3200 GGGAAATTCCTCTCGGCGCGCGCTGAGCCCGCCCTTTATGTCATCTCCCATTTGCGCC 3259
DB 3001 GGGAAATTCCTCTCGGCGCGCGCTGAGCCCGCCCTTTATGTCATCTCCCATTTGCGCC 3060
QY 3260 TCCGCTCAGGCAATTTGACAGGCGACCCCGAGCCCGCCCGCTTCTCCCGGCGCTCG 3319
DB 3061 TCCGCTCAGGCAATTTGACAGGCGACCCCGAGCCCGCCCGCTTCTCCCGGCGCTCG 3120
QY 3320 AGCATTTCCGGGTTTACCTTTCTAAGAGAGCGAGCGGAAGCTGCTAAGTGGAAATCG 3379
DB 3121 AGCATTTCCGGGTTTACCTTTCTAAGAGAGCGAGCGGAAGCTGCTAAGTGGAAATCG 3180
QY 3380 TGCATTAAGAGAACTTTCTGCTGCGACGCGCTAAGGACAGCGGAGAGCGAATCCGAGC 3439
DB 3181 TGCATTAAGAGAACTTTCTGCTGCGACGCGCTAAGGACAGCGGAGAGCGAATCCGAGC 3240
QY 3440 GTCTGAAGCGGACGTCTCCAGAAAGTGGACTTGGCACTGAAACAGTGGGACATCCGCG 3499
DB 3241 GTCTGAAGCGGACGTCTCCAGAAAGTGGACTTGGCACTGAAACAGTGGGACATCCGCG 3300
QY 3500 AGTACGAAACAGCGCTGAAAGTGGAGCGGAGGTCAGACAGTGTAGCCGCGCTCG 3559
DB 3301 AGTACGAAACAGCGCTGAAAGTGGAGCGGAGGTCAGACAGTGTAGCCGCGCTCG 3360
QY 3560 GGTGGGTGGCGGAGCGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3619
DB 3361 GGTGGGTGGCGGAGCGCTGAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
QY 3620 CTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3641
DB 3421 TTGACCTGATGGGTGCCAAGA 3442

RESULT 13

ADSL2778 standard; cDNA; 3810 BP.

ADSL2778;

16-DEC-2004 (first entry)

Human TRPM4a splicing variant cDNA sequence.

transient receptor potential cation channel; subfamily M; member 4;

TRPM4; phospholipase A1-A; PLALA; butyryl coenzyme A synthetase 1; BUCS1;

prostate cancer; TRPM4a; gene; ss; splicing variant.

Homo sapiens.

Key Location/Qualifiers

CDS 324..3374

FT /tag= a

FT /product= "Human TRPM4a splicing variant protein"

JP2004267118-A.

30-SEP-2004.

10-MAR-2003; 2003JP-00063578.

10-MAR-2003; 2003JP-00063578.

WPI; 2004-693915/68.

P-PSDB; ADSL2779.

Detecting prostatic cancer, comprises extracting RNA fractions from test

PT substance of subject and normal human, measuring and analyzing the
PT difference in e.g., phospholipase A1-A and butyryl coenzyme A synthetase
PT expression levels.

PS Claim 1; SEQ ID NO 5; 126bp; Japanese.

CC The invention comprises a method for detecting prostatic cancer in a
CC subject. The method involves measuring the expression levels of specific
CC genes: transient receptor potential cation channel, subfamily M, member 4
CC (TRPM4); phospholipase A1-A (PLALA); and butyryl coenzyme A synthetase 1
CC (BUCS1). The method of the invention is useful for the detection and
CC treatment of prostate cancer. The present cDNA sequence encodes the human
CC TRPM4a splicing variant protein of the invention.

XX Sequence 3810 BP; 669 A; 1177 C; 1203 G; 761 T; 0 U; 0 Other;

Query Match 93.9%; Score 3421.2; DB 13; Length 3810;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 3429; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 200 CCAGGAGAAAGCCCAACCGATGCTTACGAGAGCTGAGCTTACGAGGCGCGCGCAAGC 259
DB 1 CCAGGAGAAAGCCCAACCGATGCTTACGAGAGCTGAGCTTACGAGGCGCGCGCAAGC 60
QY 260 ACAGCAATTTCTCCGGCTCTGACCGAAGGATCCAGCTGACGTTTATGTCGTGCA 319
DB 61 ACAGCAATTTCTCCGGCTCTGACCGAAGGATCCAGCTGACGTTTATGTCGTGCA 120
QY 320 CACGCAATGGGAGGCTTCCGTCGCCGAACCTGATGTCAGTCTGAGGAGATCGGAGG 379
DB 121 CACGCAATGGGAGGCTTCCGTCGCCGAACCTGATGTCAGTCTGAGGAGATCGGAGG 180
QY 380 GCCCGTCTTCCAGACCTGCTGCGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 439
DB 181 GCCCGTCTTCCAGACCTGCTGCGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
QY 440 AGAGCAGAGAGCGCTGATTTGCTCACTGAGGAGTGGCAACGAGGATGGCCGAGATGG 499
DB 241 AGAGCAGAGAGCGCTGATTTGCTCACTGAGGAGTGGCAACGAGGATGGCCGAGATGG 300
QY 500 GTGTGCTGTACGAGGACCATCAGATGCGCAGACTGAGGAGGCCAAGGTGTGCGATGG 559
DB 301 GTGTGCTGTACGAGGACCATCAGATGCGCAGACTGAGGAGGCCAAGGTGTGCGATGG 360
QY 560 GTGTGCGCCCTGGGAGTGTGCTCGGAATAGAGACCTTCATCAACCCCAAGGCTGCT 619
DB 361 GTGTGCGCCCTGGGAGTGTGCTCGGAATAGAGACCTTCATCAACCCCAAGGCTGCT 420
QY 620 TCCCTGAGAGGTACCGGTGGGCGGTGACCCGAGAGCGGGGTCCAGTTTCCCTGAGCT 679
DB 421 TCCCTGAGAGGTACCGGTGGGCGGTGACCCGAGAGCGGGGTCCAGTTTCCCTGAGCT 480
QY 680 ACAACTACTCGGCTTCTTCTGCTGAGACGAGCACAACGCTGCTGAGGAGCGAGA 739
DB 481 ACAACTACTCGGCTTCTTCTGCTGAGACGAGCACAACGCTGCTGAGGAGCGAGA 540
QY 740 ACCGCTTCCGCTTGGCGCTGAGTCTTCACTTCAACGAGAGACGCGCGTGGAGGGA 799
DB 541 ACCGCTTCCGCTTGGCGCTGAGTCTTCACTTCAACGAGAGACGCGCGTGGAGGGA 600
QY 800 CTGGAATTGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
DB 601 CTGGAATTGACATCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
QY 860 GAATAGAGAGCGCACCGAGCTCAGTCCCATGCTCTGCTGCTGCTGCTGCTGCTGCTG 919
DB 661 GAATAGAGAGCGCACCGAGCTCAGTCCCATGCTCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 920 CTGCGACTGCTGCGGAGAGACCTTGAAGACACTGCTGCTGCTGCTGCTGCTGCTGCTG 979
DB 721 CTGCGACTGCTGCGGAGAGACCTTGAAGACACTGCTGCTGCTGCTGCTGCTGCTGCTG 780
QY 980 GGCAAGCGAAGCCGAGATGATCAAGGCTTCTTCCCAAGGAGACTTGAAGTCC 1039

Db 781 GGAAGGGGAGGCCGAGATCGAATCAGGCGTTCTTTCCCAAAGGGGACCTTGAGTGC 840
Qy 1040 TGCAGGCCAGGTGAGAGATTAATGACCCGGAAGAGACTCTGTGACATCTATTCTTCTG 1099
Db 841 TGCAGGCCAGGTGAGAGATTAATGACCCGGAAGAGACTCTGTGACATCTATTCTTCTG 900
Qy 1100 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTGAAGGCCCTTGGAAGGCTGTGGGA 1159
Db 901 AGGATGGGTCTGAGGAATTCGAGACCATAGTTTGAAGGCCCTTGGAAGGCTGTGGGA 960
Qy 1160 GCTCGAGGCTCTAGCCTTACCTGATGAGCTGCTTGGCTGTGGCTTGGAAACGCGTGG 1219
Db 961 GCTCGAGGCTCTAGCCTTACCTGATGAGCTGCTTGGCTGTGGCTTGGAAACGCGTGG 1020
Qy 1220 ACATTGCCAGATGAACTTTTGGGGGAGAAATCCAAATGAGGCTTCCATCTCGAAG 1279
Db 1021 ACATTGCCAGATGAACTTTTGGGGGAGAAATCCAAATGAGGCTTCCATCTCGAAG 1080
Qy 1280 CTTCCTGATGAGCGCCCTGGAATGACCGGCTGAGTGGTGGCGCTTGTCTATTTCC 1339
Db 1081 CTTCCTGATGAGCGCCCTGGAATGACCGGCTGAGTGGTGGCGCTTGTCTATTTCC 1140
Qy 1340 ACGGCTCAGGCTGGGCACTTCTGACCCCGATGCGCTGGCCCACTTACAGCGGG 1399
Db 1141 ACGGCTCAGGCTGGGCACTTCTGACCCCGATGCGCTGGCCCACTTACAGCGGG 1200
Qy 1400 CGGCTCTCACTGCTCATCCGCAACCTTTTGGACAGGCGCTCCCAAGCGGACCA 1459
Db 1201 CGGCTCTCACTGCTCATCCGCAACCTTTTGGACAGGCGCTCCCAAGCGGACCA 1260
Qy 1460 AAGCCCAAGCCCTTAAAGGGGGAGCTGCGAGAGCTCGGCGCCCTGACGTTGGGAGATGTC 1519
Db 1261 AAGCCCAAGCCCTTAAAGGGGGAGCTGCGAGAGCTCGGCGCCCTGACGTTGGGAGATGTC 1320
Qy 1520 TGAGATGCTGCTGGGGAAGATGTGCGCGCGAGGTACCCCTCGGGGGGCGCTTGGAGC 1579
Db 1321 TGAGATGCTGCTGGGGAAGATGTGCGCGCGAGGTACCCCTCGGGGGGCGCTTGGAGC 1380
Qy 1580 CTCACCCAGGCGGAGGCTTGGGGGAGAGATGTATGTGCTCTCGGACAAAGGCACTCTGC 1639
Db 1381 CTCACCCAGGCGGAGGCTTGGGGGAGAGATGTATGTGCTCTCGGACAAAGGCACTCTGC 1440
Qy 1640 CGCTCTGCTGATGTGCGCTCGGGGAGGCGCCCGTGGAGCGACCTGCTTCTTGGGAGC 1699
Db 1441 CGCTCTGCTGATGTGCGCTCGGGGAGGCGCCCGTGGAGCGACCTGCTTCTTGGGAGC 1500
Qy 1700 TGTTCGTGAACAGGAGCAGATGCGCATGTACTTCTGGAGATGGGTTCCAAATGCAATT 1759
Db 1501 TGTTCGTGAACAGGAGCAGATGCGCATGTACTTCTGGAGATGGGTTCCAAATGCAATT 1560
Qy 1760 CCTCAGCTTTTGGGGCTGTTTGTGCTCTCGGGTGAATGAGCGCTTGGAGCTGAGCTG 1819
Db 1561 CCTCAGCTTTTGGGGCTGTTTGTGCTCTCGGGTGAATGAGCGCTTGGAGCTGAGCTG 1620
Qy 1820 AAGAGGAGCAGAGAGAGAAAGACTGGGAGTTCAAGTTTGAAGGAGATGGGCTTGAACCTT 1879
Db 1621 AAGAGGAGCAGAGAGAGAAAGACTGGGAGTTCAAGTTTGAAGGAGATGGGCTTGAACCTT 1680
Qy 1880 TTGGGAGTGTATCGCAGCAGTGAAGTGAAGGCTGCGCGCTCTCTCTCGTCTGCTGCG 1939
Db 1681 TTGGGAGTGTATCGCAGCAGTGAAGTGAAGGCTGCGCGCTCTCTCTCGTCTGCTGCG 1740
Qy 1940 CGCTCTGGGGGAGTGCACCTTGGCTCTCAGCTGGCCATGCAAGCTGACGCGCTGCTTCT 1999
Db 1741 CGCTCTGGGGGAGTGCACCTTGGCTCTCAGCTGGCCATGCAAGCTGACGCGCTGCTTCT 1800
Qy 2000 TTGGCCAGGATGGGAGTGAAGTCTGCTGACACAGAGTGTGGGGAGATATGGCCAGCA 2059
Db 1801 TTGGCCAGGATGGGAGTGAAGTCTGCTGACACAGAGTGTGGGGAGATATGGCCAGCA 1860
Qy 2060 CTACACCACTTGGGCGCTGCTTCTGCGCTTCTTGGCCCTCAGTCACTACACCGCGC 2119

Db 1861 CTACACCACTTGGGCGCTGCTTCTGCGCTTCTTGGCCCTCAGTCACTACACCGCGC 1920
Qy 2120 TCATCACCCTCAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTAGATTGACATG 2179
Db 1921 TCATCACCCTCAGAAATCAGAAAGAGAGCCCAACGAGGAGAGCTAGATTGACATG 1980
Qy 2180 ATAGTGTATTATGGGAGAGGCTGTGGGAGCGGCGGACCCAGCCGAAAGACGCGC 2239
Db 1981 ATAGTGTATTATGGGAGAGGCTGTGGGAGCGGCGGACCCAGCCGAAAGACGCGC 2040
Qy 2240 TGGGGTCCCGCCAGTGGGCGCTCGGGTGTGCGGGGGCGCGCGGGGGGGCGC 2299
Db 2041 TGGGGTCCCGCCAGTGGGCGCTCGGGTGTGCGGGGGCGCGCGGGGGGGCGC 2100
Qy 2300 GATGCTACGCGCTGCTTCCACTTCTGGGGCGCGCGGTAACATCTTCAATGGGCAAG 2359
Db 2101 GATGCTACGCGCTGCTTCCACTTCTGGGGCGCGCGGTAACATCTTCAATGGGCAAG 2160
Qy 2360 TGTTCAGCTACCTGCTGTCTGCTGCTTCTGCGGGGCTGCTGCTGATTTCCAGC 2419
Db 2161 TGTTCAGCTACCTGCTGTCTGCTGCTTCTGCGGGGCTGCTGCTGATTTCCAGC 2220
Qy 2420 CGGCGCGCCCGGCTCCCTGAGAGCTGCTCTATTTCTGGGCTTTCAAGCTGCTGTCG 2479
Db 2221 CGGCGCGCCCGGCTCCCTGAGAGCTGCTCTATTTCTGGGCTTTCAAGCTGCTGTCG 2280
Qy 2480 AGGAATGCGCGCAGAGGCTGAGCGGAGGCGGGGAGAGCTCGCAAGCGGGGGCCCGGGC 2539
Db 2281 AGGAATGCGCGCAGAGGCTGAGCGGAGGCGGGGAGAGCTCGCAAGCGGGGGCCCGGGC 2340
Qy 2540 CTGGCATGCTCTCATGAGCAGCGCTGCGCTCTCATCTGCGGACAGCTGGAACAGT 2599
Db 2341 CTGGCATGCTCTCATGAGCAGCGCTGCGCTCTCATCTGCGGACAGCTGGAACAGT 2400
Qy 2600 GCGACCTAGTGTCTTCACTGCTTCTCTGAGGAGTGGGCTGCGGCTGACCCGGGTT 2659
Db 2401 GCGACCTAGTGTCTTCACTGCTTCTCTGAGGAGTGGGCTGCGGCTGACCCGGGTT 2460
Qy 2660 TGTACCACTGGGCGCGCACTGCTCTCTGATGCACTTCAATGATTTTCAAGTGGCGGCTGC 2719
Db 2461 TGTACCACTGGGCGCGCACTGCTCTCTGATGCACTTCAATGATTTTCAAGTGGCGGCTGC 2520
Qy 2720 TTCAATCTTTCAGGTCACAAACAGCTGGGGCCCAAGATGCTCATCTGAGCAAGATGA 2779
Db 2521 TTCAATCTTTCAGGTCACAAACAGCTGGGGCCCAAGATGCTCATCTGAGCAAGATGA 2580
Qy 2780 TGAAGAAGTGTCTTCTTCT 2839
Db 2581 TGAAGAAGTGTCTTCTTCT 2640
Qy 2840 CCAGGAGGAGCTCTGAGGAGCCAGGAGCAATGCACTTCCAAATGATCTGCGCGGCTCT 2899
Db 2641 CCAGGAGGAGCTCTGAGGAGCCAGGAGCAATGCACTTCCAAATGATCTGCGCGGCTCT 2700
Qy 2900 TCTACCTGCTTACCTGAGATCTTGGGAGATTTCCCAAGAGACATGAGCTGGGCC 2959
Db 2701 TCTACCTGCTTACCTGAGATCTTGGGAGATTTCCCAAGAGACATGAGCTGGGCC 2760
Qy 2960 TCATGAGCAGCAGCACTGCTGTGAGAGCCGCGCTTCTGGGCAACCTCTTGGGGGCC 3019
Db 2761 TCATGAGCAGCAGCACTGCTGTGAGAGCCGCGCTTCTGGGCAACCTCTTGGGGGCC 2820
Qy 3020 AAGCGGGGACCTGCGCTCCAGTATGACCACTGGGCTGGTGTGCTCTCTGATCT 3079
Db 2821 AAGCGGGGACCTGCGCTCCAGTATGACCACTGGGCTGGTGTGCTCTCTGATCT 2880
Qy 3080 TCTGCTGTGAGCAACATCTGCTGTCACTTCTCAATGCACTTCAATGCACTTCAAT 3139
Db 2881 TCTGCTGTGAGCAACATCTGCTGTCACTTCTCAATGCACTTCAATGCACTTCAAT 2940
Qy 3140 TGGGCAAGTACAGGCAACAGGATCTTATCTGGAAGCGAGGTTACCGCTCATGCG 3199
Db 2941 TGGGCAAGTACAGGCAACAGGATCTTATCTGGAAGCGAGGTTACCGCTCATGCG 3000

QY 3200 GGAATTCACGCTCTGAGCCGCGCTGAGCCGCTTATGTCATCTCCCACTTGGGCC 3259
DB 3001 GGGAAATTCACCTCTGCGCCGCGCTGAGCCGCTTATGTCATCTCCCACTTGGGCC 3060
QY 3360 TCCTGCTAGGCAATTGTGACAGCGACCCCGAGCCGCTCTCTCCCGGCGCTCG 3319
DB 3061 TCCTGCTAGGCAATTGTGACAGCGACCCCGAGCCGCTCTCTCTCCCGGCGCTCG 3120
QY 3320 AGCATTTCCGGGTTTACTTTCTAAAGAACCGGAGAGCTGCTAACTGGGATCGG 3379
DB 3121 AGCATTTCCGGGTTTACTTTCTAAAGAACCGGAGAGCTGCTAACTGGGATCGG 3180
QY 3380 TGCAATAGGAGAACTTTGCTGCGACGCGCTAGGAGAAACCGGAGAGCACTCCGAGC 3439
DB 3181 TGCAATAGGAGAACTTTGCTGCGACGCGCTAGGAGAAACCGGAGAGCACTCCGAGC 3240
QY 3440 GTCTGAAGCGACGCTCCAGAAAGTGACTTGACCTGAAACAGCTGGAGACATCCGCG 3439
DB 3241 GTCTGAAGCGACGCTCCAGAAAGTGACTTGACCTGAAACAGCTGGAGACATCCGCG 3300
QY 3500 AGTACGAACACGCGCTGAAAGTGCTGAGCGGAGAGTCCAGCACTGTAAGCGGCTCTGG 3559
DB 3301 AGTACGAACACGCGCTGAAAGTGCTGAGCGGAGAGTCCAGCACTGTAAGCGGCTCTGG 3360
QY 3560 GGTGGGTGGCGGAGCGCCCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3619
DB 3361 GGTGGGTGGCGGAGCGCCCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3420
QY 3620 CTGACCTGCTGGGTCCAAAGA 3641
DB 3421 TTGACCTGCAATGGGTCCAAAGA 3442

RESULT 14
AAH76383
ID AAH76383 standard; cDNA; 3900 BP.

XX AAH76383;

DT 30-NOV-2001 (first entry)

XX Human TLCC polypeptide encoding cDNA.

XX TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
XX hepatotropic; candidant; antiarteriosclerotic; antiinflammatory; vitruclide;
XX cytosolic; analgesic; cerebroprotective; nootropic; neuroprotective;
XX gene therapy; ss.

XX Homo sapiens.

XX Key location/Qualifiers

XX CDS 138..3527

XX /product= "TLCC polypeptide"
XX /note= "coding sequence (AAH76384) specifically claimed"

XX MO200162794-A2.

XX 30-AUG-2001.

XX 20-FEB-2001; 2001WO-US005529.

XX 22-FEB-2000; 2000US-00510706.

XX 31-MAY-2000; 2000US-00583373.

XX 08-AUG-2000; 2000US-00634669.

XX (MILL-) MILLENNIUM PHARM INC.

XX Gluckmann MA, Curtis RAJ, Lora JM;

XX WPI; 2001-557700/62.

XX P-PSDB; AAB85974.

XX New isolated nucleic acid encoding a transient receptor potential-like
PT calcium channel for identifying modulators that can be used to treat
PT hepatic or cardiovascular disorders.

XX Claim 1; Fig 1A-D; 160pp; English.

XX The invention provides isolated nucleic acids encoding a human transient
CC receptor potential (TRP) family member, called TRP-like calcium channel
CC (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC recombinant methodology. The TLCC polynucleotides and polypeptide are
CC used to identify modulators that can be used to treat a hepatic or a
CC cardiovascular disorder, such as liver fibrosis or atherosclerosis. Other
CC disorders that can be treated are hepatitis, liver tumours, cirrhosis of
CC the liver, hemochromatosis, liver parasite induced disorders, central
CC nervous system disorders, pain disorders, or disorders of cellular
CC growth, differentiation or migration. The TLCC polynucleotides,
CC polypeptide, protein homologs and antibodies to the proteins can be used
CC in predictive medicine (e.g. diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenetics). Anti-TLCC antibodies
CC can isolate TLCC proteins, regulate the bioavailability of TLCC
CC proteins, and modulate TLCC activity. The present sequence represents a
CC cDNA encoding the human TLCC polypeptide

XX Sequence 3900 BP; 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;

XX Query Match 92.7%; Score 3374.4; DB 5; Length 3900;

XX Best Local Similarity 99.5%; Pred. No. 0;

XX Matches 3384; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 243 GGGGGCGCGCGCAAGCAATTCCTCCGCTCTGACCGAAGCAATCCAGCTGC 302
DB 125 GTGCCCGCTCCATGTGTCCACAGTTCCTCCGCTCTGACCGAAGCAATCCAGCTGC 184
QY 303 AGTTATAGTCTGTGTCACAGCAATGAGGCTTCGTCGCCCAAGCTGTGTGTCAGT 362
DB 185 AGTTATAGTCTGTGTCACAGCAATGAGGCTTCGTCGCCCAAGCTGTGTGTCAGT 244
QY 363 GCTGGGGGATCGGGGGGCGCCGCTCTCCAGACTGCTGAGGACTGCTGCTGCTG 422
DB 245 GCTGGGGGATCGGGGGGCGCCGCTCTCCAGACTGCTGAGGACTGCTGCTGCTG 304
QY 423 GCTGTGCGGGCTGCGCCAGAGACAGAGGCTGATGTCATCTGGGGGTCTGCAACGG 482
DB 305 GCTGTGCGGGCTGCGCCAGAGACAGAGGCTGATGTCATCTGGGGGTCTGCAACGG 364
QY 483 CATGCGCGGATGTTGTGTGCTGTAGCGGACATCAATGAGCCAGACTGCGGGGCTAC 542
DB 365 CATGCGCGGATGTTGTGTGCTGTAGCGGACATCAATGAGCCAGACTGCGGGGCTAC 424
QY 543 CAAGGTGTGGCCATGTGGTGTGCGCCCTGTGGGTGTGGTCCGAATAGACACTTCAT 602
DB 425 CAAGGTGTGGCCATGTGGTGTGCGCCCTGTGGGTGTGGTCCGAATAGACACTTCAT 484
QY 603 CAACCCCAAGGGCTGTTCCCTGAGAGTACCGGTGCGGGGTATACCCGAGAGCGGGGT 662
DB 485 CAACCCCAAGGGCTGTTCCCTGAGAGTACCGGTGCGGGGTATACCCGAGAGCGGGGT 544
QY 663 CCAAGTTTCCCTGATACAACTACTGAGGCTTCTTCTCTGTGAGAGAGGACACACGG 722
DB 545 CCAAGTTTCCCTGATACAACTACTGAGGCTTCTTCTCTGTGAGAGAGGACACACGG 604
QY 723 CTGCTGGGGGCGAGAACCGCTTCCGCTTGGCGCTGAGTCTTAATCTTCACAGAGAA 782
DB 605 CTGCTGGGGGCGAGAACCGCTTCCGCTTGGCGCTGAGTCTTAATCTTCACAGAGAA 664
QY 783 GACGGGCGTGGAGAGACTGGAATTGACATCCCTGTCTCTCTCTCTGATGATGATGA 842
DB 665 GACGGGCGTGGAGAGACTGGAATTGACATCCCTGTCTCTCTCTCTGATGATGATGA 724
QY 843 TGAGAAATGTTGACGGAATTAGAGAACGACACCGAGCTCAGTCCCATGCTCTCTGCT 902
DB 725 TGAGAAATGTTGACGGAATTAGAGAACGACACCGAGCTCAGTCCCATGCTCTCTGCT 784

903 GGCTGCTCAGGGGAGCTGCGGACTGCTGCGGAGACCTGGAAGACACTTGAGCCC 962
785 GGTGCTCAGGGGAGGAGCTGCGGACTGCTGCGGAGACCTGGAAGACACTTGAGCCC 844
963 AGGAGTGGGGAGCCAGGCAAGCGAGACCCGAGATCGAATCAGGCGTTCTTTCCAA 1022
845 AGGGATGGGGAGGCGAGGCAAGCGAGACCCGAGATCGAATCAGGCGTTCTTTCCAA 904
1023 AGGGACCTTGAAGTCCGCGAGGCGGAGTGAAGGATTAAGACCCGGAAGAGACTCT 1082
905 AGGGACCTTGAAGTCCGCGAGGCGGAGTGAAGGATTAAGACCCGGAAGAGACTCT 964
1083 GACAGTCTATTTCTTCTGAGAGTGGGTCTGAGGAATTCGAGACCATAGTTTGAAGCCCT 1142
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RESULT 15
ABSS8041
ID ABSS8041 standard; cDNA; 3900 BP.
XX
AC ABSS8041;
XX
DT 14-FEB-2003 (first entry)
XX
DE Human transient receptor potential (TRP)-like calcium channel (TLCC).
XX
KW Human; gene; 89; transient receptor potential-like calcium channel; TRP;
KW TLCC; 18607; calcium signalling; growth; differentiation;
KW capacitative calcium channel; store-operated calcium channel; SOC;
KW plasma membrane; calcium ion; cytosol; modulator; membrane excitability;
KW action potential; excitation; neurite outgrowth; synaptogenesis;
KW signal transduction; angiogenesis; cell proliferation; vascular tone;
KW gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;
KW reneurosis; endothelial cell disorder; tumour metastasis; psoriasis;
KW rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;
KW central nervous system disorder; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; cancer;
KW cellular proliferation disorder; migration disorder; therapeutic.
XX
OS Homo sapiens.
XX
FH Key 1. 137
FH 5'UTR
FT
FT CDS
FT
FT
FT
FT 3'UTR

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XX      (CURT/) CURTIS R A J.
XX      (LORA/) LORA J M.
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XX      Glucksmann MA, Curtis RAJ, Lora JM,
XX      WPI; 2003-102516/09.
XX      P-PSDB; ABG72088.
XX
XX      Isolated transient receptor potential-like calcium channel polypeptide,
XX      useful for treating cardiovascular, hepatic, central nervous system
XX      disorders, pain, cellular proliferation, or migration disorder.
XX
XX      Claim 1; Fig 1; 80pp; English.
XX
XX      The invention discloses an isolated transient receptor potential (TRP)-
XX      like calcium channel (TLCC) polypeptide (18607). Calcium signalling has
XX      been implicated in the regulation of a variety of cellular responses,
XX      such as growth and differentiation. TLCC is a member of the capacitative
XX      calcium channel group or store-operated calcium channel (SOC) which is
XX      activated in the plasma membrane to import calcium ions from the
XX      extracellular environment to the cytosol. The nucleic acids, polypeptides
XX      and antibodies of TLCC are useful for detecting its presence in a sample,
XX      for identifying a compound which binds to it and identifying a compound
XX      which modulates its activity. Modulators of TLCC can be used to modulate
XX      membrane excitability, wave forms and frequencies of action potentials,
XX      thresholds of excitation, neurite outgrowth and synaptogenesis, signal
XX      transduction, angiogenesis, endothelial cell proliferation and vascular
XX      tone. The nucleic acid and polypeptide are also useful (using gene
XX      therapy) for diagnosing and treating cardiovascular disorders, such as
XX      atherosclerosis and restenosis, endothelial cell disorders, such as
XX      tumour metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic
XX      disorders such as hepatitis and cirrhosis, central nervous system disorders,
XX      such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and
XX      epilepsy, cellular proliferation disorders, such as cancer, and growth,
XX      differentiation or migration disorders. TLCC can also be used in
XX      predictive medicine (e.g. diagnostic assays, prognostic assays,
XX      monitoring clinical trials and pharmacogenomics) and in methods of
XX      treatment (e.g. therapeutic and prophylactic). The sequence presented is
XX      the human TLCC, 18607, cDNA
XX
XX      Sequence 3900 BP, 655 A; 1232 C; 1216 G; 795 T; 0 U; 2 Other;
XX
XX      Query Match 92.7%; Score 3374.4; DB 8; Length 3900;
XX      Best Local Similarity 99.5%; Pred. No. 0;
XX      Matches 3384; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1158	31.8	1524	3	US-09-020-956-109 Sequence 109, App
2	1158	31.8	1524	3	US-09-030-607-109 Sequence 109, App
3	1158	31.8	1524	3	US-09-439-313-109 Sequence 109, App
4	1158	31.8	1524	3	US-09-352-616A-109 Sequence 109, App
5	1158	31.8	1524	3	US-09-232-149A-109 Sequence 109, App
6	1158	31.8	1524	4	US-09-159-812-109 Sequence 109, App
7	1158	31.8	1524	4	US-09-636-215-109 Sequence 109, App
8	1158	31.8	1524	4	US-09-685-166A-109 Sequence 109, App
9	1158	31.8	1524	4	US-09-115-453-109 Sequence 109, App
10	1158	31.8	1524	4	US-09-688-489-109 Sequence 109, App
11	1158	31.8	1524	4	US-09-679-426-109 Sequence 109, App
12	1158	31.8	1524	4	US-09-759-143-109 Sequence 109, App
13	1158	31.8	1524	4	US-09-651-236-109 Sequence 109, App
14	1095.2	30.1	1297	2	US-08-727-688-9 Sequence 9, Appli
15	815.8	22.4	3498	4	US-09-949-016-1003 Sequence 1003, Ap
16	814.2	22.4	3498	4	US-09-949-016-5521 Sequence 5521, Ap
17	428.6	11.8	6220	4	US-09-600-087-1 Sequence 1, Appli
18	428.6	11.8	6220	4	US-09-949-016-470 Sequence 470, App
19	427	11.7	6221	4	US-09-949-016-5229 Sequence 5229, Ap
20	358	9.8	384	3	US-09-030-607-185 Sequence 185, App
21	358	9.8	384	3	US-09-439-313-185 Sequence 185, App
22	358	9.8	384	3	US-09-352-616A-185 Sequence 185, App
23	358	9.8	384	3	US-09-232-149A-185 Sequence 185, App
24	358	9.8	384	4	US-09-159-812-185 Sequence 185, App
25	358	9.8	384	4	US-09-636-215-185 Sequence 185, App
26	358	9.8	384	4	US-09-685-166A-185 Sequence 185, App
27	358	9.8	384	4	US-09-115-453-185 Sequence 185, App

28	358	9.8	384	4	US-09-688-489-185 Sequence 185, App
29	358	9.8	384	4	US-09-679-426-185 Sequence 185, App
30	358	9.8	384	4	US-09-759-143-185 Sequence 185, App
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33	348.6	9.6	380	3	US-09-030-607-84 Sequence 84, Appl
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35	348.6	9.6	380	3	US-09-352-616A-84 Sequence 84, Appl
36	348.6	9.6	380	3	US-09-232-149A-84 Sequence 84, Appl
37	348.6	9.6	380	4	US-09-159-812-84 Sequence 84, Appl
38	348.6	9.6	380	4	US-09-636-215-84 Sequence 84, Appl
39	348.6	9.6	380	4	US-09-685-166A-84 Sequence 84, Appl
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41	348.6	9.6	380	4	US-09-688-489-84 Sequence 84, Appl
42	348.6	9.6	380	4	US-09-679-426-84 Sequence 84, Appl
43	348.6	9.6	380	4	US-09-759-143-84 Sequence 84, Appl
44	348.6	9.6	380	4	US-09-651-236-84 Sequence 84, Appl
45	304	8.3	367	2	US-08-727-688-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-020-956-109
Sequence 109, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121,427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 1524 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-09-020-956-109
Query Match 31.8%; Score 1158; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264; Indels 0; Gaps 0;
Matches 1158; Conservative 0; Mismatches 0;
2485 CTGGCCAGAGGCTTGTAGCGAGAGCGGAGGAGCTTCCGACGAGGAGGAGCCGAGGCTTGGC 2544
DB 10 CTGGCCAGAGGCTTGTAGCGAGAGCGGAGGAGCTTCCGACGAGGAGGAGCCGAGGCTTGGC 69

QY 2545 CATGCTCTGAGCAGGCGCTGAGCCTCTACCTGCGCAGAGCTGAAACAGTGGCAG 2604
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DB 70 CATGCTCTGAGCAGGCGCTGAGCCTCTACCTGCGCAGAGCTGAAACAGTGGCAG 129
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QY 2605 CTAGTGGCTCTGACCTGCTTCTCTGAGCGTGGCTGCGCTGACCCCGGGTTTGAAC 2664
| | | | |
DB 130 CTAGTGGCTCTGACCTGCTTCTCTGAGCGTGGCTGCGCTGACCCCGGGTTTGAAC 189
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QY 2665 CACCTGGGCGGACCTGTCTCTGATCGACTTCAATGTTTTCAGCGTGGCTGCTTAC 2724
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DB 190 CACCTGGGCGGACCTGTCTCTGATCGACTTCAATGTTTTCAGCGTGGCTGCTTAC 249
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QY 2725 ATCTTCAGCGTCAAAAGAGCTGGGGCCCAAGATGTCATGTCAGTGAAGTGAAG 2784
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DB 250 ATCTTCAGCGTCAAAAGAGCTGGGGCCCAAGATGTCATGTCAGTGAAGTGAAG 309
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QY 2785 GACGTGTTCTTCTCTCTCTCTCTGAGCGTGGCTGAGTGGTGGTGGTGGTGG 2844
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DB 310 GACGTGTTCTTCTCTCTCTCTCTCTGAGCGTGGCTGAGTGGTGGTGGTGGTGG 369
| | | | |
QY 2845 GAGGGGCTCTGAGGCGCAGGAGCAGTGAATCTCCAGATATCTGCGCGCTTCTTAC 2904
| | | | |
DB 370 GAGGGGCTCTGAGGCGCAGGAGCAGTGAATCTCCAGATATCTGCGCGCTTCTTAC 429
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QY 2905 CGTCCCTACCTGAGATCTTCCGGGAGATTCGCCAGAGAGATGAGAGCTGGCCCTCATG 2964
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DB 430 CGTCCCTACCTGAGATCTTCCGGGAGATTCGCCAGAGAGATGAGAGCTGGCCCTCATG 489
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QY 2965 GAGCAGCAGCACTGCTGTCGAGAGCCCGGCTTCTGGGCAACCTCTCTGGGGCCAGGGC 3024
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DB 490 GAGCAGCAGCACTGCTGTCGAGAGCCCGGCTTCTGGGCAACCTCTCTGGGGCCAGGGC 549
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QY 3025 GGCACCTGGCTCTCCAGATATGCAATGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 3084
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QY 3085 CTGCTGGCAACATCTGCTGGTCAACTGCTCATATGCTGAGTGAACATTTCCGAC 3144
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DB 610 CTGCTGGCAACATCTGCTGGTCAACTGCTCATATGCTGAGTGAACATTTCCGAC 669
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DB 670 AAAGTACAGGGCAACAGCGATCTTAAGTGAAGCGGAGCGTTCAGCGCTCATCCGGGA 729
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QY 3265 CTGAGGCAATTTGAGGAGCAGCCGAGAGCCCGCAGCGCTCTCCCGGCTCTGAGCAT 3324
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QY 3325 TTCCGGGTTTACCTTTCTAAGAGCGAGCGAGAGCTTAACGTGGGAATCGGTGAT 3384
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DB 850 TTCCGGGTTTACCTTTCTAAGAGCGAGCGAGAGCTTAACGTGGGAATCGGTGAT 909
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QY 3385 AAGGAGAACTTTCTGCTGGCAGCGCTTAAGGAGCAAGCGGAGAGAGCGACTCCGAGGCTCG 3444
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DB 910 AAGGAGAACTTTCTGCTGGCAGCGCTTAAGGAGCAAGCGGAGAGAGCGACTCCGAGGCTCG 969
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QY 3505 GAAACAGCGCTTAAGTGTGAGCGGAGGATTCAGCAGATGTAAGCGGCTCTGGGAGTGG 3564
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DB 1030 GAAACAGCGCTTAAGTGTGAGCGGAGGATTCAGCAGATGTAAGCGGCTCTGGGAGTGG 1089
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QY 3565 GTGGCGGAGGCGCTGAGCGGCTCTGCTTGGCTGGCGCCAGAGTGGGCGCGACCCCTGAC 3624
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DB 1090 GTGGCGGAGGCGCTGAGCGGCTCTGCTTGGCTGGCGCCAGAGTGGGCGCGACCCCTGAC 1149
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QY 3625 CTGCTGGGATCCAAAGAC 3642
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DB 1150 CTGCTGGGATCCAAAGAC 1167
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RESULT 2
US-09-030-607-109
; Sequence 109, Application US/09030607
; Patent No. 6262245
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 224
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,607
; FILING DATE: 25-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; TELEPHONE/DOCKET NUMBER: 210121.427C3
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1524 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-09-030-607-109
Query Match 31.8%; Score 1158; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2485 CTGCGCCAGGGCTTGAAGGAGGCGGGGAGCGCTGCGCAGCGGGGCTCCGGGCTTGGC 2544
| | | | |
DB 10 CTGCGCCAGGGCTTGAAGGAGGCGGGGAGCGCGGAGCGCTGCGCAGCGGGGCTCCGGGCTTGGC 69
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QY 2545 CATGCTCTGAGCAGGCGCTGAGCGCTCTTAACCTGCGCAGAGCTGGAACAGTGGCAG 2604
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DB 70 CATGCTCTGAGCAGGCGCTGAGCGCTCTTAACCTGCGCAGAGCTGGAACAGTGGCAG 129
| | | | |
QY 2605 CTAGTGGCTCTGACCTGCTTCTCTGAGCGTGGCTGCGCTGACCCCGGGTTTGAAC 2664
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DB 130 CTAGTGGCTCTGACCTGCTTCTCTGAGCGTGGCTGCGCTGACCCCGGGTTTGAAC 189
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QY 2665 CACCTGGGCGGACCTGTCTCTGATCGACTTCAATGTTTTCAGCGTGGCTGCTTAC 2724
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DB 190 CACCTGGGCGGACCTGTCTCTGATCGACTTCAATGTTTTCAGCGTGGCTGCTTAC 249
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QY 2725 ATCTTCAGCGTCAAAAGAGCTGGGGCCCAAGATGTCATGTCAGTGAAGTGAAG 2784
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DB 250 ATCTTCAGCGTCAAAAGAGCTGGGGCCCAAGATGTCATGTCAGTGAAGTGAAG 309
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QY 2785 GACGTGTTCTTCTCTCTCTCTCTGAGCGTGGCTGAGTGGTGGTGGTGGTGGTGG 2844
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[illegible]

RESULT 3
US-09-439-313-109
Sequence 109, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, James C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlockee, Susan Louise
APPLICANT: Jiang Yugu
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
APPLICANT: Fanger, Gary

```

: APPLICANT: Retter, Mark
: APPLICANT: Solk, Craig
: APPLICANT: Day, Craig
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C9
: CURRENT APPLICATION NUMBER: US/09/439,313
: CURRENT FILING DATE: 1999-11-12
: NUMBER OF SEQ ID NOS: 575
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 109
: LENGTH: 1524
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-439-313-109

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Query Match	31.8%;	Score 1158;	DB 3;	Length 1524;
Best Local Similarity	100.0%;	Prod. No. 1.7e-264;		
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			Indels	0;
			Gaps	0;
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QY	2545	CATGCTTCACTGAGCCAGGCGCTGCGCTTAACTCTGCGGACAGCTGGAACCAAGTGGCAC	2604	
Db	70	CATGCTTCACTGAGCCAGGCGCTGCGCTTAACTCTGCGGACAGCTGGAACCAAGTGGCAC	129	
QY	2605	CTAGTGGCTCACCTGGCTTCTCCTGGGGCGTGGGGCTGCGCGGCTGACCCCGGGATTGTAC	2666	
Db	130	CTAGTGGCTCACCTGGCTTCTCCTGGGGCGTGGGGCTGCGCGGCTGACCCCGGGATTGTAC	189	
QY	2665	CACCTGGGCGGCACTGTCTCTGATGACTTCAATGATTTTACGGTGGCGCTGCTTAC	2722	
Db	190	CACCTGGGCGGCACTGTCTCTGATGACTTCAATGATTTTACGGTGGCGCTGCTTAC	249	
QY	2725	ATCTTACGGTCAACAACAGCTGGGGCGCAAGATCGTATCGAGACAATGATGAG	2788	
Db	250	ATCTTACGGTCAACAACAAGCTGGGGCGCAAGATCGTATCGAGACAATGATGAG	309	
QY	2785	GACGTGTCTTCTTCTTCTTCTTCTGCGCGCTGTGGCTGTAGCTATGAGCGTGGACAG	2844	
Db	310	GACGTGTCTTCTTCTTCTTCTTCTGCGCGCTGTGGCTGTAGCTATGAGCGTGGACAG	369	
QY	2845	GAGGGGCTCTGAGGGCCAGGGACAAGTACTTCCAAATATCTGGCGCGCTTCTTAC	2904	
Db	370	GAGGGGCTCTGAGGGCCAGGGACAAGTACTTCCAAATATCTGGCGCGCTTCTTAC	429	
QY	2905	CGTCCCTAACCTGAGATTTTGGGGCAGATTTCCCGAGAGGACATGGAAGTGGCCCTTAC	2966	
Db	430	CGTCCCTAACCTGAGATTTTGGGGCAGATTTCCCGAGAGGACATGGAAGTGGCCCTTAC	489	
QY	2965	GAGCACAAGCACTGCTCGTGGAGCCCGGCTTGTGGGACACCTCTTGGGGCCAGGCG	3022	
Db	490	GAGCACAAGCACTGCTCGTGGAGCCCGGCTTGTGGGACACCTCTTGGGGCCAGGCG	549	
QY	3025	GGCACCCTGCGCTTCTCCAGTATGACCACCTGGGTGGTGGTCTCTCTGATCTTCTG	3088	
Db	550	GGCACCCTGCGCTTCTCCAGTATGACCACCTGGGTGGTGGTCTCTCTGATCTTCTG	609	
QY	3085	CTCTGGGCAACATCTGCTGGTGAACCTTGCTCATTTGCGATGTTACATACATTGGC	3144	
Db	610	CTCTGGGCAACATCTGCTGGTGAACCTTGCTCATTTGCGATGTTACATACATTGGC	669	
QY	3145	AAAGTACAAGGCAACAGGATCTTACTGGAAGCGCAGCGTTACCGCTCATTCGGGA	3204	
Db	670	AAAGTACAAGGCAACAGGATCTTACTGGAAGCGCAGCGTTACCGCTCATTCGGGA	729	
QY	3205	TTCACACTGGGCGCGGCTGGGCCCGGCTTATATGATCTGCGAATTGCGGCTCTG	3266	
Db	730	TTCACACTGGGCGCGGCTGGGCCCGGCTTATATGATCTGCGAATTGCGGCTCTG	789	
QY	3265	CTAAGGCAATTGTGACAGGCAACCCCGAGCCCGAGCGTCTTCCCGGCTTGAAGAT	3324	

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Db 790 CTCAGCAATTGTGAGGCGACCCCGACCCCGCCTCCCTCCCGCCTCGAGCAT 849
Qy 3325 TTCGGGTTTACCTTCTTAAGGAAGCCGGAAGCTCTAAGCTGGGAATCGTGAT 3384
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Qy 3385 AAGGAATCTTCTGCTGACGCGCTAGAGCAAGCGGAGAGCGACTCCGAGCGCTTG 3444
Db 910 AAGGAATCTTCTGCTGACGCGCTAGAGCAAGCGGAGAGCGACTCCGAGCGCTTG 969
Qy 3445 AAGCCAGCTCCCAAGAGTGAATTTGGACTGGAACAGCTGGGACACTCCGAGATAC 3504
Db 970 AAGCCAGCTCCCAAGAGTGAATTTGGACTGGAACAGCTGGGACACTCCGAGATAC 1029
Qy 3505 GAACAGCCGCTGAAGTGTGAGCGGAGGTCACAGCTAGCGCGCTCGGGGTG 3564
Db 1030 GAACAGCCGCTGAAGTGTGAGCGGAGGTCACAGCTAGCGCGCTCGGGGTG 1089
Qy 3565 GTGGCCGAGGCGCTGAGCGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 3624
Db 1090 GTGGCCGAGGCGCTGAGCGGCTTGCTGCTGCTGCTGCTGCTGCTGCTGAC 1149
Qy 3625 CTGCTGGGTCCAAAGAC 3642
Db 1150 CTGCTGGGTCCAAAGAC 1167
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RESULT 4

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US-09-352-616A-109
; Sequence 109, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yugu
; APPLICANT: Xu, Jianshun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-109
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Query Match 31.8%; Score 1158; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2485 CTGGCCAGAGGCTTGAAGCGAGGCGGAGCGAGCTTGCAGCGGAGCGCTGAGC 2544
Db 10 CTGGCCAGAGGCTTGAAGCGAGGCGGAGCGAGCTTGCAGCGGAGCGCTGAGC 69
Qy 2545 CATGCTCACTAGGCGAGGCGCTGAGCGCTTACCTTGCAGAGCTGGAACTAGTGCAC 2604
Db 70 CATGCTCACTAGGCGAGGCGCTGAGCGCTTACCTTGCAGAGCTGGAACTAGTGCAC 129
Qy 2605 CTAGTGGCTCTACCTGCTTCTCCGAGGCGTGGGCTGCGGCTGACCCCGGTTTATC 2664
Db 130 CTAGTGGCTCTACCTGCTTCTCCGAGGCGTGGGCTGCGGCTGACCCCGGTTTATC 189
Qy 2665 CACCTGGGCGGAGCTGCTCTGATCACTTCACTGTTTTCACGAGTGGCTGCTTAC 2724
Db 190 CACCTGGGCGGAGCTGCTCTGATCACTTCACTGTTTTCACGAGTGGCTGCTTAC 249
Qy 2725 ATCTTACGCTCAACAAGCTGGGCGGCAAGATGCTATGTAAGCAATGATGAAG 2784
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Db 250 ATCTTACGCTCAACAAGCTGGGCGGCAAGATGCTATGTAAGCAATGATGAAG 309
Qy 2785 GACGTGTTCTTCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2844
Db 310 GACGTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 369
Qy 2845 GAGGGGCTCTGAGGCGGAGGAGGAGTATTTCCCAAGTATCTTCCGCGGCTTCTTAC 2904
Db 370 GAGGGGCTCTGAGGCGGAGGAGGAGTATTTCCCAAGTATCTTCCGCGGCTTCTTAC 429
Qy 2905 GCTCCCTACCTGCAATCTTGGGAGCATTTCCCGAGGAGGAGTATGAGTGGGCTTCTAC 2964
Db 430 GCTCCCTACCTGCAATCTTGGGAGCATTTCCCGAGGAGGAGTATGAGTGGGCTTCTAC 489
Qy 2965 GAGCAGCAGCACTGCTGCTGAGGCGGAGGCTTCTTGGGAGCAGCTTCTTGGGAGC 3024
Db 490 GAGCAGCAGCACTGCTGCTGAGGCGGAGGCTTCTTGGGAGCAGCTTCTTGGGAGC 549
Qy 3025 GGCACCTGCTCTCCAGTATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3084
Db 550 GGCACCTGCTCTCCAGTATGCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 609
Qy 3085 CTGCTGGGCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3144
Db 610 CTGCTGGGCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
Qy 3145 AAAGTACAGGCGCAACAGGATCTTCTTGAAGGCGGAGGCTTACCGGCTTACCGGGA 3204
Db 670 AAAGTACAGGCGCAACAGGATCTTCTTGAAGGCGGAGGCTTACCGGCTTACCGGGA 729
Qy 3205 TTCCACTCTGCGGCGGCGGCTGCGGCGGCTTATGCTGATCTTCCACTTGGGCTTCTG 3264
Db 730 TTCCACTCTGCGGCGGCGGCTGCGGCGGCTTATGCTGATCTTCCACTTGGGCTTCTG 789
Qy 3265 CTCAGGCAATTGTGAGGCGGAGCCCGGAGGCGGCGGCTTCCCGGCGGCTGAGGAT 3324
Db 790 CTCAGGCAATTGTGAGGCGGAGCCCGGAGGCGGCGGCTTCCCGGCGGCTTCCCGGAT 849
Qy 3325 TTCGGGTTTACCTTCTTAAGGAAGCCGGAAGCTCTAAGCTGGGAATCGTGAT 3384
Db 850 TTCGGGTTTACCTTCTTAAGGAAGCCGGAAGCTCTAAGCTGGGAATCGTGAT 909
Qy 3385 AAGGAATCTTCTGCTGACGCGCTAGAGCAAGCGGAGAGCGACTCCGAGCGCTTG 3444
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Db 1030 GAACAGCCGCTGAAGTGTGAGCGGAGGTCACAGCTAGCGCGCTCGGGGTG 1089
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Db 1150 CTGCTGGGTCCAAAGAC 1167
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RESULT 5

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US-09-232-149A-109
; Sequence 109, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; CANCER AND METHODS FOR THEIR USE
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FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232.149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 109
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapien
US-09-232-149A-109

Query Match 31.8%; Score 1158; DB 3; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2485 CTGCGCCAGGGCTCTAGCGGAGGCGGGGCGAGCCTTCGCCAGCGGGGGCCCCGGGCTTGGC 2544
DB 10 CTGCGCCAGGGCTCTAGCGGAGGCGGGGCGAGCCTTCGCCAGCGGGGGCCCCGGGCTTGGC 69
OY 2545 CATGCTCACTAGGAGCGGCGCTTGCGCTCTACCTCGCGACAGCTGGAAACAGTGGAC 2604
DB 70 CATGCTCACTAGGAGCGGCGCTTGCGCTCTACCTCGCGACAGCTGGAAACAGTGGAC 129
OY 2605 CTAGTGGCTCTACCTGCTTCTCTCTGCGCGTGGCGTGGCGCTGACCCCGGGTTTGTAC 2664
DB 130 CTAGTGGCTCTACCTGCTTCTCTCTGCGCGTGGCGTGGCGCTGACCCCGGGTTTGTAC 189
OY 2665 CACCTGGGCGCGACTGTCTCTCTGTCATCGACTTATGTTTTCACGGTGGCGCTGCTTAC 2724
DB 190 CACCTGGGCGCGACTGTCTCTCTGTCATCGACTTATGTTTTCACGGTGGCGCTGCTTAC 249
OY 2725 ATCTTCACGTCACAAACAGTGGGCGCGCAAGTCATCGTACGTAAGCAAGATGATGAG 2784
DB 250 ATCTTCACGTCACAAACAGTGGGCGCGCAAGTCATCGTACGTAAGCAAGATGATGAG 309
OY 2785 GACGTTCTTCTTCTCTCTCTCTGCGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGC 2844
DB 310 GACGTTCTTCTTCTCTCTCTCTCTGCGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGC 369
OY 2845 GAGGGGCTCTGAGGCGCAAGGAGAGTATCCCAAGTATCTGCGCGCTCTTCTAC 2904
DB 370 GAGGGGCTCTGAGGCGCAAGGAGAGTATCCCAAGTATCTGCGCGCTCTTCTAC 429
OY 2905 CGTCTCTACCTGTCATCTTCTGCGGAGATTTCCCGAGAGATGAGATGAGTGGCTCTAC 2964
DB 430 CGTCTCTACCTGTCATCTTCTGCGGAGATTTCCCGAGAGATGAGATGAGTGGCTCTAC 489
OY 2965 GAGCAGCAGCACTGCTGCTGCGAGGCGCGCTTCTGCGGAGACCTTCTGCGGCGCGAC 3024
DB 480 GAGCAGCAGCACTGCTGCTGCGAGGCGCGCTTCTGCGGAGACCTTCTGCGGCGCGAC 549
OY 3025 GGCACCTGCGTCTCCAGTATGCACTGGCTGAGTGGCTGCTGCTGCTGCTTCTG 3084
DB 550 GGCACCTGCGTCTCCAGTATGCACTGGCTGAGTGGCTGCTGCTGCTGCTTCTG 609
OY 3085 CTGCGGCGCAACATCTGCTGTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3144
DB 610 CTGCGGCGCAACATCTGCTGTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 669
OY 3145 AAAGTACAGGGGCAAGGAGATCTTACTGGAAGGCGGAGCTTACCGGCTTACCGGGGA 3204
DB 670 AAAGTACAGGGGCAAGGAGATCTTACTGGAAGGCGGAGCTTACCGGCTTACCGGGGA 729
OY 3205 TTCCACTCTGCGCGCGCGTGGCGCGCGCTTATGTCATCTCCACTTGGCGCTCTG 3264
DB 730 TTCCACTCTGCGCGCGCGTGGCGCGCGCTTATGTCATCTCCACTTGGCGCTCTG 789
OY 3265 CTGAGGCAATTGTGAGGCGAGACCCCGGAGCCCTGCTGCTGCTGCTGCTGAGAT 3324
DB 790 CTGAGGCAATTGTGAGGCGAGACCCCGGAGCCCTGCTGCTGCTGCTGAGAT 849
OY 3325 TTCCGGGTTTACTTTTAAAGAGCCGAGGAGCTTACAGTGGGAATCGGTGAT 3384
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DB 850 TTCCGGGTTTACTTTCTTAAGGAACCGAGCGAAGCTGTACGTGGGAATCGGTGAT 909
OY 3385 AAGGAGAACTTCTGCTGGACGCGCTAGAGCAAGCGGAGAGAGACTTCCGAGGTCTG 3444
DB 910 AAGGAGAACTTCTGCTGGACGCGCTAGAGCAAGCGGAGAGAGACTTCCGAGGTCTG 969
OY 3445 AAGGCAAGTCCGAGAGGTGACTTGTGCACTGAAACAGTGGAGCAATCCGAGTAC 3504
DB 970 AAGGCAAGTCCGAGAGGTGACTTGTGCACTGAAACAGTGGAGCAATCCGAGTAC 1029
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DB 1030 GAACAGCGCTGAAGTGTGCTGAGCGGAGGCTCCAGCATGTATGCGGCTCTGAGGTG 1089
OY 3565 GTGCGCGAGGCGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3624
DB 1090 GTGCGCGAGGCGCTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
OY 3625 CTGCGTGGGTCCAAAGAC 3642
DB 1150 CTGCGTGGGTCCAAAGAC 1167
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RESULT 6
US-09-159-812-109
Sequence 109; Application US/09159812A
Patent No. 6613872
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
FILE REFERENCE: 210121.428C5
CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 109
LENGTH: 1524
TYPE: DNA
ORGANISM: Homo sapien
US-09-159-812-109

Query Match 31.8%; Score 1158; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2485 CTGCGCCAGGGCTCTAGCGGAGGCGGGGCGAGCCTTCGCCAGCGGGGGCCCCGGGCTTGGC 2544
DB 10 CTGCGCCAGGGCTCTAGCGGAGGCGGGGCGAGCCTTCGCCAGCGGGGGCCCCGGGCTTGGC 69
OY 2545 CATGCTCACTAGGAGCGGCGCTTGCGCTCTACCTCGCGACAGCTGGAAACAGTGGAC 2604
DB 70 CATGCTCACTAGGAGCGGCGCTTGCGCTCTACCTCGCGACAGCTGGAAACAGTGGAC 129
OY 2605 CTAGTGGCTCTACCTGCTTCTCTCTGCGGAGTGGGCTGCGGCTGAGACCCCGGGTTTGTAC 2664
DB 130 CTAGTGGCTCTACCTGCTTCTCTCTGCGGAGTGGGCTGCGGCTGAGACCCCGGGTTTGTAC 189
OY 2665 CACCTGGGCGCGACTGTCTCTGATGCACTTCAATGATTTTCAAGTTCGAGTGGCTGCTTAC 2724
DB 190 CACCTGGGCGCGACTGTCTCTGATGCACTTCAATGATTTTCAAGTTCGAGTGGCTGCTTAC 249
OY 2725 ATCTTCACGTCACAAACAGCTGGGCGCGCAAGTGTGATCTGAGCAAGATGATGAG 2784
DB 250 ATCTTCACGTCACAAACAGCTGGGCGCGCAAGTGTGATCTGAGCAAGATGATGAG 309
OY 2785 GACGTTCTTCTTCTTCTTCTTCTGCGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGC 2844
DB 310 GACGTTCTTCTTCTTCTTCTTCTTCTGCGCGTGGCGTGGCGTGGCGTGGCGTGGCGTGGC 369
OY 2845 GAGGGGCTCTGAGGCGCAAGGAGAGTATCCCAAGTATCTGCGCGGCTCTTCTAC 2904
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Db 370 GAGGGGCTTCGAGGCCACGGGACAGTGACTTCCCAAGTATCTGCGCCGCTCTTCTAC 429
Qy 2905 CGTCCCTACCTGACATCTTCCGGGAGATTCCCGAGAGACATGAGCGTGGCCCTCATG 2964
Db 430 CGTCCCTACCTGACATCTTCCGGGAGATTCCCGAGAGACATGAGCGTGGCCCTCATG 489
Qy 2965 GAGCAGACAACTGCTGCTGGAGCCCGGCTTCTGAGGACACCCCTCTGGGGCCGAGGCG 3024
Db 490 GAGCAGACAACTGCTGCTGGAGCCCGGCTTCTGAGGACACCCCTCTGGGGCCGAGGCG 549
Qy 3025 GGCACCTGCTGCTGCTGAGTGAAGGCACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 3084
Db 550 GGCACCTGCTGCTGCTGAGTGAAGGCACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 609
Qy 3085 CTCGTGGCCAACTCTGCTGAGTGAAGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGG 3144
Db 610 CTCGTGGCCAACTCTGCTGAGTGAAGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGG 669
Qy 3145 AAAGTACAGGGGCAACAGGCACTCTAAGTGAAGGCGGAGCGTTACCGGCTCATCCGGGAA 3204
Db 670 AAAGTACAGGGGCAACAGGCACTCTAAGTGAAGGCGGAGCGTTACCGGCTCATCCGGGAA 729
Qy 3205 TTCCACTCTCGGCGCCGCGCTGGCGCCGCTTATGCTATCTCCCACTTGGGCTCTCTG 3264
Db 730 TTCCACTCTCGGCGCCGCGCTGGCGCCGCTTATGCTATCTCCCACTTGGGCTCTCTG 789
Qy 3265 CTCAGGCAATTGAGAGGCAAGCCGAGAGCCCGGAGCGCTCTCCCGGCGCTCTGAGCAT 3324
Db 790 CTCAGGCAATTGAGAGGCAAGCCGAGAGCCCGGAGCGCTCTCCCGGCGCTCTGAGCAT 849
Qy 3325 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGGAAAGCTGCTAAGTGGAAATCGGTGAT 3384
Db 850 TTCCGGGTTTACCTTTCTAAGGAAGCCGAGGAAAGCTGCTAAGTGGAAATCGGTGAT 909
Qy 3385 AAGGAACCTTCTGCTGAGCAAGCGCTGAGGCAAGCGGAGAGAGCACTCCGAGGCTCTG 3444
Db 910 AAGGAACCTTCTGCTGAGCAAGCGCTGAGGCAAGCGGAGAGAGCACTCCGAGGCTCTG 969
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Db 970 AAGGCAAGTCCCAAGAGGTGAGCTTGGCACTGAAGACAGCTGGGACACATCCGAGTAC 1029
Qy 3505 GAAAGAGCGCTGAAAGTGTGAGGCGGAGGTCAGAGCACTGATGAGCGGCTCTGAGGTG 3564
Db 1030 GAAAGAGCGCTGAAAGTGTGAGGCGGAGGTCAGAGCACTGATGAGCGGCTCTGAGGTG 1089
Qy 3565 GTGGCCGAGGCGCTGAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 3624
Db 1090 GTGGCCGAGGCGCTGAGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAC 1149
Qy 3625 CTGCTGGGTCGAAAGAC 3642
Db 1150 CTGCTGGGTCGAAAGAC 1167

RESULT 7
US-09-636-215-109
; Sequence 109, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
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; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.4271C17
; CURRENT APPLICATION NUMBER: US/09/636.215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-109
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Query Match 31.8%; Score 1158; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1.7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2485 CTGGGCGAGGGCTGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2544
Db 10 CTGGGCGAGGCGTGAAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 69
Qy 2545 CATGCTCACTGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2604
Db 70 CATGCTCACTGAGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 129
Qy 2605 CTAGTGGCTCTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2664
Db 130 CTAGTGGCTCTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 189
Qy 2665 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2724
Db 190 CACCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 249
Qy 2725 ATCTTCAAGGTCACAAACAGCTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2784
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Qy 2785 GACGTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2844
Db 310 GACGTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 369
Qy 2845 GAGGGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2904
Db 370 GAGGGGCTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 429
Qy 2905 CGTCCCTACCTGACATCTTCCGGGAGATTCCCGAGAGACATGAGCGTGGCCCTCATG 2964
Db 430 CGTCCCTACCTGACATCTTCCGGGAGATTCCCGAGAGACATGAGCGTGGCCCTCATG 489
Qy 2965 GAGCAGACAACTGCTGCTGGAGCCCGGCTTCTGAGGACACCCCTCTGGGGCCGAGGCG 3024
Db 490 GAGCAGACAACTGCTGCTGGAGCCCGGCTTCTGAGGACACCCCTCTGGGGCCGAGGCG 549
Qy 3025 GGCACCTGCTGCTGCTGAGTGAAGGCACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 3084
Db 550 GGCACCTGCTGCTGCTGAGTGAAGGCACTGGCTGGTGGTGGTGGTGGTGGTGGTGG 609
Qy 3085 CTCGTGGCCAACTCTGCTGAGTGAAGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGG 3144
Db 610 CTCGTGGCCAACTCTGCTGAGTGAAGGCACTGGTGGTGGTGGTGGTGGTGGTGGTGG 669
Qy 3145 AAAGTACAGGGGCAACAGGCACTCTAAGTGAAGGCGGAGCGTTACCGGCTCATCCGGGAA 3204
Db 670 AAAGTACAGGGGCAACAGGCACTCTAAGTGAAGGCGGAGCGTTACCGGCTCATCCGGGAA 729
Qy 3205 TTCCACTCTCGGCGCCGCGCTGGCGCCGCTTATGCTATCTCCCACTTGGGCTCTCTG 3264
Db 730 TTCCACTCTCGGCGCCGCGCTGGCGCCGCTTATGCTATCTCCCACTTGGGCTCTCTG 789
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Db	70	CATGCTTCACTGAGCCAGCGCTGCGCTTCACTTCCGCCAGACAGCTGGAAACAATGGCAC	129
Qy	2605	CTAGTGGCTCTACACTGCTCTTCTCTG3GCGTGG3CTGCGGCTGACCCGG3TTTGTAC	2664
Db	130	CTAGTGGCTCTCACTGCTTCTCTG3GCGTGG3CTGCGGCTGACCCCG3TTTGTAC	189
Qy	2665	CACCTGGGCGGCATCTGTCCTCTGATATGACATTACATG3TTTCAAGTGGCGGCTGCTTAC	2724
Db	190	CACCTGGGCGGCATCTGTCCTCTGATATGACTTACATG3TTTCAAGTGGCGGCTGCTTAC	249
Qy	2725	ATCTTCAAGGTCAACAACAGCTGGGCGCCAGATGCTCATCTGAGACAAGATGATGAAG	2784
Db	250	ATCTTCAAGGTCAACAACAGCTGGGCGCCAGATGCTCATCTGAGACAAGATGATGAAG	309
Qy	2785	GACGTGTTCTTCTTCTCTTCTTCTCTGCGCGTGTGGCTG3TGAAGCTTATG3GTTGGCAAG	2844
Db	310	GACGTGTTCTTCTTCTCTTCTTCTCTGCGCGTGTGGCTG3TGAAGCTTATG3GTTGGCAAG	369
Qy	2845	GAGGGGCTCTGAGAGGCCAGAGGACAGTGAATTCCCAAGTATCTTGGCCCGCGTTTCTAC	2904
Db	370	GAGGGGCTCTGAGAGGCCAGAGGACAGTGAATTCCCAAGTATCTTGGCCCGCGTTTCTAC	429
Qy	2905	CGTCCCTAATCTGACGATCTTTCGGGCAAGTTCGCCAGAGAGACATGAGCGTGGCCCTCATG	2964
Db	430	CGTCCCTAATCTGACGATCTTTCGGGCAAGTTCGCCAGAGAGACATGAGCGTGGCCCTCATG	489

RESULT 8

QY	3025	GGGACCTGGCGTCTCCAGTAGGCCAACGGGTGGTGGAGCGCTCTGGTCACTTCTCG	3084
Db	550	GGGACCTGGCGTCTCCAGTAGGCCAACGGGTGGTGGAGCGCTCTGGTCACTTCTCG	609
QY	3085	CTCGTGGCCAAACATCTGCTGGTCAACTGGCTCACTTCCATGTTCAATTACATTCCGC	3144
Db	610	CTCGTGGCCAAACATCTGCTGGTCAACTGGCTCACTTCCATGTTCAATTACATTCCGC	669
QY	3145	AAAGTACAGGCGCAACAGCGATCTTCTACTGGAGCGCAGCGTTACCGCTCATCCGGGA	3204
Db	670	AAAGTACAGGCGCAACAGCGATCTTCTACTGGAGCGCAGCGTTACCGCTCATCCGGGA	729
QY	3205	TTCACACTCTGGGCCCCGGCTGGCCCCCGCCCTTTATGTCATCTCCCACTTGGCGCTCTG	3264
Db	730	TTTCAACTCTGGCCCCGGCTGGCCCCCGCCCTTTATGTCATCTCCCACTTGGCGCTCTG	789
QY	3265	CTCAGGCAATTGTGCAGGCGCACCCCGGAGCCCCAGCGGTCTCTCCCGGACCTCGAGCAT	3324
Db	790	CTCAGGCAATTGTGCAGGCGCACCCCGGAGCCCCAGCGGTCTCTCCCGGACCTCGAGCAT	849
QY	3325	TTCCGGGTTTACCTTCTTAAGAAAGCCGAGCGGAAGCTGCTTAAGTGGGAATCGGTGAT	3384
Db	850	TTCCGGGTTTACCTTCTTAAGAAAGCCGAGCGGAAGCTGCTTAAGTGGGAATCGGTGAT	909
QY	3385	AAGAGAACTTTCGTCTGGCACTGGCTTAAGGACAAGCGGAGAGACGATCTCGACGCTCTG	3444
Db	910	AAGAGAACTTTCGTCTGGCACTGGCTTAAGGACAAGCGGAGAGACGATCTCGACGCTCTG	969
QY	3445	AAGGCGACGTCCGAGGAAGTGGACTTGGGCACTGAACAGCGTGGGACATCCGCGGAGTAC	3504
Db	970	AAGGCGACGTCCGAGGAAGTGGACTTGGGCACTGAACAGCGTGGGACATCCGCGGAGTAC	1029

1030 GAACAGCGCTGAAGTCTGAGCGGAGGTCCAGCAGTGTAGCCCGCTCTTGGGGTGG 1089

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QY 3625 CTGCTGGGCTCCAAAGAC 3642

	Db	1150	CTGCCTGGGTCCAAAGAC	1167
			RESULT 9	
			US-09-115-453-109	
			; Sequence 109; Application US/09115453B	
			; Patent No. 6657056	
			; GENERAL INFORMATION:	
			; APPLICANT: Xu, Jiangchun	
			; APPLICANT: Dillon, Davin C.	
			; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND	
			; TITLE OF INVENTION: METHODS FOR THEIR USE	
			; FILE REFERENCE: 210121.427C4	
			; CURRENT APPLICATION NUMBER: US/09/115.453B	
			; NUMBER OF SEQ ID NOS: 228	
			; SOFTWARE: FastSeq for Windows Version 3.0	
			; SEQ ID NO 109	
			; LENGTH: 1524	
			; TYPE: DNA	
			; ORGANISM: Homo sapien	
			US-09-115-453-109	
			Query Match	31.8%; Score 1158; DB 4; Length 1524;
			Best Local Similarity	100.0%; Pred. No. 1.7e-264;
			Matches 1158; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	2485	CTGCGCCAGGCGCTCATGAGCGAGCCGGGGCAGCCTCGCACGGGGGCCCGGCGCTTGGC	2544	4A
Db	10	CTGCGCCAGGCGCTCATGAGCGAGCGGGGCAAGCTTCGCACGGGGGCCCGGCGCTTGGC	69	
Oy	2545	CATGCTTACTTGAGCCAGCGCCCTGTGGCTTTACTTCTGCGGAACAGTGAACCAATGGCAC	2604	A
Db	70	CATGCTTACTTGAGCCAGCGCCCTGTGGCTTTACTTCTGCGGAACAGTGAACCAATGGCAC	129	
Oy	2605	CTAGTGGCTTCACCTGCTTCTCTCTGGGGCGTGGGCTCCGGCTGACCCCGGGTTTTCAC	2666	G
Db	130	CTAGTGGCTTCACCTGCTTCTCTCTGGGGCGTGGGCTCCGGCTGACCCCGGGTTTTCAC	189	
Oy	2665	CACCTGGGCGCGACGTGCTCTCTGACATGACATTATGATTTTTCACGGTGGGCTTTCAC	2724	A
Db	190	CACCTGGGCGCGACGTGCTCTCTGACATGACATTATGATTTTTCACGGTGGGCTTTCAC	249	
Oy	2725	ATCTTCACGGTCAACAACAAACAGCTGGGGGCCAAGAATGTCATCTGTAGCAAGATGATAAG	2784	A
Db	250	ATCTTCACGGTCAACAACAAACAGCTGGGGGCCAAGAATGTCATCTGTAGCAAGATGATAAG	309	
Oy	2785	GACGTGTTCTTCTTCTCTTCTTCTCTGCGCGTGGCTGGTAGCTTAAGCGTGGCCACG	2844	A
Db	310	GACGTGTTCTTCTTCTCTTCTTCTCTGCGCGTGGCTGGTAGCTTAAGCGTGGCCACG	369	
Oy	2845	GAGGGGCTCTGAGGCGACGGGACAGTAGACTTCCCAGATTCCTGCGCGGCTTTTCAC	2904	A
Db	370	GAGGGGCTCTGAGGCGACGGGACAGTAGACTTCCCAGATTCCTGCGCGGCTTTTCAC	429	
Oy	2905	CGTCCCTACTGACAGATCTTCTGGGCGAGATTCCTCCAGAGGACATGAGCGTGGCCCTCATG	2964	T
Db	430	CGTCCCTACTGACAGATCTTCTGGGCGAGATTCCTCCAGAGGACATGAGCGTGGCCCTCATG	489	
Oy	2965	GAGCAGCAACTGCTCTGTGGAGCCCGGCTTTCTGGGCAACACCCTCTGGGGCCCAAGCG	3024	G
Db	490	GAGCAGCAACTGCTCTGTGGAGCCCGGCTTTCTGGGCAACACCCTCTGGGGCCCAAGCG	549	
Oy	3025	GGCAGCTGCTGCTCCAGATGACCAATGCGCTGGTGGTGGGCTCTGTCATCTTCTGTG	3084	T
Db	550	GGCAGCTGCTGCTCCAGATGACCAATGCGCTGGTGGTGGGCTCTGTCATCTTCTGTG	609	
Oy	3085	CTCGTGGCCAACATCTGTGGTCAACTGTGCTCATTTGCGCATGTTAGTTACATTTCCGC	3144	G
Db	610	CTCGTGGCCAACATCTGTGGTCAACTGTGCTCATTTGCGCATGTTAGTTACATTTCCGC	669	
Oy	3145	AAAGTACAGGGGCAACAGCGATCTTACTGAAAGGCGACGTTACCGGCTCATTCGGGAA	3204	A

Db	670	AAAGTACAGGGCAACAGAGATCTCTACTGGAAAGCGCAGAGGTTACCGCTCATCCGGAA	729
Qy	3205	TTCCACTCTCGGCCCGCGCTGAGCCCGCCTTTATGTGTCATCTCCACTTGGCCTCTCG	3264
Db	730	TTCCACTCTCGGCCCGCGCTGAGCCCGCCTTTATGTGTCATCTCCACTTGGCCTCTCG	789
Qy	3255	CTCAGGGCAATTGATGCAGGCGACCCCGGAGCCCGAGCGTCCTCCCGGCGCTCGACAT	3324
Db	790	CTCAGGCAATTGTCTCAGGCGACCCCGGAGCCCGAGCGTCCTCCCGGCGCTCGACAT	849
Qy	3325	TTCCGGGTTTACCTTTCTTGAAGAAAGCCGAGCGGAGCTGTAACTGTGGATCGTGTCAT	3384
Db	850	TTCCGGGTTTACCTTTCTTGAAGAAAGCCGAGCGGAGCTGTAACTGTGGATCGTGTCAT	909
Qy	3385	AAGAGAACTTCTGCTGCTGACACGCGCTAAGGACCAAGCTGGAGAACCTCCGAGCTCTG	3444
Db	910	AAGAGAACTTCTGCTGCTGACACGCGCTAAGGACCAAGCTGGAGAACCTCCGAGCTCTG	969
Qy	3445	AAGGCGACCTGCCGAGAGTGGGACTTGGCACTGAAACAGCTGGGACCATCCGAGATAC	3504
Db	970	AAGGCGACCTGCCGAGAGTGGGACTTGGCACTGAAACAGCTGGGACCATCCGAGATAC	1029
Qy	3505	GAAAGAGCCCTGAAAGTGTCTGAGACGGGAGGTCAGACAGTGTAGCCGCTCTTGGGCTGG	3564
Db	1030	GAAAGAGCCCTGAAAGTGTCTGAGACGGGAGGTCAGACAGTGTAGCCGCTCTTGGGCTGG	1089
Qy	3565	GTGGCCGAGGCGCTGAGGCGCTCTGCTTGTCTGCTGCCCCAGGTGGGCGGCCACCCCTGTAC	3624
Db	1090	GTGGCCGAGGCGCTGAGGCGCTCTGCTTGTCTGCTGCCCCAGGTGGGCGGCCACCCCTGTAC	1149
Qy	3625	CTGCCTGGGATCCAAAGAC	3642
Db	1150	CTGCCTGGGATCCAAAGAC	1167
RESULT 10			
US-09-688-489-109			
/ Sequence 109, Application US/09688489			
/ Patent No. 6664377			
/ GENERAL INFORMATION:			
/ APPLICANT: Xu, Jiaqun			
/ APPLICANT: Dillon, Devin C.			
/ TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE			
/ TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE			
/ FILE REFERENCE: 210121.427D2			
/ CURRENT APPLICATION NUMBER: US/09/688,489			
/ CURRENT FILING DATE: 2000-10-13			
/ NUMBER OF SEQ ID NOS: 338			
/ SOFTWARE: FastSeq for Windows Version 3.0			
/ SEQ ID NO 109			
/ LENGTH: 1524			
/ TYPE: DNA			
/ ORGANISM: Homo sapien			
US-09-688-489-109			
Query Match			
Best Local Similarity 100.0%; Pred. No. 1,7e-264;			
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2485	CTGGCGCCAGGGCTGAGCGAGGCGGGGGCAGCTCTGCGCAGCGGGGCTCCCGGCTGGC	2544
Db	10	CTGGCGCCAGGGCTGAGCGAGGCGGGGGCAGCTCTGCGCAGCGGGGCTCCCGGCTGGC	69
Qy	2545	CATGCTTACTGAGCCAGCGCTTGGCTCTAAGCTTGGCCGACAGCTTGGAACTCATGTGGAC	2604
Db	70	CATGCTTACTGAGCCAGCGCTTGGCTCTAAGCTTGGCCGACAGCTTGGAACTCATGTGGAC	129
Qy	2605	CTAGTGGCTTACCTGCTTCTCTGCTGGGCGTGGAGCTGCGGCTGACCCCGGGTTTGTAC	2664
Db	130	CTAGTGGCTTCTCAGCTGCTTCTCTCTGAGCGTGGAGCTGCGGCTGACCCCGGGTTTGTAC	189
Qy	2665	CACCTGGGCGCACATGCTCTCTGATGACTTTCATGTGTTTTCACGATGCGGCTGCTTAC	2724

QY	3085	CTGCTGGCCAAACATCTGCTGTGTCTAACTTGCTCACTTGCCATGTTGACGTTACATTCGACATTCGGC	3144
Db	610	CTGCTGGCCAAACATCTGCTGTGTCTAACTTGCTCACTTGCCATGTTGACGTTACATTCGACATTCGGC	669
QY	3145	AAAGTACAGGGCAACACGATCTCTTACTGTGAAAGCGACGCTTACCCCTCATCCGGGAAA	3204
Db	670	AAAGTACAGGGCAACACGATCTCTTACTGTGAAAGCGACGCTTACCCCTCATTCGGGAAA	729
QY	3205	TTCCACTCTGGGCCCGCGCTGTGGCCCGCCCTTTATTCGTCACTCTCCACTTGGCGCTCTG	3264
Db	730	TTCCACTCTGGGCCCGCGCTGTGGCCCGCCCTTTATTCGTCACTCTCCACTTGGCGCTCTG	789
QY	3265	CTCAGGCAATTGTGTACAGGCGACCCCGGAGCCCGACGCTCTCCCGCGCTGTGACAT	3324
Db	790	CTCAGGCAATTGTGTACAGGCGACCCCGGAGCCCGACGCTCTCCCGCGCTGTGACAT	849
QY	3325	TTCCGGGTTTACCTTTCTTGAAGAAAGCGAGCGGAAGCTGTAACTGTGGAAATCGGTGCAT	3384
Db	850	TTCCGGGTTTACCTTTCTTGAAGAAAGCGAGCGGAAGCTGTAACTGTGGAAATCGGTGCAT	909
QY	3385	AAGGAAACTTTCCTGTGTGGCACTGGCTTAAAGGAGCGGAGAGCGCATCTCCGACGCTG	3444
Db	910	AAGGAAACTTTCCTGTGTGGCACTGGCTTAAAGGAGCGGAGAGCGCATCTCCGACGCTG	969
QY	3445	AAGGCACTTTCCTGAAAGGTGTGACTTTGGCACTGAAACAGCTGTGGACACATTCGGGATAC	3504
Db	970	AAGGCACTTTCCTGAAAGGTGTGACTTTGGCACTGAAACAGCTGTGGACACATTCGGGATAC	1029
QY	3505	GAACAGAGCGCTGAAAGGTGTGAGACGGGAGGCTCCAGCAGTGTAGCCCGCTCTGGGGTGG	3564
Db	1030	GAACAGAGCGCTGAAAGGTGTGAGACGGGAGGCTCCAGCAGTGTAGCCCGCTCTGGGGTGG	1089
QY	3565	GTGGCCGAGGCGCTCTGAGCCGCTCTGTGCTTGTGCCCCCAGGTGGAGCCGACCCCTGCAC	3624
Db	1090	GTGGCCGAGGCGCTCTGAGCCGCTCTGTGCTTGTGCCCCCAGGTGGAGCCGACCCCTGCAC	1149
QY	3625	CTGCTGGGTTCGCAAGAC	3642
Db	1150	CTGCTGGGTTCGCAAGAC	1167

RESULT 12
US-09-759-143-109
: Sequence 109, Application US/09/759143
: Patent No. 6800746
: GENERAL INFORMATION:
: APPLICANT: Xu, Jiangchun
: APPLICANT: Dillon, Davin C.
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Harlocker, Susan L.
: APPLICANT: Jiang, Yugu
: APPLICANT: Henderson, Robert A.
: APPLICANT: Kaios, Michael D.
: APPLICANT: Fanger, Gary R.
: APPLICANT: Retter, Marc W.
: APPLICANT: Stolck, John A.
: APPLICANT: Day, Craig H.
: APPLICANT: Vedvick, Thomas S.
: APPLICANT: Carter, Darriek
: APPLICANT: Li, Samuel
: APPLICANT: Wang, Aljun
: APPLICANT: Skeiky, Yasir A.W.
: APPLICANT: Hepler, William
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
: TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
: FILE REFERENCE: 210121.427C23
: CURRENT APPLICATION NUMBER: US/09/759,143
: CURRENT FILING DATE: 2001-01-12
: NUMBER OF SEQ ID NOS: 934
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 109
: LENGTH: 1524

[illegible]

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Db 1030 GAACAGCCCTGAAAGTGTGTGAGGCGGAGCTGACAGTGAAGCCGCTCTGGGGTGG 1089
Qy 3565 GTGGCGAGGCGCTGAGCGCTGTGCTGTGCTGCCCCAGGTGGGCGCCACCCCTGAC 3624
Db 1090 GTGGCGAGGCGCTGAGCGCTGTGCTGTGCTGCCCCAGGTGGGCGCCACCCCTGAC 1149
Qy 3625 CTGCTGGGTCCAAAGAC 3642
Db 1150 CTGCTGGGTCCAAAGAC 1167

RESULT 13
US-09-651-236-109
; Sequence 109, Application US/09651236
; Patent No. 6818751
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianshun
; APPLICANT: Dillon, David C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Patrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.4271818
; CURRENT APPLICATION NUMBER: US/09/651.236
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FaestSeq for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 1524
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-109

Query Match 31.8%; Score 1158; DB 4; Length 1524;
Best Local Similarity 100.0%; Pred. No. 1,7e-264;
Matches 1158; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 70 CATGCTCACTGAGCAGCGCTGCGCTTCACTGCGGACAGCTGGAAACAAGTGCAG 129
Qy 2605 CTAGTGCTCTCACTGCTTCTCTCTGAGCGGTGGGCTGCGGCTGACCCCGGGTTTGTAC 2664
Db 130 CTAGTGCTCTCACTGCTTCTCTCTGAGCGGTGGGCTGCGGCTGACCCCGGGTTTGTAC 189
Qy 2665 CACCTGGGCGGCACTGTCTCTGTGATCGACTTCAAGTTTTCACGGTGGCTGTTTAC 2724
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Db 310 GACGTTCTTCTTCTCTCTCTCTCTGAGCGTGTGGCTGATGAGGCTATGAGGTGGCCAG 369
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Db 1090 GTGGCGAGGCGCTGAGCGCTGTGCTGTGCTGCCCCAGGTGGGCGCCACCCCTGAC 1149
Qy 3625 CTGCTGGGTCCAAAGAC 3642
Db 1150 CTGCTGGGTCCAAAGAC 1167

RESULT 14
US-08-727-688-9
; Sequence 9, Application US/08727688
; Patent No. 5919638
; GENERAL INFORMATION:
; APPLICANT: Russell, John C.
; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
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86 ACTTGGAGAGGCTCTGGGAAGAACGAGCACTTTGTACGGGTGCGAGCGGAGTGGCCC 145
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416 GTCTGTGGCTGTGCGGGCTGCCAGAGCACAGAGCTGATTTGTCACTGGGGGTGTC 475
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476 ACACGGGATGCGCGGACATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 535
326 GGTGTGGCTGTGCGCAGGATGTGCGGCGAGGCGGTGCGACCACTGTGGCGACAGT 385
536 GGGGCA---CGAAGGTGGGCGCATGGGTGTGGCCCCCTGGGGGTGTGGTCCGGAATAG 592
386 CCACCAAGGTCTGT 445
593 ACACCTCATCAACCCCAAGGGCTGTCTCTGTGAGGATACGGTGGCGGCTGTACCG 652
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2009 ATGGGATACAGTCTGT 2068
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1940 TCTGTGGGCTGT 1999
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2309 GCGGCTGT 2368

